

# A new species of day gecko (Reptilia, Gekkonidae, *Cnemaspis* Strauch, 1887) from Sri Lanka with an updated *ND2* gene phylogeny of Sri Lankan and Indian species

Suranjan Karunarathna<sup>1</sup>, Anslem De Silva<sup>2</sup>, Dinesh Gabadage<sup>3</sup>, Madhava Botejue<sup>3,4</sup>,  
Majintha Madawala<sup>5</sup>, Kanishka D.B. Ukuwela<sup>6</sup>

1 *Nature Explorations and Education Team, No: B-1 / G-6, De Soysapura Flats, Moratuwa 10400, Sri Lanka*

2 *Amphibia and Reptile Research Organization of Sri Lanka, 15/1, Dolosbage Road, Gampola, Sri Lanka*

3 *Biodiversity Conservation Society, 150/6, Stanley Thilakarathne Mawatha, Nugegoda 10250, Sri Lanka*

4 *Central Environmental Authority, 104, Denzil Kobbekaduwa Mawatha, Battaramulla 10120, Sri Lanka*

5 *Victorian Herpetological Society, P.O. box 4208, Ringwood, VIC 3134, Australia*

6 *Department of Biological Sciences, Faculty of Applied Sciences, Rajarata University of Sri Lanka, Mihintale 50300, Sri Lanka*

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Corresponding authors: Suranjan Karunarathna ([suranjan.karu@gmail.com](mailto:suranjan.karu@gmail.com)); Kanishka D.B. Ukuwela ([kanishkaku@gmail.com](mailto:kanishkaku@gmail.com))

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## Abstract

A new day gecko of the genus *Cnemaspis* Strauch, 1887 is described from the intermediate bioclimatic zone (Haputale Forest and Idalgashinna Forest in Badulla District) of Sri Lanka. The new species belongs to the *Cnemaspis kandiana* clade and was recorded from granite caves and abandoned buildings within forested areas. The region in which these habitats are located, receives relatively high annual rainfall (2500–3500 mm) and has fairly cool, moist and well-shaded conditions. The new species is medium in size (30.2–32.9 mm SVL) and can be differentiated from all other Sri Lankan *Cnemaspis* by the presence of small subcaudals, heterogeneous dorsal scales, smooth pectoral and ventral scales, 7 or 8 supralabials and infralabials, 143–159 ventral scales, 15–17 belly scales, 95–103 mid-body scales, 122–132 paravertebrals, 3 pre-anal pores, 4 or 5 femoral pores and 17 or 18 lamellae on 4<sup>th</sup> toe. The species described herein is categorised as Critically Endangered (CR) under the IUCN Red List Criteria. The major threats for the new species are habitat loss due to expansion of commercial-scale agriculture and illicit forest encroachments. Therefore, we recommend relevant authorities to take immediate conservation action to ensure the protection of these forest areas in Haputale and Idalgashinna along with the buffer zone in the near future.

## Key Words

Conservation, genetic distance, granite caves, mtDNA, montane rainforests, species delimitation, taxonomy

## Introduction

The tropical island of Sri Lanka has a rich and diverse assemblage of reptiles that comprises a total of 238 species, of which 155 (65%) are endemic and 107 are threatened with extinction (MoE-SL 2012; Batuwita 2016; Batuwita and Edirisinghe 2017; de Silva and Ukuwela 2020; Wickramasinghe et al. 2017, 2019, 2020; Karunarathna et al. 2019a, 2019b, 2020; Batuwita et al. 2020). Amongst the

diverse reptile community of the Island, the diversity of geckos (Family Gekkonidae) are remarkable; 59 species have been recognised so far which accounts for 25% of the overall reptilian richness (Karunarathna et al. 2019b; Amarasinghe and Karunarathna 2020). Forty-nine (~ 83%) of them are endemic to the Island (Batuwita and Udugampola 2017; de Silva and Ukuwela 2020; Batuwita et al. 2019; de Silva et al. 2019; Karunarathna et al. 2019a, 2019b, 2019c; Karunarathna and Ukuwela 2019;

Amarasinghe and Karunarathna 2020) and 31 (~53%) are threatened with extinction (MoE-SL 2012). Though the Sri Lankan gecko fauna consists of seven genera: *Calodactylodes*, *Cnemaspis*, *Cyrtodactylus*, *Gehyra*, *Hemidactylus*, *Hemiphyllodactylus* and *Lepidodactylus*, none is endemic to the country (Somaweera and Somaweera 2009; de Silva and Ukuwela 2020). With 37 nominal species in Sri Lanka, *Cnemaspis* is considered as the most speciose reptile genus in the country, with 100% species endemism (Karunarathna et al. 2019b; Amarasinghe and Karunarathna 2020). *Cnemaspis* are diurnal geckos distributed in Africa and Asia comprising three distinct paraphyletic groups in Africa, Indian subcontinent and Sri Lanka and Southeast Asia (Gamble et al. 2015).

During the past two decades, the number of species recognised in the genus *Cnemaspis* in Sri Lanka has grown rapidly with more than a nine-fold increase (from 4 to 37 species) as a result of the recent taxonomic renaissance (Deraniyagala 1953; Bauer et al. 2007; Batuwita et al. 2019; de Silva et al. 2019; Karunarathna et al. 2019b; Amarasinghe and Karunarathna 2020). Recent molecular phylogenetic analyses have indicated two distinct Sri Lankan clades of *Cnemaspis*, namely: *C. kandiana* and *C. podihuna* (Agarwal et al. 2017) and eight subclades (Karunarathna et al. 2019c) in the two clades; four subclades in the *C. podihuna* clade and four sub-clades in the *C. kandiana* clade. The use of molecular phylogenetics, detailed elucidation of morphological characters, as well as their polarity, greater access to remote locations and enhanced knowledge on geology and geography of the region have contributed to the taxonomic advances of *Cnemaspis* in Sri Lanka (Batuwita et al. 2019; de Silva et al. 2019). During recent field excursions to Badulla District of Sri Lanka, a *Cnemaspis* species which had been previously confused with *C. kandiana* (Kelaart 1852) was discovered from Haputhale and Idalgashinna. Here, we describe this as a new species using a combination of morphological and molecular data.

## Methods

### Field sampling and specimens

We conducted field surveys in 165 different locations distributed across several bioclimatic regions (e.g. dry zone, intermediate zone and wet zone) in Sri Lanka as a part of an on-going island-wide survey of lizards under permit number WL/3/2/42/18 (a & b), issued by the Department of Wildlife Conservation and permit number R&E/RES/NFSRCM/2019-04, issued by the Forest Department of Sri Lanka. At each location, we surveyed and documented gecko species found with special attention on the focal genus *Cnemaspis*. On average, per location, we spent 12 man-hours per survey. Museum acronyms follow Uetz et al. (2019). The type material discussed in this paper is deposited in the National Museum of Sri Lanka (NMSL), Colombo. Specimens were caught by hand and were pho-

tographed in life. They were euthanised using halothane and fixed in 10% formaldehyde for two days, washed in water and transferred to 70% ethanol for long-term storage. Tail tips were collected as tissue samples before fixation and were stored in 95% ethanol. For comparison, we examined 458 *Cnemaspis* specimens (catalogued and uncatalogued) representing all recognised Sri Lankan species, including all type specimens housed at the National Museum of Sri Lanka (NMSL), The Natural History Museum, London (BMNH) and specimens collected by Ansem de Silva (bearing the field codes ADS, Aaron Bauer (bearing the field codes AMB) and Suranjan Karunarathna (bearing the field codes SSK), which have been deposited in the NMSL (Appendix 1). Specimens that formerly belonged to the Wildlife Heritage Trust (WHT) collection which bears WHT numbers are currently deposited at the NMSL, catalogued under their original numbers.

Additional information on the morphology and natural history of Sri Lankan *Cnemaspis* species was extracted from the relevant literature (Bauer et al. 2007; Manamendra-Arachchi et al. 2007; Wickramasinghe and Munindradasa 2007; Vidanapathirana et al. 2014; Wickramasinghe et al. 2016; Agarwal et al. 2017; Batuwita and Udugampala 2017; Batuwita et al. 2019; de Silva et al. 2019; Karunarathna et al. 2019a; Karunarathna et al. 2019b; Karunarathna et al. 2019c; Karunarathna and Ukuwela 2019; Amarasinghe and Karunarathna 2020). Assignment of unidentified specimens to the new species was based on their morphometric, meristic and molecular characters, colour patterns and the level of geographic isolation. The new species described in the present paper has been included in previous phylogenies of the genus as *Cnemaspis* sp. 5 (NMSL AA87 and AA87B collected from Haputhale, Sri Lanka) in Agarwal et al. (2017) and *Cnemaspis* sp. 4 in Karunarathna et al. (2019c). In this paper, we initially refer to this species as *Cnemaspis* sp. 5 following Agarwal et al. (2017). The tissue voucher (bearing the Field number SK5) was sampled from one of the paratypes collected from Idalgashinna, Sri Lanka.

### DNA-based species delimitation

To determine the genetic distinction of the new species to already-known species of *Cnemaspis*, we examined the mitochondrial *NADH dehydrogenase subunit 2* (ND2) gene. ND2 gene is commonly used as a barcode marker for geckos and the majority of DNA sequences available on GenBank for Sri Lankan and Indian *Cnemaspis* species are of this gene. Additionally, we included two *Cnemaspis* (*C. rammalensis* [ $n = 2$ ] and *C. rajakarunai* [ $n = 3$ ]) species that have not been included in previous phylogenies. Genetic distinction was determined through examining the haplotype clusters through phylogenetic analysis (Wiens and Penkrot 2002), uncorrected pairwise genetic distances and species delimitation analyses.

Whole genomic DNA was isolated from the tissue samples using a Qiagen DNeasy blood and tissue DNA

isolation kit (Valencia, CA, USA) following the manufacturer's protocols. The quality of the isolated DNA was determined through gel electrophoresis in ethidium bromide stained 1% Agarose gel. The concentration of the isolated DNA samples was quantified using a Nabi Nano-spectrophotometer (MicroDigital Company Ltd, Korea). We PCR amplified a 1040 bp fragment of the *ND2* gene using already-published primers L4437a, AAGCTTTTCGGCCCATACC and H5934, AGRGTGCCAATGTCTTTGTGRTT (Macey et al. 1997). The PCR was carried out in 25 µl reactions with a primer concentration of 0.4 µM for each primer employing 35 cycles with an annealing temperature of 50 °C (Macey et al. 1997) following standard PCR protocols with Promega PCR master mix (Promega Corporation, Madison, Wisconsin, USA). The success of the PCR amplification and size of the amplified fragment was checked through gel electrophoresis in ethidium bromide stained 1% Agarose gel using a Promega 100 bp ladder (Promega Corporation, Madison, Wisconsin, USA). The PCR products of the successfully amplified samples were purified and sequenced in both directions at the Genetech Sri Lanka Pvt. Ltd., Colombo, Sri Lanka.

