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 Karunarathna1, Anslem De Silva2, Dinesh Gabadage3, Madhava Botejue3,4, Majinthia Madawala5, Kanishka D.B. Ukuwela6

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 Thilakaratne 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

http://zoobank.org/401B344F-6CA0-48C5-BC22-7E28B345F3CD

Corresponding authors: Suranjan Karunarathna (suranjan.karu@gmail.com); Kanishka D.B. Ukuwela (kanishkauku@gmail.com)

Academic editor: Rafe Brown ♦ Received 23 April 2020 ♦ Accepted 24 February 2021 ♦ Published 25 March 2021

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 4th 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 Udagampola 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, Corydactylus, 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 Idalgashinha. 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 photographed 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 Anslem 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 Idalgashinha, 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, AAGCTTTTG-GGCCCATACC and H5934, AGRGTGCAATATGCTTTTGGTTGRTT (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 unresolved lineage from the South Asian Cnemaspis. However, C. modiglianii, C. taninathyri 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 to 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-climbing 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 anterior most point of the orbit and the posterior border of the nostril; snout length (ES), the distance between anterior most point of the orbit and the tip of snout; snout to nostril length (SN), the distance between tip of snout and the anterior most 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 anterior most 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-
Meric 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 left and right supraciliary scale rows; number of postmentals (PM) bounded by chin scales, 1st infralabial on the left and right and the mental; number of chin scales (CHS) touching medial edge of infralabials on the left and right and the mental; number of supralabials (SUP) 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, 1st infralabial on the left and right and the mental; number of chin scales (CHS) touching medial edge of infralabials and mental between juncture of 1st and 2nd infralabials on of chin scales (CHS) touching medial edge of infralabials on the left and right and the mental; number of supralabials (SUP) 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, 1st infralabial on the left and right and the mental; number of chin scales (CHS) touching medial edge of infralabials and mental between juncture of 1st and 2nd 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 anterior-most point of the orbit; total lamellae on manus I–V (TLM) counted from first proximal enlarged scansor greater than twice the 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 sequenc-
Figure 1. Bayesian all compatible ND2 gene tree of South Asian *Cnemaspis* lineage. Dark circles depict nodes with Bayesian posterior probability ≥ 0.95 and Bootstrap support ≥ 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. C. buletai | 2. C. kumarasingheii | 3. C. gotaibinari | 4. C. ingerorum | 5. C. kalima | 6. C. kandiana | 7. C. kokukurumburi | 8. C. latna | 9. C. modiglianii | 10. C. nandimithrai | 11. C. pava | 12. C. pulchra | 13. C. retigalensis | 14. C. samanalensis | 15. C. silvula | 16. Cnemaspis sp. 1 | 17. Cnemaspis sp. 3 | 18. Cnemaspis sp. 4 | 19. Cnemaspis sp. 5 | 20. C. upendrai |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 8.2 7.0 9.9 7.2 | 5.1 5.8 5.9 6.8 | 7.7 7.4 6.6 8.8 | 5.4 | 8.2 7.0 8.9 6.2 | 4.6 | 7.4 8.0 9.9 6.3 | 5.1 5.8 | 8.5 8.7 9.7 7.2 | 5.7 7.2 4.5 | 9.1 9.4 9.5 7.9 | 9.4 9.4 9.5 7.8 | 9.0 6.6 8.3 7.9 | 10.4 8.2 6.8 8.6 | 10.7 9.4 9.5 7.8 | 9.1 9.2 9.3 7.4 | 5.1 5.1 5.1 4.6 | 6.6 8.3 7.8 7.5 | 9.2 8.3 6.6 7.1 | 7.4 | 2.2 |

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 pairwise 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 kandiana* clade. The average uncorrected pairwise genetic distance between *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 kandiana* clade. The average uncorrected pairwise genetic distance between *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 kandiana* clade.

Species delimitation analyses using PTP implementing the Maximum Likelihood (PTP) approach indicated the presence of a single species exclusive of the members of the *C. kandiana* clade. The average uncorrected pairwise 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 kandiana* clade.

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, Vidalgashinna, 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 lokugai* 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 precloacal 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 100%); supraocular ridges moderately developed; ear opening small (EL/HL ratio 9.0%), deep, taller than wide, larger than nostrils; two
rows of scales separate orbit from supralabials; interorbital 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

**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: Suranjana Karunarathna).
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 smooth, larger than nostrils, partially in contact with first supralabials; 1/1 postnasals, smooth, smaller than nostrils.