Consensus sequences from forward and reverse reads were assembled in Geneious v.5.6 software (Drummond et al. 2009). We downloaded all the available *ND2* sequences for *Cnemaspis* species of the South Asian radiation (Appendix 1). We did not include the Southeast Asian *Cnemaspis* as they are known to be a separate unrelated lineage from the South Asian *Cnemaspis*. However, *C. modiglianii*, *C. tanintharyi* and *C. thayawthadangyi* (Agarwal et al. 2017; Lee et al. 2019) are known to be nested within the South Asian *Cnemaspis* radiation and are closely related to each other (Lee et al. 2019) and thus *C. modiglianii* has been included in the phylogenetic analyses. The total dataset included 104 taxa comprising 27 of the 37 *Cnemaspis* species known from Sri Lanka, four putative species from Sri Lanka, 17 *Cnemaspis* species from India and one species from Southeast Asia. *Calodactylodes illingworthorum* was used as the outgroup since it has been shown to be the sister lineage of the South Asian *Cnemaspis* radiation (Agarwal et al. 2017). DNA sequences were aligned using Geneious alignment (Drummond et al. 2009) in Geneious v.5.6 software using default settings and refined manually. The sequences were translated to amino acid sequences using the vertebrate mitochondrial genetic code to check for premature stop codons that might indicate amplification of pseudogenes and to determine the correct reading frame.

The mitochondrial *ND2* gene tree was reconstructed using Bayesian and Maximum Likelihood (ML) methods. Partitioning schemes and best-fit substitution models for each partition were assessed using the Bayesian Information Criterion (BIC) implemented in Partitionfinder 2 (Lanfear et al. 2017). BIC indicated three partitions based on the three codon positions with GTR+I+G substitution model for each partition. Partitioned ML analysis was implemented in RAxML 7.2.6. (Stamatakis et al. 2008) with 200 independent ML searches using the rapid hill-climb-

ing algorithm. Branch support was estimated using 1000 bootstrap pseudoreplicates. Partitioned Bayesian analysis was performed in MrBayes 3.2.6 (Ronquist and Huelsenbeck 2003) with unlinked model parameters using default priors for 80 million generations with two independent runs and four chains (one hot and three cold chains) sampling every 10000 generations. Convergence of the independent runs was assessed by examining split frequencies (< 0.01) of clades across runs, effective sample sizes (ESS values) and likelihood plots in Tracer v.1.4.1 (Rambaut et al. 2018). An all-compatible consensus tree was built after first 25% of sampled trees were discarded as burn-in. Uncorrected pairwise distances (p-distances) between species were calculated in MEGA X with an average site cut-off of 95% (Kumar et al. 2018).

Species delimitation analysis using Poisson Tree Process (PTP) (Zhang et al. 2013) was conducted using the rooted Bayesian tree as input tree (ML and Bayesian). The calculations were performed on the PTP web server (<http://species.h-its.org/ptp/>), with 200,000 MCMC generations, thinning set to 100 and burn-in set at 25% and performing a Bayesian search. The probability of each node to represent a species node was calculated in both Bayesian and Maximum Likelihood methods.

## Morphometric characters

Forty morphometric measurements were taken using a Mitutoyo digital Vernier calliper (to the nearest 0.1 mm) and detailed observations of scales and other structures were made through Leica Wild M3Z and Leica EZ4 dissecting microscopes. The following symmetrical meristic characters were taken on the left side of the body: eye diameter (ED), horizontal diameter of eye ball; orbital diameter (OD), the greatest diameter of orbit; eye to nostril length (EN), the distance between anteriormost point of the orbit and the posterior border of the nostril; snout length (ES), the distance between anteriormost point of the orbit and the tip of snout; snout to nostril length (SN), the distance between tip of snout and the anteriormost point of the nostril; nostril width (NW), the maximum horizontal width of the nostrils; eye to ear distance (EE), the distance between the posterior border of eye and the anteriormost point of ear opening; snout to axilla distance (SA), the distance between axilla and tip of snout; ear length (EL), the maximum length of the ear opening; interorbital width (IO), the shortest distance between the left and right supraciliary scale rows; inter-ear distance (IE) the distance across the head between the two ear openings; head length (HL), the distance between posterior edge of mandible and the tip of the snout; head width (HW), the maximum width of the head in-between the ears and the orbits; head depth (HD), the maximum height of the head at the level of the eye; jaw length (JL), the distance between the tip of snout and the corner of the mouth; internarial distance (IN), the smallest distance between the inner margins of nostrils; snout to ear dis-

tance (SED), the distance between the tip of snout and anteriormost point of the ear; upper-arm length (UAL), the distance between the axilla and the angle of the elbow; lower-arm length (LAL), the distance from the elbow to the wrist with palm flexed; palm length (PAL), the distance between the wrist (carpus) and the tip of longest finger excluding the claw; length of digits I–V of manus (DLM), the distance between the juncture of the basal phalanx with the adjacent digit and the tip of the digit, excluding the claw; snout-vent length (SVL), the distance between tip of snout and the anterior margin of vent; trunk length (TRL), the distance between the axilla and the groin; trunk width (TW), the maximum width of body; trunk depth (TD), the maximum depth of body; femur length (FEL), the distance between the groin and the knee; tibia length (TBL), the distance from the knee to the heel with ankle dorsiflexed; heel length (HEL), the distance between ankle (tarsus) and the tip of longest toe (excluding the claw) with both foot and tibia flexed; length of pedal digits I–V (DLP), the distance between the juncture of the basal phalanx with the adjacent digit and the digit tip, excluding the claw; tail length (TAL), the distance between the anterior margin of the vent and the tail tip; tail base depth (TBD), the maximum height of the tail base; tail base width (TBW), the widest point of the tail base.

### Meristic characters

Thirty discrete characters were observed and recorded using Leica Wild M3Z and Leica EZ4 dissecting microscopes on both the left (L) and the right (R) side of the body (reported in the form L/R): number of supralabials (SUP) and infralabials (INF) between the first labial scale and the corner of the mouth; number of interorbital scales (INOS) between the left and right supraciliary scale rows; number of postmentals (PM) bounded by chin scales, 1<sup>st</sup> infralabial on the left and right and the mental; number of chin scales (CHS) touching medial edge of infralabials and mental between juncture of 1<sup>st</sup> and 2<sup>nd</sup> infralabials on the left and right; number of supranasal (SUN) scales between nares; presence of the postnasal (PON) scales posterior to the naris; presence of the internasal (INT) scale between supranasals; number of supraciliary scales (SUS) above the eye; number of scales between the eye and tympanum (BET) from posterior-most point of the orbit to anterior-most point of the tympanum; number of canthal scales (CAS), number of scales from posterior-most point of naris to anteriormost point of the orbit; total lamellae on manus I–V (TLM) counted from first proximal enlarged scansor, greater than twice width of the largest palm scale, to distalmost lamella at tip of digits; number of dorsal paravertebral granules (PG) between pelvic and pectoral limb insertion points along a straight line immediately left of the vertebral column; number of mid-body 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 belly scales (BLS) across the ventre between the lowest rows of granular dorsal scales; total lamellae on pes I–V (TLP), counted from first proximal enlarged scansor greater than twice the width of the largest heel scale, to distalmost lamella at tip of digits; number of precloacal pores (PCP) anterior to the cloaca; number of femoral pores (FP) present on the femur; numbers of non-pored proximal femoral scales (PFS) counted from proximal ends of femoral pore rows to precloacal pores; numbers of non-pored distal femoral scales (DFS) counted from distal ends of femoral pore rows to knee. In addition, we also evaluated the texture [keeled (KD) or smooth (SM)] of the ventral scales, the texture [heterogeneous (HET) or homogeneous (HOM)] of the dorsal scales, the number of spinous scales on the flanks (FLSP) and characteristics, such as appearance of the caudal scales (except in specimens with regenerated tails). Colouration was determined from digital images of living specimens and also from direct observations in the field.

### Distribution and natural history

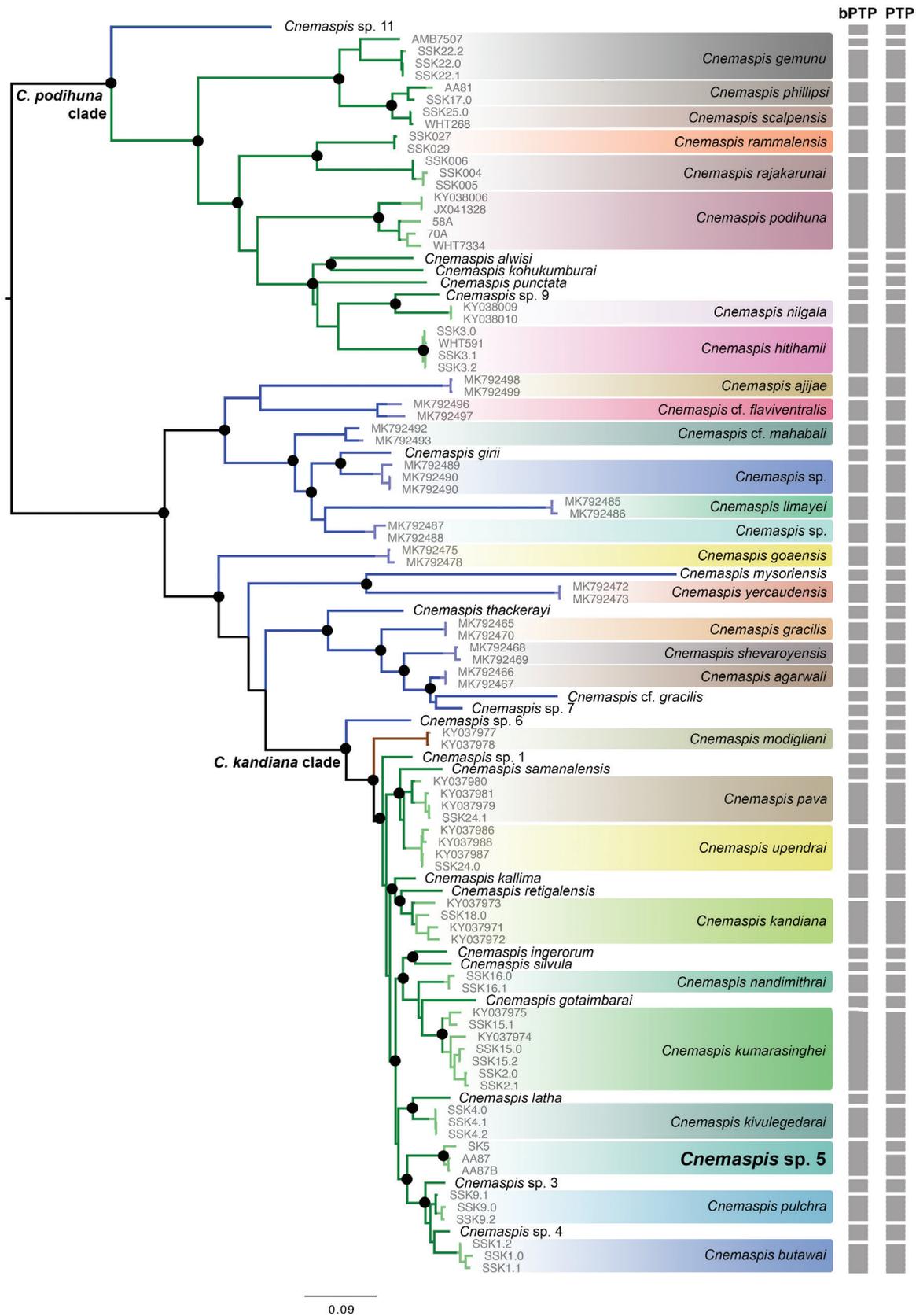
During the surveys, behavioural and other aspects of natural history of the focal species were observed through opportunistic and non-systematic means. The ambient temperature and the substrate temperature were measured using a standard thermometer and a N19 Q1370 infrared thermometer (Dick Smith Electronics, Shanghai, China), respectively. The relative humidity and light intensity were measured with a QM 1594 multifunction environment meter (Digitek Instruments Co., Ltd., Hong Kong, China). To record elevation and georeference species locations, an eTrex 10 GPS (Garmin) was used. Sex was determined by the presence of hemipenial bulges, precloacal and femoral pores in males (M) or absence of the above in females (F). The conservation status of the species was evaluated using IUCN Red List Categories and Criteria version 14 (IUCN 2019).

## Results

### DNA-based species delimitation

Both ML (Supplementary Fig. 1) and Bayesian analyses recovered highly similar topologies and branch lengths and hence only the Bayesian tree is shown (Fig. 1). *Cnemaspis* sp. 5 was recovered in the *C. kandiana* clade (Agarwal et al. 2017) and was sister to a clade comprising *Cnemaspis* sp. 3, *Cnemaspis* sp. 4, *C. pulchra* and *C. butewai* (BPP = 0.98, BS = 70). All three sequences of the new species were monophyletic (BPP = 1.0, BS = 100) (Fig. 1).

The average uncorrected pair-wise genetic distance between *Cnemaspis* sp. 5 and other taxa in the *C. podihuna* clade was 26.3% (range 23.9–28.3%), while it



**Figure 1.** Bayesian all compatible *ND2* gene tree of South Asian *Cnemaspis* lineage. Dark circles depict nodes with Bayesian posterior probability  $\geq 0.95$  and Bootstrap support  $\geq 70$ . The outgroup *Calodactylodes illingworthorum* is not shown. Scale bar indicates the number of substitutions per site. Colours of the branches indicate the geographical origin of the taxa where green, blue and brown depict Sri Lankan, Indian and Southeast Asian taxa, respectively. Results of molecular species delimitation analyses (bPTP and PTP) are shown in grey bars on the right.

**Table 1.** Uncorrected pairwise genetic distances in the *ND2* gene between the *Cnemaspis* sp.5 (*Cnemaspis* sp. 4 in Karunarathna et al. 2019c) and the members of the *Cnemaspis kandiana* clade, the clade to which *Cnemaspis* sp. 5 species belongs.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1. <i>C. butewai</i>	–																		
2. <i>C. kumarasinghei</i>	9.5	–																	
3. <i>C. gotaimbarai</i>	11.2	8.5	–																
4. <i>C. ingerorum</i>	8.8	7.7	8.5	–															
5. <i>C. kallima</i>	7.4	6.6	8.8	5.4	–														
6. <i>C. kandiana</i>	8.2	7.0	8.9	6.2	4.6	–													
7. <i>C. kohukumburai</i>	7.4	8.0	9.9	6.3	5.1	5.8	–												
8. <i>C. latha</i>	8.5	8.7	9.7	7.2	5.7	7.2	4.5	–											
9. <i>C. modiglianii</i>	10.6	9.5	11.7	8.1	6.3	7.3	7.6	8.1	–										
10. <i>C. nandimithrai</i>	8.6	6.5	7.6	5.9	5.5	6.1	6.2	6.7	8.2	–									
11. <i>C. pava</i>	7.7	7.7	9.3	6.3	5.5	5.9	6.3	6.1	8.4	7.6	–								
12. <i>C. pulchra</i>	5.0	9.0	10.6	7.9	6.6	7.6	6.4	7.3	9.8	7.4	7.7	–							
13. <i>C. retigalensis</i>	9.5	7.7	10.9	7.6	4.6	5.6	6.4	8.1	8.1	7.6	7.2	8.5	–						
14. <i>C. samanalensis</i>	9.8	8.7	11.1	8.5	6.3	7.2	7.5	8.2	8.7	8.8	5.8	8.6	8.4	–					
15. <i>C. silvula</i>	9.4	8.0	9.0	5.4	6.0	6.5	6.7	7.8	8.4	6.2	7.6	8.1	7.9	8.4	–				
16. <i>Cnemaspis</i> sp. 1	8.2	7.0	9.4	6.4	4.5	6.3	6.1	6.7	7.8	6.5	6.7	7.5	6.7	7.3	6.4	–			
17. <i>Cnemaspis</i> sp. 3	5.8	9.3	10.3	7.5	7.0	8.2	6.3	7.2	10.5	7.6	8.1	2.8	9.1	9.3	8.2	8.2	–		
18. <i>Cnemaspis</i> sp. 4	5.1	9.1	10.8	8.2	7.0	7.9	7.0	7.8	10.3	7.6	7.8	2.7	8.8	9.4	8.8	6.6	3.6	–	
19. <b><i>Cnemaspis</i> sp. 5</b>	<b>8.3</b>	<b>8.6</b>	<b>10.4</b>	<b>7.4</b>	<b>6.6</b>	<b>7.7</b>	<b>6.8</b>	<b>7.9</b>	<b>9.0</b>	<b>6.6</b>	<b>8.2</b>	<b>6.9</b>	<b>7.5</b>	<b>9.2</b>	<b>8.3</b>	<b>6.6</b>	<b>7.1</b>	<b>7.4</b>	–
20. <i>C. upendrai</i>	8.2	7.0	9.9	7.2	5.1	5.8	5.9	6.8	7.7	7.4	3.7	7.3	6.6	5.3	7.2	5.7	7.9	7.8	7.8

Bold numbers indicate uncorrected pairwise genetic distance between *Cnemaspis* sp. 5 and other members of the *C. kandiana* clade.

was 20.0% (range 22.1–34.3%) between *Cnemaspis* sp. 5 and Indian *Cnemaspis* species exclusive of the members of the *C. kandiana* clade. The average uncorrected pair-wise genetic distance between *Cnemaspis* sp. 5 and other taxa in the *C. kandiana* clade was 7.8% (range 6.6–10.4%) (Table 1) which was greater than the mean (5.6%, range 3.7–8.5%) uncorrected pair-wise genetic distances between sister species pairs in the *C. kandiana* clade. *Cnemaspis nandimithrai* shares the lowest uncorrected pair-wise genetic distance (6.6%) with *Cnemaspis* sp. 5.

Species delimitation analyses using PTP implementing the Maximum Likelihood (PTP) approach indicated the presence of two species within *Cnemaspis* sp. 5, but with low support (ML support: 0.29). However, Bayesian approach (bPTP) indicated the presence of a single species within *Cnemaspis* sp. 5 (Bayesian support: 0.71).

## Systematics

### *Cnemaspis lokugei* sp. nov.

<http://zoobank.org/91469423-CEBA-4BB2-BAF0-386C9572A588>

Figs 2–3; Tables 2–3

Lokuge's day gecko (English)

Lokugege diva-seri hoona (Sinhala)

*Cnemaspis* sp. 5 Agarwal et al. 2017

*Cnemaspis* sp. 4 Karunarathna et al. 2019c

**Holotype.** NMSL.2021.01.01, adult male, 32.9 mm SVL, collected from a granite cave bordering a stream, Haputale, Badulla District, Uva Province, Sri Lanka (6.7753°N; 80.9667°E, WGS1984; elevation 1510 m; around 10:00 hrs) on 18 December 2019 by Suranjan Karunarathna.

**Paratypes.** NMSL.2021.01.02, adult female, 30.8 mm SVL and NMSL.2021.01.03, adult female, 30.2 mm SVL, collected from a granite cave bordering a stream, Idalgashinna, Badulla District, Uva Province, Sri Lanka (6.7791°N; 80.8967°E, WGS1984; elevation 1565 m; around 09:00 hrs) on 19 December 2019 by Suranjan Karunarathna.

**Diagnosis.** *Cnemaspis lokugei* sp. nov., can be readily distinguished from its Sri Lankan congeners by a combination of the following morphological and meristic characteristics: maximum SVL 32.9 mm; dorsum scalation heterogeneous, mixed with smooth and keeled large granular scales; 1/1 supranasals, 1 internasal, 1/1 postnasal; 3 enlarged postmentals; postmentals bounded by 5 enlarged chin scales; chin, gular, pectoral and abdominal scales smooth, subimbricate; 15–17 belly scales across mid-body; 5 or 6 feebly-developed tubercles on posterior flank; 122–132 paravertebral granules linearly arranged; 3 precloacal pores, 4 or 5 femoral pores in males, separated by 8 or 9 proximal femoral scales lacking pores, 7 or 8 distal femoral scales lacking pores; 143–159 ventral scales; 95–103 mid-body scales; smooth subcaudals, median row comprising an irregular series of diamond shaped, small scales; 7 or 8 supralabials; 7 or 8 infralabials; 15 or 16 total lamellae on fourth digit of manus and 17 or 18 total lamellae on fourth digit of pes.