Mental, sub-rhomboïd 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 1st infrabial; ventral scales smaller than chin scales. Smooth, rounded, juxtaposed scales on the chin and the gular region; pectoral and abdominal scales smooth, subimbricate towards precoxal region, abdominal scales slightly larger than dorsals; 17 belly scales across ventre; smooth scales around vent and base of tail, subimbricate; 3 precoxal 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, subrhomboïd, 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). Subdigital 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    |
|------------------------------|-----------------|-----------------|-----------------|-------------|------------|
| 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             | 0.2–0.2     | 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             | 1.5             | 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) | 2.3             | 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 individuals 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. parvimaculatus* 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
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 km² (3.84 km² 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*, *C. rajakarunai*, and *C. rammalensis*. The new species also differs from *C. biliva*, *C. anslemi*, *C. gemunu*, *C. godagedarai*, *C. hithamii*, *C. kandambyi*, *C. kohukumburai*, *C. molligoda*, *C. nilgala*, *C. phillipsi*, *C. podihuna*, *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 cool, humid montane forests (Agarwal et al. 2017; Karunarathna et al. 2019c).

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**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 |
|-----------|-----------------|-----------------|-----------------|-------|
| Supralabials (L, R) | 7.7 | 7.7 | 7.7 | 7-8 |
| Infrafalabial (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 | 5 | 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 | 15.19 | 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 | 15 | 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 |
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; Karunarathna 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 (Karunarathna 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*,
### 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 | Supralabials | Ventral scales | Belly scales | Mid-body scales | Paravertebrals | Flank spines | Pre-anal pores | Femoral pores | Lamellae on 4th finger | Lamellae on 4th toe |
|-------------------|------------------|---------------|-----------------|----------------|--------------|----------------|--------------|-----------------|----------------|--------------|----------------|--------------|------------------------|------------------|
| *C. pava*         | 32.4 HET KD KD Sml 7-8 7-8 | 139-145 22-25 | 64-75 | 83-98 | 9-11 | 2-4 | 4-5 | 16-17 | 18-19 |
| *C. pulchra*      | 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 |
| *C. samanalenisis*| 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 |
| *C. silvula*      | 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 |
| *C. tropidogaster*| 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 |
| *C. upendrai*     | 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 |
| *C. ingerorum*    | 26.9 HET SM SM Sml 7-8 7-8 | 88-95 17-21 | 62-69 | 93-101 | 7-8 | 2-3 | 4-5 | 15-16 | 17-18 |
| *C. kivulegedarai*| 31.2 HET SM SM Sml 7-8 7-8 | 109-114 17-19 | 69-76 | 131-133 | 4-5 | 2-3 | 4-5 | 13-15 | 14-16 |
| *C. kallima*      | 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 |
| *C. kotagamai*    | 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 |
| **C. lokugei** sp. nov. | **32.9 HET SM SM Sml 7-8 7-8** | **143-159 15-17** | **95-103** | **122-132** | **5-6** | **3** | **4-5** | **15-16** | **17-18** |
| *C. butewai*      | 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 |
| *C. kandiana*     | 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 |
| *C. menikay*      | 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 | 17-17 |
| *C. retigalensis* | 30.8 HET SM SM Sml 7-8 7-8 | 121-128 16-20 | 69-77 | 82-86 | 4-6 | 1 | 3-4 | 14-15 | 16-20 |
| *C. amith*        | 33.0 HOM SM SM Sml 7-8 7-8 | 123-131 19-21 | 67-74 | 79-84 | 4-6 | 3 | 3 | 16-17 | 18-19 |
| *C. dissanayakai* | 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 |
| *C. gotaimbarai*  | 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 |
| *C. kawminiae*    | 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 |
| *C. kumarasinghei*| 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 |
| *C. latha*        | 30.4 HOM SM SM Sml 7-8 7-8 | 108-115 13-15 | 69-73 | 72-79 | 5-7 | 2-3 | 4-5 | 15-17 | 17-18 |
| *C. nandimithrai* | 31.7 HOM SM SM Sml 5-6 5-6 | 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), *Gymnodactyulus 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 scelation. However, *C. kandiana* has heterogenous dorsal scelation 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 heterogenous dorsal scelation, while *C. malabarica* has homogeneous dorsal scelation. 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*) many other differences (see comparison for details), the name *C. tropidogaster* is also not applicable to the new species described here. *Gymnodactyulus 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 Kandy Region. Due to the fact that *C. kandiana* and *C. lokugei* sp. nov., are morphologically and genetically distinct and allopatric, we believe that *Gymnodactyulus 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 Haputhale. 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 km² (i.e. AOO < 10 km², EOO < 100 km²) 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.

Acknowledgements

We thank to the Director General, the Research Director, the research committee and the field staff of the Department of Wildlife Conservation of Sri Lanka for granting research permits (WL/3/2/42/18a, b) and assisting us during the field surveys. The Additional Conservator and field staff of the Department of Forest Conservation are acknowledged for issuing research permits (R&E/RES/NFSRCM/2019-04) and the support provided during the field surveys. Further, we are grateful to Nanda Wickramasinghe, Sanuja Kasthuriarachchi, Lankani...
Somaratne, Chandrika Munasinghe, Tharushi Gamage, Rasika Dasanayake, Thushari Dasanayake, Ravindra Wickramanayake and Panmilage Gunasiri at NMSL for assisting us during examining collections under their care. Thilina Surasinghe, Thasun Amarasinghe, Nirama Perera, Sulakshana Wickramarachchi, Hasantha Wijethunga, Angelo Hettige, Nimantha Aherathna, Mendis Wickramasinghe, Tharaka Kusuminda, Buddhika Madurapperuma, Sanjaya Bandara and Niranjan Karunarathna provided valuable assistance in numerous stages of the study. Dimanthi Jayatilake and Danesha Nanayakkara are thanked for providing laboratory facilities and assistance with laboratory work. Finally, we would like to thank Mark Scherz and three anonymous reviewers and the editor, Rafe Brown for constructive comments that immensely helped to improve the manuscript.

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Appendix 1

Comparative material examined from Sri Lanka

Museum acronyms

BMNH  The Natural History Museum, London, UK
NMSL  National Museum of Sri Lanka, Colombo, Sri Lanka
DWC  Museum of the Department of Wildlife Conservation, Giritale, Sri Lanka
WHT  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 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 (parallectotype), BMNH 80.2.2.119B (paralecotype), BMNH 80.2.2.119C (paralecotype), 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. kivulegedarai: NMSL 2019.08.01 (holotype), NMSL 2019.08.02 (paratype), NMSL 2019.08.03 (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. 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. 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. 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. 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. 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. 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 |
|--------------------------------------|----------------------|--------|
| Calodactylodes illingworthorum       | AMB7415 JX041318     | Gamble et al. 2012 |
| Cnemaspis agarwali                   | AK107 MK792466       | Khandekar et al. 2019 |
|                                      | AK108 MK792467       | Khandekar et al. 2019 |
|                                      | AK429 MK792498       | Khandekar et al. 2019 |
|                                      | AK432 MK792499       | Khandekar et al. 2019 |
| Cnemaspis alwisi                     | AMB7447 KY037997     | Agarwal et al. 2017 |
| Cnemaspis butewai                    | SSK1.0/ NMSL.2019.07.01 MK562351 Karunarathna et al. 2019c |
|                                      | SSK1.1/ NMSL.2019.07.02 MK562352 Karunarathna et al. 2019c |
|                                      | SSK1.2/ NMSL.2019.07.03 MK562353 Karunarathna et al. 2019c |
| Cnemaspis cf. flaviventris           | AK518 MK792496       | Khandekar et al. 2019 |
|                                      | AK517 MK792464       | Khandekar et al. 2019 |
| Cnemaspis cf. gracilis               | AK213 MK792464       | Khandekar et al. 2019 |
| Cnemaspis cf. kumarasinghei          | AA13/NMSL KY037975   | Agarwal et al. 2017 |
| Cnemaspis cf. mahabali               | AK398 MK792492       | Khandekar et al. 2019 |
|                                      | AK389 MK792493       | Khandekar et al. 2019 |
| Cnemaspis cf. gemunu                 | AMB7507/NMSL KY038000 Agarwal et al. 2017 |
| Cnemaspis cf. podilhuna              | AMB7449/NMSL KY038006 Agarwal et al. 2017 |
| Cnemaspis latha                       | WHT214/ NMSL KY037976 Agarwal et al. 2017 |
| Cnemaspis limayeii                    | AK DJ MK792485       | Khandekar et al. 2019 |