**Description of holotype.** An adult male, 32.9 mm SVL and 36.9 mm TAL (regenerated). Body slender, relatively short (TRL/SVL ratio 39.9%). Head relatively small (HL/SVL ratio 27.7% and HL/TRL ratio 69.5%), narrow (HW/SVL ratio 14.2% and HW/HL ratio 51.2%), depressed (HD/SVL ratio 10.1% and HD/HL ratio 36.4%) and distinct from neck. Snout relatively long (ES/HW ratio 75.5% and ES/HL ratio 38.6%), less than twice the eye diameter (ED/ES ratio 53.4%), more



**Figure 2.** *Cnemaspis lokugei* sp. nov. male holotype (NMSL.2021.01.01), (a) dorsal head, (b) lateral head, (c) ventral head, (d) heterogeneous scales on dorsal surface of trunk, (e) lateral surface of trunk, (f) smooth ventral scales, (g) cloacal characters with preloacal and femoral pores (h) subdigital lamellae on manus, (i) subdigital lamellae on pes; female paratype (NMSL.2021.01.03), (j) dorsal side of tail, (k) lateral side of tail, (l) subrhomboid-shaped small subcaudals. Scale bar: 1 mm (Photos: Suranjan Karunarathna).

than half length of jaw (ES/JL ratio 64.8%), snout slightly concave in lateral view; eye relatively small (ED/HL ratio 20.6%), larger than the ear (EL/ED ratio 43.6%), pupil round; orbit length greater than eye to ear distance

(OD/EE ratio 125.8%) and equal to length of digit IV of manus (OD/DLM IV ratio 100%); supraocular ridges moderately developed; ear opening small (EL/HL ratio 9.0%), deep, taller than wide, larger than nostrils; two



**Figure 3.** *Cnemaspis lokugei* sp. nov. male holotype (NMSL.2021.01.01) in life in-situ (a) dorsal view of the full body with typical colour pattern, (b) ventral aspect showing gular and ventral colouration, (b) lateral aspect with spines on flank and labial colouration from Haputale (Photos: Suranjan Karunaratna).

rows of scales separate orbit from supralabials; inter-orbital distance is a little shorter than snout length (IO/ES ratio 97.7%), shorter than head length (IO/HL ratio 37.8%); eye to nostril distance greater than the eye to ear distance (EN/EE ratio 102.8%).

Dorsal surface of the trunk with smooth scales intermixed with keeled heterogeneous granules, 132 paravertebral granules; 148 smooth, mid-ventral scales; 95 mid-body scales; 6/5 weakly-developed tubercles on the flanks; ventrolateral scales small, irregular; granules on snout

oval, keeled and raised, larger than those on interorbital and occipital regions; canthus rostralis nearly absent, 13/13 smooth oval scales from eye to nostril; scales of the interorbital region circular and keeled; short tubercles present both on the sides of the neck and around the ear; ear opening vertically oval, slanting from anterodorsal to posteroventral, 21/20 scales between anterior margin of the ear opening and the posterior margin of the eye. Supralabials 7/7, infralabials 8/7, becoming smaller towards the posterior end of the mouth. Rostral scale wider than long, partially divided (80%) by a median groove and in contact with first supralabial. Nostrils separated by 1/1 enlarged supranasals with 1 internasal; few enlarged scales behind the supranasals. Nostrils oval, dorsolaterally orientated, not in contact with first supralabials; 1/1 postnasals, smooth, larger than nostrils, partially in contact with first supralabial (Fig. 2).

Mental, sub-rhomboid in shape, as wide as long, posteriorly in contact with 3 enlarged postmentals (smaller than mental and larger than chin scales); postmentals in contact and bordered posteriorly by 5 unkeeled chin scales (larger than nostrils), in contact with the 1<sup>st</sup> infralabial; ventral scales smaller than chin scales. Smooth, rounded, juxtaposed scales on the chin and the gular region; pectoral and abdominal scales smooth, subimbricate towards precloacal region, abdominal scales slightly larger than dorsals; 17 belly scales across ventre; smooth scales around vent and base of tail, subimbricate; 3 precloacal pores; 4/5 femoral pores; 8/9 proximal femoral scales lacking pores on each side; 7/8 enlarged distal femoral scales. Regenerated tail little longer than the snout-vent length (TAL/SVL ratio 112.2%); hemipenial bulge moderately swollen (TBW 2.8 mm), heterogeneous scales on the dorsal aspect of the tail directed backwards, spine-like tubercles present at the base of tail; tail with 3 or 4 enlarged flattened obtuse scales forming whorls; a large, blunt post-cloacal spur on each side, dorsoventrally flattened and narrow; subcaudals smooth and small, sub-rhomboidal, arranged in a single median series (Fig. 2).

Forelimbs very short, slender (LAL/SVL ratio 11.6% and UAL/SVL ratio 13.1%); hind limbs long, tibia little longer than the femur (TBL/SVL ratio 16.7% and FEL/SVL ratio 15.8%). Scales on anterior, upper, posterior and ventral surfaces of upper arm with keeled granules and less imbricate scales, scales of the anterior surface twice as large as those of the other surfaces; anterior, upper, posterior and ventral surfaces of lower arm with keeled and less imbricate scales, scales of the upper surface twice as large as those of the other surfaces. Scales on anterior, upper, posterior surfaces of femur keeled, ventral surface with smooth, subimbricate scales, scales on the ventral surface twice the size of those of other aspects; anterior, upper, posterior surfaces of tibia keeled, ventral surface with smooth, imbricate scales, scales on the upper surface twice the size of those of other aspects. Dorsal and ventral surfaces of manus and pes with keeled granules; dorsal surfaces of digits with granular scales (Fig. 2H, I). Digits elongate and slender with inflected distal phalanges, all bearing slightly recurved claws (Fig. 2). Subdigi-

tal lamellae entire (except divided at first interphalangeal joint), unnotched; total lamellae on manus (left/right): digit I (10/11), digit II (13/14), digit III (16/16), digit IV (16/15), digit V (15/15); total lamellae on pes (left/right): digit I (11/10), digit II (15/15), digit III (17/18), digit IV (18/18), digit V (17/17); interdigital webbing absent; relative length of left manual digits: I (1.4 mm), II (1.8 mm), V (2.3 mm), III (2.5 mm), IV (3.1 mm); relative length of left pedal digits: I (1.5 mm), II (2.9 mm), III (3.4 mm), V (3.5 mm), IV (3.9 mm).

**Variation in the type series** (Tables 2 and 3). The SVL of adult specimens in the type series of *Cnemaspis lokugei* sp. nov. ( $n = 3$ ) ranges from 30.2 to 32.9 mm; interorbital scales 24–26; supraciliaries above the eye 14–16; supralabials 7 or 8, infralabials 7 or 8; scales from eye to tympanum 19–21; canthal scales 12 or 13; tubercles on posterior flank 5 or 6; ventral scales 143–159 (Tables 2–3); mid-body scales 95–103; paravertebral granules 122–132; belly scales across ventre 15–17; femoral pores in males 4 or 5; proximal femoral scales lacking pores in males 8 or 9; distal femoral scales lacking pores in males 7 or 8; total lamellae on digit of the manus: digit I (10 or 11), digit II (13 or 14), digit III (15 or 16), digit IV (15 or 16), digit V (14 or 15); total lamellae on digit of the pes: digit I (10 or 11), digit II (14 or 15), digit III (17 or 18), digit IV (17 or 18), digit V (16 or 17).

**Colour in life.** Dorsum of head, body and limbs generally reddish-brown; yellow spot with black outer edge on neck dorsally; broken faded, yellow vertebral stripe running from occiput to tail (Fig. 3); seven irregular blackish-brown, chevron shaped paravertebral markings present. Tail dark brown dorsally, with 10 faded brown irregular cross-bands; pupil circular and black with the surrounding iris yellow; two very faint postorbital stripes on each side; supralabials and infralabials yellowish with tiny black spots; chin and gular scales yellow, with dark spots; pectoral, abdominal, cloacal and subcaudal scales are cream and intermixed with irregular stippling; dorsum of limbs with faded black markings; manus and pes with alternating black and cream-white cross bands.

**Colour in preservation.** Dorsally grey brown with seven distinct dark, irregular blotches; pale spot with dark outer edge on neck dorsally; supralabials and infralabials dirty white; two dark postorbital stripes on each side; chin and gular scales grey; ventral surface uniformly dirty white colour with some scales on thigh, tail base and arms with dark brown margins.

**Etymology.** The specific epithet is an eponym Latinised (*lokugei*) in the masculine genitive singular, honouring Mr. Ajith Nethkelum Lokuge, a pioneer ecologist, analogue forestry specialist and a senior member of Young Zoologist's Association of Sri Lanka, for his significant contribution towards environmental conservation and research in Sri Lanka.

**Distribution and natural history.** The specimens of the type series were collected from the two locations, Haputale and Idalgashinna (Badulla District, Uva Province), which are situated in the central highlands of Sri

**Table 2.** Morphometric measurements (mm) of holotype from Haputale and two paratypes from Idalgashinna of *Cnemaspis lokugei* sp. nov. from Badulla District, Sri Lanka (“–” = not applicable).

Measurement	NMSL.2021.01.01	NMSL.2021.01.02	NMSL.2021.01.03	Range	Mean±SD
	Holotype (M)	Paratype (F)	Paratype (F)		
Snout-vent length	32.9	30.8	30.2	30.2–32.9	31.3±1.4
Trunk length	13.1	12.3	12.4	12.3–13.1	12.6±0.4
Trunk width	5.2	5.4	5.3	5.2–5.4	5.3±0.1
Trunk depth	3.6	3.4	3.4	3.4–3.6	3.5±0.1
Head length	9.1	8.9	8.9	8.9–9.1	9.0±0.1
Head width	4.7	4.6	4.4	4.4–4.7	4.6±0.1
Head depth	3.3	2.8	2.8	2.8–3.3	3.0±0.3
Snout to axilla distance	15.9	14.3	14.4	14.3–15.9	14.9±0.9
Jaw length	5.4	5.3	5.3	5.3–5.4	5.4±0.1
Tail length	36.9	35.1	34.4	34.4–36.9	35.5±1.3
Tail base width	2.8	2.4	2.4	2.4–2.8	2.6±0.2
Tail base depth	2.5	2.1	2.2	2.2–2.5	2.3±0.2
Eye diameter	1.9	1.7	1.7	1.7–1.9	1.7±0.1
Orbital diameter	3.1	2.9	2.9	2.9–3.1	3.0±0.1
Eye to nostril length	2.6	2.4	2.5	2.4–2.6	2.5±0.1
Snout length	3.5	3.1	3.1	3.1–3.5	3.3±0.2
Snout to nostril length	1.3	1.2	1.2	1.2–1.3	1.2±0.1
Nostril width	0.2	0.2	0.2	–	0.2±0.0
Eye to ear distance	2.5	2.4	2.3	2.3–2.5	2.4±0.1
Ear length	0.8	0.7	0.7	0.7–0.8	0.8±0.1
Interorbital width	3.4	3.3	3.4	3.3–3.4	3.4±0.1
Inter-ear distance	3.6	3.5	3.5	3.5–3.6	3.5±0.0
Internarial distance	1.5	1.3	1.4	1.3–1.5	1.4±0.1
Snout to ear distance	8.3	8.2	8.2	8.2–8.3	8.2±0.1
Upper-arm length	4.3	4.3	4.2	4.2–4.3	4.3±0.1
Lower-arm length	3.8	3.7	3.6	3.6–3.8	3.7±0.1
Palm length	3.2	2.9	3.1	2.9–3.2	3.1±0.1
Digits length of manus (i)	1.4	1.5	1.5	1.4–1.5	1.5±0.1
Digits length of manus (ii)	1.8	1.8	1.9	1.8–1.9	1.8±0.1
Digits length of manus (iii)	2.5	2.4	2.3	2.3–2.5	2.4±0.1
Digits length of manus (iv)	3.1	2.9	3.1	2.9–3.1	3.0±0.1
Digits length of manus (v)	2.3	2.2	2.1	2.1–2.3	2.2±0.1
Femur length	5.2	5.1	5.1	5.1–5.2	5.2±0.1
Tibia length	5.5	5.4	5.3	5.3–5.5	5.4±0.1
Heel length	4.1	3.9	3.9	3.9–4.1	4.0±0.1
Digits length of pes (i)	1.5	1.3	1.4	1.3–1.5	1.4±0.1
Digits length of pes (ii)	2.9	2.7	2.6	2.6–2.9	2.7±0.1
Digits length of pes (iii)	3.4	3.5	3.2	3.2–3.5	3.4±0.1
Digits length of pes (iv)	3.9	3.8	3.8	3.8–3.9	3.8±0.0
Digits length of pes (v)	3.5	3.4	3.3	3.3–3.5	3.4±0.1