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| Species               | Field No./ Museum Voucher No. | GenBank Accession No. | Source                        |
|----------------------|------------------------------|-----------------------|-------------------------------|
| *Cnemaspis modiglianii* | MVZ239314                    | KY037977              | Agarwal et al. 2017          |
|                      | MVZ239315                    | KY037978              | Agarwal et al. 2017          |
| *Cnemaspis mysorizensis* | NA                           | MK792474              | Khandekar et al. 2019        |
| *Cnemaspis nandithirai* | SSK16.0/ NMSL.2019.03.01     | MK562362              | Karunarathna et al. 2019c    |
|                      | SSK16.1/ NMSL.2019.03.02     | MK562363              | Karunarathna et al. 2019c    |
| *Cnemaspis nilgala*   | AMB7418/ NMSL                | KY038009              | Agarwal et al. 2017          |
|                      | AMB7436/ NMSL                | KY038010              | Agarwal et al. 2017          |
| *Cnemaspis pava*      | 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              | Karunarathna et al. 2019c    |
| *Cnemaspis phillipi*  | AA81/ NMSL                   | KY038001              | Agarwal et al. 2017          |
|                      | SSK17.0/ ADS220/ NMSL        | MK562343              | Karunarathna et al. 2019c    |
| *Cnemaspis podihuna*  | 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          |
| *Cnemaspis pulchra*   | SSK0.0/ ADS205               | MK562354              | Karunarathna et al. 2019c    |
|                      | SSK0.1/ ADS206               | MK562355              | Karunarathna et al. 2019c    |
|                      | SSK0.2/ ADS207               | MK562356              | Karunarathna et al. 2019c    |
|                      | AAAO/ NMSL                   | KY038007              | Agarwal et al. 2017          |
| *Cnemaspis rajakarunai* | SSK004                  | MW594285              | This study                   |
|                      | SSK005                      | MW594286              | This study                   |
|                      | SSK006                      | MW594287              | This study                   |
| *Cnemaspis rammalensis* | SSK027                 | MW594288              | This study                   |
|                      | SSK029                      | MW594289              | This study                   |
| *Cnemaspis retigalensis* | AMB7448/ NMSL             | KY037982              | Agarwal et al. 2017          |
| *Cnemaspis samanalaensis* | AMB7505/ NMSL          | KY037983              | Agarwal et al. 2017          |
| *Cnemaspis scalpensis* | SSK25.0/ ADS219            | MK562344              | Karunarathna et al. 2019c    |
|                      | WHT7268/ NMSL                | KY038008              | Agarwal et al. 2017          |
| *Cnemaspis shevaroyensis* | AK204                  | MK792468              | Khandekar et al. 2019        |
|                      | AK205                      | MK792469              | Khandekar et al. 2019        |
| *Cnemaspis silvula*   | AA88/ NMSL                  | KY037984              | Agarwal et al. 2017          |
| *Cnemaspis sp. 1 (Sri Lanka)* | AA17/ NMSL             | KY037989              | Agarwal et al. 2017          |
| *Cnemaspis sp. 3 (Sri Lanka)* | AMB7508/ NMSL         | KY037991              | Agarwal et al. 2017          |
| *Cnemaspis sp. 4 (Sri Lanka)* | AMB7529/ NMSL         | KY037992              | Agarwal et al. 2017          |
| *Cnemaspis sp. 6 (India)* | SB048                   | KY037995              | Agarwal et al. 2017          |
| *Cnemaspis sp. 7 (India)* | JB239                   | KY037996              | Agarwal et al. 2017          |
| *Cnemaspis sp. 9 (Sri Lanka)* | 47A/ NMSL             | KY038011              | Agarwal et al. 2017          |
| *Cnemaspis sp. 11 (India)* | SB151                  | KY038013              | Agarwal et al. 2017          |
| *Cnemaspis sp. (India)* | G349                      | MK792490              | Khandekar et al. 2019        |
| *Cnemaspis sp. (India)* | VG407                     | MK792487              | Khandekar et al. 2019        |
| *Cnemaspis sp. (India)* | VG408                     | MK792488              | Khandekar et al. 2019        |
| *Cnemaspis thackerayi* | CES G143                  | MK792471              | Khandekar et al. 2019        |
| *Cnemaspis upendrai*  | AA83                      | KY037986              | Agarwal et al. 2017          |
|                      | AA12                       | KY037987              | Agarwal et al. 2017          |
|                      | AMB7488                    | KY037988              | Agarwal et al. 2017          |
|                      | SSK24.0/ ADS213            | MK562345              | Karunarathna et al. 2019c    |
| *Cnemaspis yercaudensis* | AK280                  | MK792472              | Khandekar et al. 2019        |
|                      | G133                       | MK792473              | Khandekar et al. 2019        |