Lanka (central intermediate bioclimatic zone [annual rainfall between 2000–2500 mm (Burt and Weerasinghe 2014)]) (Fig. 4). Tropical sub-montane and montane forests make up the dominant vegetation type (Gunatileke and Gunatileke 1990) of this area. The forest acreage in both areas is approximately 1200 ha and is relatively isolated from other forests due to anthropogenic habitats and tea plantations. It is very likely that the species occurs in the intervening regions between these two locations as there are similar habitats scattered between the two locations. However, this needs to be verified through a thorough field survey. These locations lie between an elevation of 1400 and 1700 m a.s.l. (Fig. 4). The mean annual rainfall is received mainly during the southwest monsoon (May–September), while the mean annual temperature is 26.1–28.9 °C. Both areas are rich in granite rock boulders with 40 identified caves. *Cnemaspis lokugei* sp. nov. appears to be a common species in the two locations as we recorded more than 50 indi-

viduals from both locations during a two-day survey. This species was observed in granite caves and relatively old buildings on vertical surfaces, about 2 m from ground within the forested area (Fig. 5). The granitic cave microhabitat of *C. lokugei* sp. nov. was poorly illuminated (light intensity: 392–476 Lux), relatively moist (relative humidity: 76–92%), well shaded (canopy cover: 62–78%) and relatively cool (ambient temperature: 29.5–31.2 °C and substrate temperature: 27.4–28.7 °C). The new species is sympatric with several other gecko species: *Cyrtodactylus* sp., *Gehyra mutilata*, *Hemidactylus frenatus*, *H. parvimaclatus* and *Hemiphyllodactylus typus*. Pure white and almost spherical shaped (mean diameter 4.9 ± 0.02 mm [ $n = 34$ ]) eggs with a slightly flattened side attached to a rocky substrate were observed in cave habitats where *Cnemaspis lokugei* sp. nov. was observed. Since these eggs were characteristic of *Cnemaspis* species and as there were no other *Cnemaspis* species observed in these habitats, it was

**Table 3.** Meristic data of holotype from Haputale and two paratypes from Idalgashinna of *Cnemaspis lokugei* sp. nov. from Badulla District, Sri Lanka (“–” = not applicable).

Character	NMSL.2021.01.01	NMSL.2021.01.02	NMSL.2021.01.03	Range
	Holotype (M)	Paratype (F)	Paratype (F)	
Supralabials (L, R)	7, 7	7, 8	7, 8	7–8
Infralabial (L, R)	8, 7	7, 7	7, 7	7–8
Lateral spines (L, R)	6, 5	5, 5	5, 6	5–6
Interorbital scales	26	24	25	24–26
Postmentals	3	3	3	–
Chin scales	5	5	5	–
Supranasal (L, R)	1, 1	1, 1	1, 1	–
Postnasal (L, R)	1, 1	1, 1	1, 1	–
Internasal	1	1	1	–
Supraciliary (L, R)	15, 14	15, 15	14, 16	14–16
Eye to tympanum scales (L, R)	21, 20	20, 20	19, 21	19–21
Canthal scales (L, R)	13, 13	13, 12	12, 12	12–13
Total lamellae on manus (i) (L, R)	10, 11	10, 10	10, 10	10–11
Total lamellae on manus (ii) (L, R)	13, 14	14, 14	13, 14	13–14
Total lamellae on manus (iii) (L, R)	16, 16	15, 16	15, 15	15–16
Total lamellae on manus (iv) (L, R)	16, 15	15, 15	15, 15	15–16
Total lamellae on manus (v) (L, R)	15, 15	14, 14	15, 15	14–15
Paravertebral granules	132	128	122	122–132
Mid-body scales	95	98	103	95–103
Mid-ventral scales	148	159	143	143–159
Belly scales	17	17	15	15–17
Total lamellae on pes (i) (L, R)	11, 10	11, 11	10, 10	10–11
Total lamellae on pes (ii) (L, R)	15, 15	14, 15	15, 15	14–15
Total lamellae on pes (iii) (L, R)	17, 18	18, 18	17, 18	17–18
Total lamellae on pes (iv) (L, R)	18, 18	17, 17	18, 17	17–18
Total lamellae on pes (v) (L, R)	17, 17	16, 17	16, 17	16–17
Precloacal pores	3	absent	absent	–
Femoral pores (L, R)	4, 5	absent	absent	4–5
Proximal femoral scales (L, R)	8, 9	absent	absent	8–9
Distal femoral scales (L, R)	7, 8	absent	absent	7–8

presumed that the eggs most likely belong to *C. lokugei* sp. nov.

**Conservation status.** Application of the IUCN Red List Criteria indicates that *C. lokugei* sp. nov. is Critically Endangered (CR) due to its having an area of occupancy (AOO) < 10 km<sup>2</sup> (3.84 km<sup>2</sup> in total assuming a 100 m radius around the seven georeferenced locations), severely fragmented habitat and a projected decline in the area, extent and the quality of habitat [Applicable criteria B2ab (iii)].

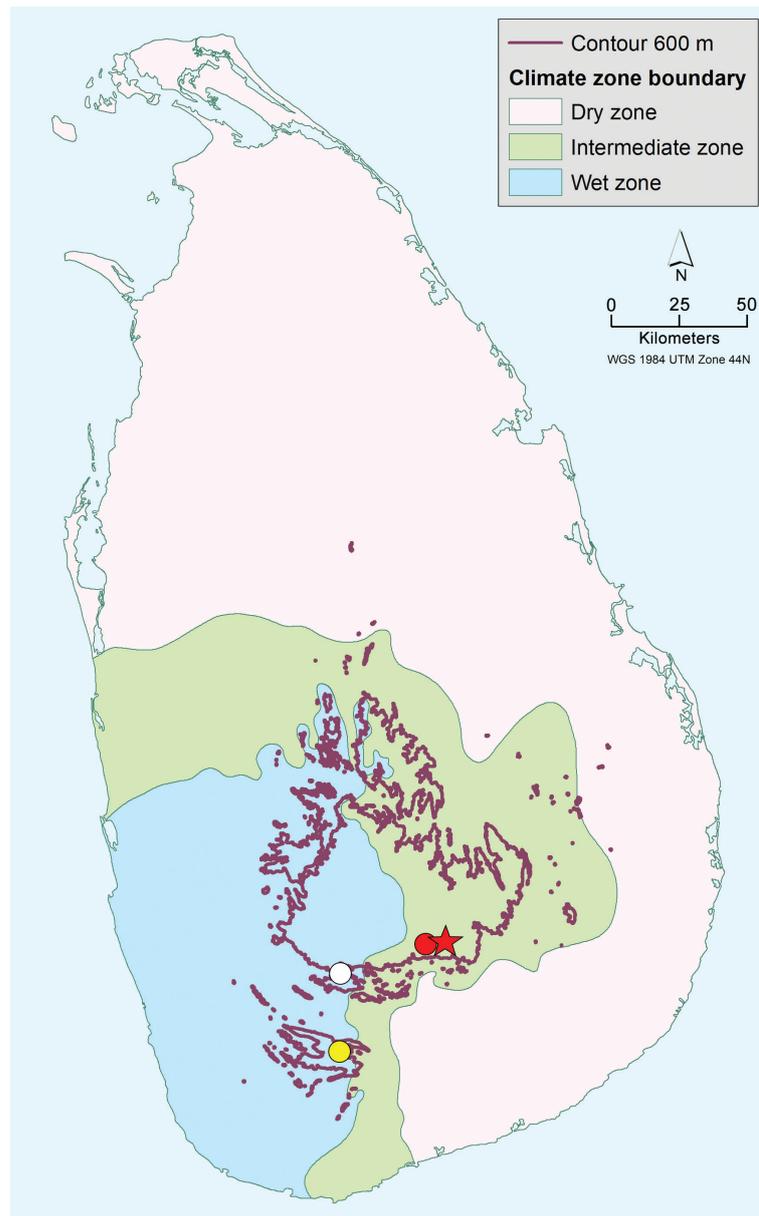
**Comparisons with other Sri Lankan species.** Morphologically, *Cnemaspis lokugei* sp. nov. most closely resembles *C. butewai*, *C. ingerorum*, *C. kivulegedarai*, *C. kallima*, *C. kandiana*, *C. kotagamai*, *C. menikay* and *C. retigalensis* because of the presence of a dorsum with heterogeneous scales and smooth belly scales (see the species comparison and Table 4 for more details). Amongst species of the *C. kandiana* clade *sensu* Agarwal et al. (2017), *Cnemaspis lokugei* sp. nov. differs by having heterogeneous (vs. homogeneous) dorsal scales from *C. amith*, *C. dissanayakai*, *C. gotaimbarai*, *C. kawminiae*, *C. kumarasinghei*, *C. latha* and *C. nandimithrai*. It can also be distinguished from *C. butewai*, *C. kandiana*, *C. menikay*, *C. pava*, *C. pulchra*, *C. retigalensis*, *C. samanensis*, *C. silvula*, *C. tropidogaster* and *C. upendurai* by having smooth (vs. keeled) gular scales. The new species differs from *C. ingerorum* and *C. kivulegedarai* by having more ventral scales (143–159 vs. 88–95 and 109–114) and by having more mid-body scales (95–103 vs. 62–69 and 69–76); from *C. kallima* by having more mid-body scales (95–103 vs. 67–74) and by having more paravertebral granules (122–132 vs. 99–107); from

*C. kotagamai* by having more mid-body scales (95–103 vs. 79–84) and by fewer scales across belly (15–17 vs. 21–22).

Amongst species of the *C. podihuna* clade *sensu* Agarwal et al. (2017), *Cnemaspis lokugei* sp. nov. differs by the absence of clearly enlarged, hexagonal or subhexagonal subcaudal scales from the following species with homogeneous dorsal scales: *C. alwisi*, *C. anslemi*, *C. gemunu*, *C. godagedarai*, *C. hitihamii*, *C. kandambyi*, *C. kohukumburai*, *C. molligodai*, *C. nilgala*, *C. phillipsi*, *C. podihuna*, *C. punctata*, *C. rajakarunai*, *C. rammalensis* and *C. scalpensis*. The new species also differs from *C. alwisi*, *C. anslemi*, *C. gemunu*, *C. godagedarai*, *C. hitihamii*, *C. kohukumburai*, *C. nilgala*, *C. phillipsi*, *C. punctata*, *C. rajakarunai*, *C. rammalensis* and *C. scalpensis* by having precloacal pores (vs. absence).

## Discussion

Our present morphological and molecular analyses and previous studies (Agarwal et al. 2017; Karunarathna et al. 2019c) strongly indicate the presence of a novel species of *Cnemaspis* in Sri Lanka, adding yet another species to the growing list of *Cnemaspis* in Sri Lanka and increasing the total number of species to 38. These *Cnemaspis* species are adapted for a scansorial and crepuscular mode of life, with most being rupicolous, while a few are arboreal or ground-dwelling (Das 2005; Karunarathna et al. 2019b). Sri Lankan representatives of the genus are microhabitat specialists with narrow niches limited to moist, cool,



**Figure 4.** Currently known distribution of *Cnemaspis lokugei* sp. nov. (holotype– red star, paratype– red circle) and its closely-related species (*C. butewai* – white circle, and *C. pulchra* – yellow circle) in Sri Lanka.

canopy-shaded rock outcrops, granite caves, trees, abandoned buildings, buildings associated with caves, wattle and daub houses and semi-naturalised rock walls, where their cryptic morphology and body colouration camouflage them in the environment (Smith 1935; Karunaratna et al. 2019c). Further, *Cnemaspis* species prefer narrow (~ 3–4 mm), long (~ 100–400 mm) and deep (~ 20–180 mm) crevices as refugia and oviposition sites (Karunaratna et al. 2019b). Likewise, the new species is also exclusively recorded from vertical surfaces about 1 to 2 m from ground in poorly illuminated, relatively moist, well shaded and relatively-cool granite caves or old buildings within forested areas (see Fig. 5B). When threatened, they readily escape to narrow crevices. These observations indicate the requirement of cool and damp

environments for the survival of these geckos signifying the narrow ecological niches they occupy. This could be one of the key drivers of speciation in these geckos where narrow ecological niches most likely have been an isolating mechanism. However, most importantly, this may also highlight the fact that these species are at a very high risk of extinction, if such habitats are destroyed. Phylogenetic analyses of the ND2 gene placed the novel species in the *C. kandiana* clade (Agarwal et al. 2017) as expected given its strong morphological resemblance to other members of the clade. The new species was sister to a clade comprising *Cnemaspis* sp. 3, *Cnemaspis* sp. 4, *C. pulchra* and *C. butewai*. The taxonomic status of *Cnemaspis* sp. 3 and *Cnemaspis* sp. 4 needs to be further investigated. Two additional species of *Cnemaspis*,



**Figure 5.** General habitat of *Cnemaspis lokugei* sp. nov. in the Uva Province of Sri Lanka (a) wet forest highland with short trees, viewed from Idalgashinna, (b) a granite cave habitat in Idalgashinna (c) communal egg clutches in Haputale. (Photos: Suranjan Karunaratna).

**Table 4.** Comparison of morphological and morphometric characters of *C. lokugei* sp. nov. with the other congeners of the *C. kandiana* clade in Sri Lanka.

Species	Maximum SVL (mm)	Dorsal scales	Pectoral scales	Abdomen scales	Subcaudals	Suprababials	Infralabials	Ventrals	Belly scales	Mid-body scales	Paravertebrals	Flank spines	Pre-anal pores	Femoral pores	Lamellae on 4 <sup>th</sup> finger	Lamellae on 4 <sup>th</sup> toe
<i>C. pava</i>	32.4	HET	KD	KD	Sml	7–8	6–7	139–145	22–25	64–75	83–98	9–11	2–4	4–5	16–17	18–19
<i>C. pulchra</i>	34.2	HET	KD	KD	Sml	7–8	7–8	120–135	24–27	67–73	94–103	5–7	3–4	4–6	15–17	17–20
<i>C. samanaiensis</i>	37.5	HET	KD	KD	Sml	8–10	8–9	128–144	19–20	61–67	64–72	5–6	3–4	3–5	16–17	18–20
<i>C. silvula</i>	28.6	HET	KD	KD	Sml	7–8	7–8	132–139	19–21	73–81	102–113	10–15	3–4	4–5	15–16	18–19
<i>C. tropidogaster</i>	31.7	HET	KD	KD	Sml	7–8	7–8	132–146	21–25	92–98	99–106	5–7	3–4	4–5	16–17	18–19
<i>C. upendrai</i>	35.2	HET	KD	KD	Sml	7–8	7–8	112–128	16–25	69–74	97–102	13–15	2–3	4–5	17–18	17–21
<i>C. ingerorum</i>	26.9	HET	SM	SM	Sml	7–8	7–8	88–95	17–21	62–69	93–101	7–8	2–3	4–5	13–16	17–18
<i>C. kivulegedarai</i>	31.2	HET	SM	SM	Sml	7–8	6–7	109–114	17–19	69–76	131–133	4–5	2–3	4–5	13–15	14–16
<i>C. kallima</i>	35.1	HET	SM	SM	Sml	7–8	7–8	131–138	19–23	67–74	99–107	12–15	3–4	4–5	16–18	18–20
<i>C. kotagamai</i>	29.8	HET	SM	SM	Sml	7–8	7–8	131–137	21–22	79–84	114–119	6–7	1	4–5	13–15	17–18
<b><i>C. lokugei</i> sp. nov.</b>	<b>32.9</b>	<b>HET</b>	<b>SM</b>	<b>SM</b>	<b>Sml</b>	<b>7–8</b>	<b>7–8</b>	<b>143–159</b>	<b>15–17</b>	<b>95–103</b>	<b>122–132</b>	<b>5–6</b>	<b>3</b>	<b>4–5</b>	<b>15–16</b>	<b>17–18</b>
<i>C. butewai</i>	31.8	HET	SM	SM	Sml	7–8	7–8	125–128	23–25	92–98	134–138	5–6	3–5	4–5	15–17	17–18
<i>C. kandiana</i>	34.6	HET	SM	SM	Sml	8–9	7–8	119–138	19–20	68–75	86–99	5–7	2–4	3–4	12–14	18–20
<i>C. menikay</i>	28.0	HET	SM	SM	Sml	7–9	7–8	124–138	20–26	71–79	83–98	13–15	1–2	3–4	14–15	15–17
<i>C. retigalensis</i>	30.8	HET	SM	SM	Sml	7–8	7–8	121–128	16–20	69–77	82–86	4–5	1	3–4	14–15	16–20
<i>C. amith</i>	33.0	HOM	SM	SM	Sml	7–8	7–8	123–131	19–21	67–74	79–84	4–5	3	3	16–17	18–19
<i>C. dissanayakai</i>	29.4	HOM	SM	SM	Sml	7–8	7–8	118–120	17–19	94–98	105–107	6–7	2–3	4–5	21–22	21–22
<i>C. gotaimbarai</i>	33.7	HOM	SM	SM	Sml	7–8	8–9	129–138	23–25	72–79	117–121	5–6	2–4	3–4	16–17	19–20
<i>C. kawminiae</i>	35.6	HOM	SM	SM	Sml	7–8	7–8	107–114	17–21	76–78	86–92	7–8	2–3	3–4	14–15	15–16
<i>C. kumarasinghei</i>	31.6	HOM	SM	SM	Sml	7–8	7–8	120–134	17–21	87–94	61–68	7–9	2–3	3–5	15–16	16–18
<i>C. latha</i>	30.4	HOM	SM	SM	Sml	7–8	7–8	109–115	13–15	69–73	72–79	5–7	2–3	4–5	15–17	17–18
<i>C. nandimithrai</i>	31.7	HOM	SM	SM	Sml	5–6	6–7	108–112	25–27	87–89	95–99	3–4	2–4	2–4	12–13	19–20

**Abbreviations:** HET – Heterogenous, HOM – Homogenous, KD – Keeled, SM – Smooth, Sml – Small. Characters that can be used to diagnose *C. lokugei* sp. nov. from other *Cnemaspis* species in Sri Lanka are shown in bold text.

*C. rammalensis* and *C. rajakarunai*, which were placed in phylogenetic analyses for the first time, were recovered in the *C. podihuna* clade (Agarwal et al. 2017). This is again expected because of their strong morphological similarity to other members of the clade characterised by the presence of enlarged hexagonal/subhexagonal subcaudal scales. The two species were recovered to be sister taxa forming a unique lineage in the *C. podihuna* clade (Fig. 1) indicating speciation in the isolated mountains (Vidanapathirana et al. 2014; Wickramasinghe et al. 2016) in the wet zone of Sri Lanka. These findings further reinforce the importance of isolated mountains for the speciation of Sri Lankan day geckos. *Cnemaspis lokugei* sp. nov. was discovered from the intermediate bioclimatic zone (see Fig. 4). Our studies illustrate that *Cnemaspis* are distributed throughout all bioclimatic zones of the Island; however, the majority, i.e. 23 species (~60%) are recorded from the wet bioclimatic zone which thus coincides with the notion that the Island's wet bioclimatic zone is home to high species richness and endemism (MoE-SL 2012). Further, the discovery of this new species from Haputale and Idalgashinna (1400–1700 m a.s.l.) suggests that the occurrence of *Cnemaspis* genus in high elevations is also considerable making this the fifth species to be described from elevations above 1000 m a. s. l. (Fig. 4) in Sri Lanka. Since 2015, we have been conducting an island-wide survey on *Cnemaspis* and sampled over 165 locations using visual encounter surveys. Our on-going studies, based on morphological and molecular analyses, have thus far discovered ~16 new species of which 14 species have been described (Botejue et al. 2019; de Silva et al. 2019; Karunarathna et al. 2019a, 2019b, 2019c; Karunarathna and Ukuwela 2019; Amarasinghe and Karunarathna 2020). In addition to this, our on-going studies indicate that there are at least another 10 new species, potentially increasing the *Cnemaspis* count to more than 50 species in Sri Lanka, resulting in the highest density of *Cnemaspis* species per land area. More field surveys in mountainous areas and detailed studies may yield promising results in the understanding of taxonomy and biogeography of this genus.

We are certain that the species that we have described here is novel and has not been previously described due to the following reasons. According to Manamendra-Arachchi et al. (2007), *Gymnodactylus malabarica* Jerdon, 1853 (= *Cnemaspis malabaricus*) described from the forests of Malabar [Kerala State] is a valid species restricted to India. Although Kluge (2001) listed *Cnemaspis malabarica* (Jerdon, 1853) in the synonymy of *C. kandiana*, according to Jerdon (1853), *C. malabarica* (type locality Kerala State, southern India) has homogeneous dorsal scalation. However, *C. kandiana* has heterogeneous dorsal scalation and has a very restricted range in Sri Lanka (Manamendra-Arachchi et al. 2007). Therefore, we consider these two species to be distinct. Similarly, *C. lokugei* sp. nov., has heterogeneous dorsal scalation, while *C. malabarica* has homogeneous dorsal scalation. Additionally, given that *C. lokugei* sp. nov., is restricted to a narrow range within

Sri Lanka and that *C. malabarica* is a species restricted to India, we believe the name *C. malabarica* is not applicable to *C. lokugei* sp. nov. Due to the presence of smooth ventrals in *C. lokugei* sp. nov., (vs. keeled ventrals in *C. tropidogaster*) and many other differences (see comparison for details), the name *C. tropidogaster* is also not applicable to the new species described here. *Gymnodactylus humei* is a species without enlarged hexagonal scales on the tail (thus a member of the *C. kandiana* clade), which was described from Kandy by Theobald (Theobald 1876). This species has been synonymised with *C. kandiana* now and *C. kandiana* is restricted to the Kandyan Region. Due to the fact that *C. kandiana* and *C. lokugei* sp. nov., are morphologically and genetically distinct and allopatric, we believe that *Gymnodactylus humei* (= *Cnemaspis humei*) is also unavailable for *Cnemaspis lokugei* sp. nov. The only *Cnemaspis* species already known from the Region is *C. latha*, which was described from Bandarawela, which is about 10 km from Haputale. However, this species is distinctly different from a suit of morphological characters (see Table 4) from *C. lokugei* sp. nov. and is also genetically distinct (see Figure 1). We therefore conclude that none of the available names or species in synonymy with *C. kandiana* is closely related, geographically proximate or relevant to the new species described here.

Most of the Sri Lankan *Cnemaspis* are point-endemics with distribution ranges limited to < 10 km<sup>2</sup> (i.e. AOO < 10 km<sup>2</sup>, EOO < 100 km<sup>2</sup>) and the new species described here corresponds with this general pattern, which has led to categorising most species as critically endangered. This restricted distribution could be a consequence of the narrow ecological niche leading to the limitation of favourable microhabitats. The known localities of the new species, Haputale and Idalgashinna are mountainous forested areas with granite caves. Although these localities are somewhat isolated from human habitations, they are susceptible to some degree of human-induced habitat degradation, including clearing and timber felling, forest fragmentation, granite mining, tea and vegetable cultivation and invasive species. Most *Cnemaspis* species, like *Cnemaspis lokugei* sp. nov. described here are restricted to forests in mountains (Fig. 5a). Therefore, the conservation of such forests and other mountainous habitats are imperative to ensure the future survival of these species.

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## Appendix 1

Comparative material examined from Sri Lanka  
Museum acronyms

<b>BMNH</b>	The Natural History Museum, London, UK
<b>NMSL</b>	National Museum of Sri Lanka, Colombo, Sri Lanka
<b>DWC</b>	Museum of the Department of Wildlife Conservation, Giritale, Sri Lanka
<b>WHT</b>	Collection of the Wildlife Heritage Trust, Sri Lanka (Now at the NMSL)

- Cnemaspis alwisi*: NMSL 2004.09.01 (holotype), NMSL 2004.09.02 (paratype), NMSL 2004.09.03 (paratype), WHT 5918, WHT 6518, WHT 6519, WHT 7336, WHT 7337, WHT 7338, WHT 7343, WHT 7344, WHT 7345, WHT 7346.
- C. anslemi*: NMSL 2019.14.01 (holotype), NMSL 2019.14.02 (paratype), NMSL 2019.14.03 (paratype).
- C. amith*: BMNH 63.3.19.1066A (holotype), BMNH 63.3.19.1066B (paratype), BMNH 63.3.19.1066C (paratype).
- C. butewai*: NMSL 2019.07.01 (holotype), NMSL 2019.07.02 (paratype), NMSL 2019.07.03 (paratype).
- C. dissanayakai*: NMSL 2019.20.01 (holotype), NMSL 2019.20.02 (paratype), NMSL 2019.20.03 (paratype).
- C. gemunu*: AMB 7495 (holotype), AMB 7507 (paratype??), WHT 7221, WHT 7347, WHT 7348, NMSL 2006.11.01, NMSL 2006.11.02, NMSL 2006.11.03, NMSL 2006.11.04.
- C. godagedarai*: NMSL 2019.09.01 (holotype), NMSL 2019.16.01 (paratype), NMSL 2019.16.02 (paratype).
- C. gotaimbarai*: NMSL 2019.04.01 (holotype), NMSL 2019.04.02 (paratype), NMSL 2019.04.03 (paratype).
- C. hitihamii*: NMSL 2019.06.01 (holotype), NMSL 2019.06.02 (paratype), NMSL 2019.06.03 (paratype).
- C. ingerorum*: WHT 7332 (holotype), WHT 7330 (paratype) WHT 7331 (paratype).
- C. kallima*: WHT 7245 (holotype), WHT 7222 (paratype), WHT 7227 (paratype), WHT 7228 (paratype), WHT 7229 (paratype), WHT 7230 (paratype), WHT 7239 (paratype), WHT 7249 (paratype), WHT 7251 (paratype), WHT 7252 (paratype), WHT 7253 (paratype), WHT 7254 (paratype), WHT 7255 (paratype).
- C. kandambyi*: WHT 9466 (holotype), WHT 9467 (paratype).
- C. kandiana*: BMNH 53.4.1.1 (lectotype), BMNH 80.2.2.119A (paralectotype), BMNH 80.2.2.119B (paralectotype), BMNH 80.2.2.119C (paralectotype), WHT 7212, WHT 7213, WHT 7267, WHT 7305, WHT 7307, WHT 7308, WHT 7310, WHT 7313, WHT 7319, WHT 7322.
- C. kawminiae*: NMSL 2019.18.01 (holotype), NMSL 2019.18.02 (paratype), NMSL 2019.18.03 (paratype).
- C. kivulegedarai*: NMSL 2019.08.01 (holotype), NMSL 2019.08.02 (paratype), NMSL 2019.08.03 (paratype).
- C. kohukumburai*: NMSL 2019.05.01 (holotype), NMSL 2019.05.02 (paratype), NMSL 2019.05.03 (paratype).
- C. kotagamai*: NMSL 2019.15.01 (holotype), NMSL 2019.15.02 (paratype), NMSL 2019.15.03 (paratype).
- C. kumarasinghei*: NMSL 2006.13.01 (holotype), NMSL 2006.13.02 (paratype).
- C. latha*: WHT 7214 (holotype).
- C. manaoe*: NMSL 2019.10.01 (holotype), NMSL 2006.10.02 (paratype), NMSL 2006.10.03 (paratype).
- C. menikay*: WHT 7219 (holotype), WHT 7218 (paratype), WHT 7349 (paratype).
- C. molligodai*: NMSL 2006.14.01 (holotype), NMSL 2006.14.02 (paratype), NMSL 2006.14.03 (paratype), NMSL 2006.14.04 (paratype), NMSL 2006.14.05 (paratype).
- C. nandimithrai*: NMSL 2019.01.01 (holotype), NMSL 2019.01.02 (paratype), NMSL 2019.01.03 (paratype).
- C. nilgala*: NMSL 2018.07.01 (holotype), NMSL 2018.06.01 (paratype), NMSL 2018.06.02 (paratype), NMSL 2018.06.03 (paratype).
- C. pava*: WHT 7286 (holotype), WHT 7281 (paratype), WHT 7282 (paratype), WHT 7283 (paratype), WHT 7285 (paratype), WHT 7288 (paratype), WHT 7289 (paratype), WHT 7290 (paratype), WHT 7291 (paratype), WHT 7292 (paratype), WHT 7293 (paratype), WHT 7294 (paratype), WHT 7295 (paratype), WHT 7296 (paratype), WHT 7297 (paratype), WHT 7298 (paratype), WHT 7299 (paratype), WHT 7300 (paratype), WHT 7301 (paratype), WHT 7302 (paratype).
- C. phillipsi*: WHT 7248 (holotype), WHT 7236 (paratype); WHT 7237 (paratype); WHT 7238 (paratype).
- C. podihuna*: BMNH 1946.8.1.20 (holotype), NMSL 2006.10.02, NMSL 2006.10.03, NMSL 2006.10.04.
- C. pulchra*: WHT 7023 (holotype), WHT 1573a (paratype), WHT 7011 (paratype), WHT 7021 (paratype), WHT 7022 (paratype).
- C. punctata*: WHT 7256 (holotype), WHT 7223 (paratype), WHT 7226 (paratype), WHT 7243 (paratype), WHT 7244 (paratype).
- C. rajakarunai*: NMSL 2016.07.01 (holotype), DWC 2016.05.01 (paratype), DWC 2016.05.02 (paratype).
- C. rammalensis*: NMSL 2013.25.01 (holotype), DWC 2013.05.001.
- C. retigalensis*: NMSL 2006.12.01 (holotype), NMSL 2006.12.02 (paratype), NMSL 2006.12.03 (paratype), NMSL 2006.12.04 (paratype).
- C. samanalis*: NMSL 2006.15.01 (holotype), NMSL 2006.15.02 (paratype), NMSL 2006.15.03 (paratype), NMSL 2006.15.04 (paratype), NMSL 2006.15.05 (paratype).
- C. scalpensis*: NMSL 2004.01.01 (neotype), NMSL 2004.02.01, NMSL 2004.03.01, NMSL 2004.04.01, WHT 7265, WHT 7268, WHT 7269, WHT 7274, WHT 7275, WHT 7276, WHT 7320.

**C. *silvula*:** WHT 7208 (holotype), WHT 7206 (paratype), WHT 7207 (paratype), WHT 7209 (paratype), WHT 7210 (paratype), WHT 7216 (paratype), WHT 7217 (paratype), WHT 7018, WHT 7027, WHT 7202, WHT 7203, WHT 7220, WHT 7354, WHT 7333.

**C. *tropidogater*:** BMNH 71.12.14.49 (lectotype), NMSL 5152, NMSL 5151, NMSL 5159, NMSL 5157, NMSL 5970, NMSL 5974.

**C. *upendrai*:** WHT 7189 (holotype), WHT 7184 (paratype), WHT 7187 (paratype), WHT 7188 (paratype), WHT 7181 (paratype), WHT 7182 (paratype), WHT 7183 (paratype), WHT 7185 (paratype), WHT 7190 (paratype), WHT 7191 (paratype), WHT 7192 (paratype), WHT 7193 (paratype), WHT 7194 (paratype), WHT 7195 (paratype), WHT 7196 (paratype), WHT 7197 (paratype), WHT 7260 (paratype).

## Appendix 2

Specimens, voucher numbers and GenBank accession numbers of the taxa used for the DNA-based species delimitation in this study.

Species	Field No./ Museum Voucher No.	GenBank Accession No.	Source
<i>Calodactylodes illingworthorum</i>	AMB7415	JX041318	Gamble et al. 2012
<i>Cnemaspis agarwali</i>	AK107	MK792466	Khandekar et al. 2019
	AK108	MK792467	Khandekar et al. 2019
<i>Cnemaspis aijijae</i>	AK429	MK792498	Khandekar et al. 2019
	AK432	MK792499	Khandekar et al. 2019
<i>Cnemaspis alwisi</i>	AMB7447	KY037997	Agarwal et al. 2017
<i>Cnemaspis butewai</i>	SSK1.0/ NMSL.2019.07.01	MK562351	Karunaratna et al. 2019c
	SSK1.1/ NMSL.2019.07.02	MK562352	Karunaratna et al. 2019c
	SSK1.2/ NMSL.2019.07.03	MK562353	Karunaratna et al. 2019c
<i>Cnemaspis cf. flaviventralis</i>	AK518	MK792496	Khandekar et al. 2019
	AK517	MK792497	Khandekar et al. 2019
<i>Cnemaspis cf. gracilis</i>	AK213	MK792464	Khandekar et al. 2019
<i>Cnemaspis cf. kumarasinghei</i>	AA13/NMSL	KY037975	Agarwal et al. 2017
<i>Cnemaspis cf. mahabali</i>	AK398	MK792492	Khandekar et al. 2019
	AK389	MK792493	Khandekar et al. 2019
<i>Cnemaspis cf. gemunu</i>	AMB7507/NMSL	KY038000	Agarwal et al. 2017
<i>Cnemaspis cf. podihuna</i>	AMB7449/NMSL	KY038006	Agarwal et al. 2017
<i>Cnemaspis lokugei</i> sp. nov.	AA87/ NMSL	KY037993	Agarwal et al. 2017
	AA87B/ NMSL	KY037994	Agarwal et al. 2017
	SK5/NMSL.2021.01.02	MW594290	This study
<i>Cnemaspis gemunu</i>	SSK22.0/ ADS217/ NMSL	MK562340	Karunaratna et al. 2019c
	SSK22.1/ ADS216/ NMSL	MK562341	Karunaratna et al. 2019c
	SSK22.2/ ADS218/ NMSL	MK562342	Karunaratna et al. 2019c
<i>Cnemaspis girii</i>	AK439	MK792491	Khandekar et al. 2019
<i>Cnemaspis goaensis</i>	VG385	MK792475	Khandekar et al. 2019
	VG399	MK792478	Khandekar et al. 2019
<i>Cnemaspis gotaimbarai</i>	SSK6.0/NMSL.2019.04.01	MK562364	Karunaratna et al. 2019c
<i>Cnemaspis gracilis</i>	CES G385	MK792465	Khandekar et al. 2019
	AK135	MK792470	Khandekar et al. 2019
<i>Cnemaspis hitihamii</i>	SSK3.0/ NMSL.2019.06.01	MK562337	Karunaratna et al. 2019c
	SSK3.1/ NMSL.2019.06.02	MK562338	Karunaratna et al. 2019c
	WHT591/ NMSL	KY038012	Agarwal et al. 2017
	SSK3.2/ NMSL.2019.06.03	MK562339	Karunaratna et al. 2019c
<i>Cnemaspis ingerorum</i>	WHT7331	KY037990	Agarwal et al. 2017
<i>Cnemaspis kallima</i>	AA82/ NMSL	KY037970	Agarwal et al. 2017
<i>Cnemaspis kandiana</i>	AA57/ NMSL	KY037971	Agarwal et al. 2017
	AMB7487/ NMSL	KY037972	Agarwal et al. 2017
	AA01/ NMSL	KY037973	Agarwal et al. 2017
	SSK18.0/ NMSL	MK562347	Karunaratna et al. 2019c
<i>Cnemaspis kivulegedarai</i>	SSK4.0/ NMSL.2019.08.01	MK562348	Karunaratna et al. 2019c
	SSK4.1/ NMSL.2019.08.02	MK562349	Karunaratna et al. 2019c
	SSK4.2/ NMSL.2019.08.03	MK562350	Karunaratna et al. 2019c
<i>Cnemaspis kohukumburai</i>	SSK23.0/ NMSL.2019.05.01	MK562336	Karunaratna et al. 2019c
<i>Cnemaspis kumarasinghei</i>	AMB7431/ NMSL	KY037974	Agarwal et al. 2017
	SSK15.0/ NMSL	MK562358	Karunaratna et al. 2019c
	SSK15.1/ NMSL	MK562359	Karunaratna et al. 2019c
	SSK15.2/ NMSL	MK562357	Karunaratna et al. 2019c
	SSK2.0/ NMSL	MK562360	Karunaratna et al. 2019c
	SSK2.1/ NMSL	MK562361	Karunaratna et al. 2019c
	AA13/ NMSL	KY037975	Agarwal et al. 2017
<i>Cnemaspis latha</i>	WHT214/ NMSL	KY037976	Agarwal et al. 2017
<i>Cnemaspis limayei</i>	AK DAJ	MK792485	Khandekar et al. 2019
	DV40.5	MK792486	Khandekar et al. 2019

Species	Field No./ Museum Voucher No.	GenBank Accession No.	Source
<i>Cnemaspis modiglianii</i>	MVZ239314	KY037977	Agarwal et al. 2017
	MVZ239315	KY037978	Agarwal et al. 2017
<i>Cnemaspis mysoriensis</i>	NA	MK792474	Khandekar et al. 2019
<i>Cnemaspis nandimithrai</i>	SSK16.0/ NMSL.2019.03.01	MK562362	Karunaratna et al. 2019c
	SSK16.1/ NMSL.2019.03.02	MK562363	Karunaratna et al. 2019c
<i>Cnemaspis nilgala</i>	AMB7418/ NMSL	KY038009	Agarwal et al. 2017
	AMB7436/ NMSL	KY038010	Agarwal et al. 2017
<i>Cnemaspis pava</i>	WHT7261/ NMSL	KY037979	Agarwal et al. 2017
	AMB7494/ NMSL	KY037980	Agarwal et al. 2017
	AA19/ NMSL	KY037981	Agarwal et al. 2017
	SSK24.1/ ADS214/ NMSL	MK562346	Karunaratna et al. 2019c
<i>Cnemaspis phillipsi</i>	AA81/ NMSL	KY038001	Agarwal et al. 2017
	SSK17.0/ ADS220/ NMSL	MK562343	Karunaratna et al. 2019c
<i>Cnemaspis podihuna</i>	70A/ NMSL	KY038002	Agarwal et al. 2017
	AMB7449/ NMSL	JX041328	Gamble et al. 2012
	58A/ NMSL	KY038005	Agarwal et al. 2017
	WHT7334/ NMSL	KY038004	Agarwal et al. 2017
<i>Cnemaspis pulchra</i>	SSK9.0/ ADS205	MK562354	Karunaratna et al. 2019c
	SSK9.1/ ADS206	MK562355	Karunaratna et al. 2019c
	SSK9.2/ ADS207	MK562356	Karunaratna et al. 2019c
	AA80/ NMSL	KY038007	Agarwal et al. 2017
<i>Cnemaspis rajakarunai</i>	SSK004	MW594285	This study
	SSK005	MW594286	This study
	SSK006	MW594287	This study
<i>Cnemaspis rammalensis</i>	SSK027	MW594288	This study
	SSK029	MW594289	This study
<i>Cnemaspis retigalensis</i>	AMB7448/ NMSL	KY037982	Agarwal et al. 2017
<i>Cnemaspis samanalensis</i>	AMB7505/ NMSL	KY037983	Agarwal et al. 2017
<i>Cnemaspis scalpensis</i>	SSK25.0/ ADS219	MK562344	Karunaratna et al. 2019c
	WHT7268/ NMSL	KY038008	Agarwal et al. 2017
<i>Cnemaspis shevaroyensis</i>	AK204	MK792468	Khandekar et al. 2019
	AK205	MK792469	Khandekar et al. 2019
<i>Cnemaspis silvula</i>	AA88/ NMSL	KY037984	Agarwal et al. 2017
<i>Cnemaspis</i> sp. 1 (Sri Lanka)	AA17/ NMSL	KY037989	Agarwal et al. 2017
<i>Cnemaspis</i> sp. 3 (Sri Lanka)	AMB7508/ NMSL	KY037991	Agarwal et al. 2017
<i>Cnemaspis</i> sp. 4 (Sri Lanka)	AMB7529/ NMSL	KY037992	Agarwal et al. 2017
<i>Cnemaspis</i> sp. 6 (India)	SB048	KY037995	Agarwal et al. 2017
<i>Cnemaspis</i> sp. 7 (India)	JB239	KY037996	Agarwal et al. 2017
<i>Cnemaspis</i> sp. 9 (Sri Lanka)	47A/ NMSL	KY038011	Agarwal et al. 2017
<i>Cnemaspis</i> sp. 11 (India)	SB151	KY038013	Agarwal et al. 2017
<i>Cnemaspis</i> sp. (India)	G349	MK792490	Khandekar et al. 2019
<i>Cnemaspis</i> sp. (India)	VG407	MK792487	Khandekar et al. 2019
<i>Cnemaspis</i> sp. (India)	VG408	MK792488	Khandekar et al. 2019
<i>Cnemaspis</i> sp. (India)	AK470	MK792489	Khandekar et al. 2019
<i>Cnemaspis thackerayi</i>	CES G143	MK792471	Khandekar et al. 2019
<i>Cnemaspis upendrai</i>	AA83	KY037986	Agarwal et al. 2017
	AA12	KY037987	Agarwal et al. 2017
	AMB7488	KY037988	Agarwal et al. 2017
	SSK24.0/ ADS213	MK562345	Karunaratna et al. 2019c
<i>Cnemaspis yercaudensis</i>	AK280	MK792472	Khandekar et al. 2019
	G133	MK792473	Khandekar et al. 2019