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A new insular species of Rock Gecko (*Cnemaspis* Boulenger) from Pulau Langkawi, Kedah, Peninsular Malaysia

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Abstract

A new, diminutive species of Rock Gecko *Cnemaspis mahsuriae* **sp. nov.** of the *affinis* group, is described from Gunung Raya on Pulau Langkawi, Kedah, Peninsular Malaysia and is differentiated from all other species in the *affinis* group by having a unique combination of characters including a maximum SVL of 36.6 mm; keeled subtibials and ventrals; 21–24 paravertebral tubercles; no tubercles in the lateral caudal furrows; caudal tubercles not encircling tail; no precloacal pores; 23–26 subdigital lamellae on the fourth toe; no white ocelli in the shoulder region; no yellow postscapular band; and faint yellow bars on the flanks. *Cnemaspis mahsuriae* **sp. nov.** is a forest-dwelling species living in close sympatry or paraptry with the insular endemic *C. roticanai* Grismer & Chan. The Langkawi Archipelago harbors a unique mix of Malaysian and Indochinese taxa and the frequency of new discoveries from this group of islands is increasing.

Key words: *Cnemaspis,* Mashuri, Pulau Langkawi, Malaysia, new species, systematics

Introduction

Pulau Langkawi lies 35 km off the northwestern coast of the Thai-Malay Peninsula on the border between Thailand and Malaysia (Fig. 1). This unique geopolitical position is mirrored by its location within the Kangar-Pattani biogeographical transition zone that demarcates a climatic hinge between Malay-type evergreen rainforest and Thai-Burmese wet seasonal evergreen rainforest (Van Steenis 1950; Wikramanayake *et al.* 2000; Woofruff 2003). As such, Pulau Langkawi and its 106 satellite islands harbor a unique and rich amalgam of Indochinese and Sundaic taxa found nowhere else on the Thai-Malay Peninsula. This is especially true for its herpetofauna whose collective phylogenetic affinities are not confined to one side of the transition zone or the other (e.g. Grismer 2008a, 2011; Grismer & Norhayati 2008; Grismer *et al.* 2006, 2012, 2014, 2015). This, coupled with the topographical and environmental complexity of Pulau Langkawi contributes to its diversity of amphibians and reptiles manifesting a wide range of adaptive types whose numbers continue to grow (Grismer *et al.* 2015). To this, we add a new species of a small Rock Gecko (genus *Cnemaspis* Boulenger) represented by six specimens collected at 400–600 m in elevation on a northwest facing slope of Gunung Raya, the island's highest and centrally located mountain. We have determined that this new population represents a separate lineage of the *affinis* group (*sensu* Grismer *et al.* 2014) in that they bear the diagnostic characters of having a SVL ranging from 36.5–65.0 mm; 7–13

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supralabials; 7–11 infralabials; keeled ventral scales; 0–10 pore-bearing precloacal scales; 18–34 paravertebral tubercles; tubercles on the flanks; a lateral row of caudal tubercles; keeled subtibials and subcaudals; no median row of enlarged subcaudal scales; 1–5 postcloacal tubercles; no enlarged femoral or subtibial scales; no enlarged submetatarsal scales on the first toe; and 21–35 lamellae beneath the fourth toe. However, it also has a unique suite of character states separating it from all other species of the *affinis* group. Additionally, a molecular phylogeny derived from the mitochondrial gene ND2 and its flanking tRNAs place this population as being most closely related to the sister species *C. harimau* Chan, Grismer, Anuar, Quah, Muin, Savage, Grismer, Norhayati, Remegio & Greer from Gunung Jerai, Kedah and *C. affinis* (Stoliczka) from Pulau Pinang, Penang (Grismer *et al.* 2014). As such we describe this population as new species.

Material and methods

Molecular phylogenetic analysis. A dataset from the mitochondrial gene NADH dehydrogenase subunit 2 gene (ND2) and its flanking tRNA's (tRNAmet, tRNAtrp, tRNAala, tRNAasn, tRNAcys; 1335 bp in total) was constructed from 48 individuals comprising all 14 species of *affinis* group plus 15 individuals from all species of the closely related *argus* group (Grismer *et al.* 2014) which constituted the outgroup (Table 1). Total genomic DNA was isolated from liver or skeletal muscle from specimens stored in 95% ethanol using the Qiagen DNeasy™ tissue kit (Valencia, CA, USA). The ND2 gene was amplified using a double-stranded Polymerase Chain Reaction (PCR) under the following conditions: 1.0 µl genomic DNA, 1.0 µl light strand primer 1.0 µl heavy strand primer, 1.0 µl dinucleotide pairs, 2.0 µl 5x buffer, 1.0 MgCl 10x buffer, 0.18 µl Taq polymerase, and 7.5 µl H_2O. PCR reactions were executed on an Eppendorf Mastercycler gradient thermocycler under the following conditions: initial denaturation at 95°C for 2 min, followed by a second denaturation at 95°C for 35 s, annealing at 47–52°C for 35 s, followed by a cycle extension at 72°C for 35 s, for 33–35 cycles (see Table 2 for details). All PCR products were visualized on a 1 % agarose gel electrophoresis. Successful targeted PCR products were vacuum purified using MANU 30 PCR Millipore plates and purified products were resuspended in DNAgrade water. Purified PCR products were sequenced using the ABI Big-Dye Terminator v3.1 Cycle Sequencing Kit in an ABI GeneAmp PCR 9700 thermal cycler. Cycle sequencing reactions were purified with Sephadex G-50 Fine (GE Healthcare) and sequenced on an ABI 3730xl DNA Analyzer at the BYU DNA Sequencing Center. Primers used for amplification and sequencing are presented in Table 2. All sequences were edited in Geneious v5.5.6 (Drummond *et al.* 2011) and aligned by eye. MacClade v4.08 (Maddison & Maddison 2005) was used to check for stop codons and to ensure the correct amino acid read frame.

The phylogenetic analysis applied two model-based methods, Maximum Likelihood (ML) and Bayesian Inference (BI). The Bayesian Information Criterion (BIC) as implemented in IQ-TREE (Nguyen *et al.* 2015) was used to calculate the best-fit model of evolution for each codon position (Table 3). Maximum Likelihood analyses using IQ-TREE employed 1000 bootstrap pseudoreplicates via the ultrafast bootstrap approximation algorithm. The Bayesian analysis was carried out in MrBayes v3.2 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003) using default priors. Two simultaneous Markov Chain Monte Carlo (MCMC) runs were performed with four chains per run (three hot and one cold) using default priors. The analysis was run for 1.5 million generations, sampled every 1500 generations, and halted after the average standard deviation split frequency was below 0.01 and convergence was assumed. The first 25% of the trees were discarded as burnin using the sumt function. Nodes having ML bootstrap support values greater than 70 and BI posterior probabilities above 0.95 were considered significantly supported (Huelsenbeck *et al.* 2001; Wilcox *et al.* 2002).

Morphological analysis. Color pattern characters were taken from digital images of living specimens cataloged in the La Sierra University Digital Photo Collection (LSUDPC) and from living specimens in the field. The following measurements on the type series were taken with Mitutoyo dial calipers to the nearest 0.1 mm under a Nikon SMZ 1500 dissecting microscope on the left side of the body where appropriate: snout-vent length (SVL), taken from the tip of snout to the vent; tail length (TL), taken from the vent to the tip of the tail, original or regenerated; tail width (TW), taken at the base of the tail immediately posterior to the postcloacal swelling; forearm length (FL), taken on the dorsal surface from the posterior margin of the elbow while flexed 90 to the inflection of the flexed wrist; tibia length (TBL), taken on the ventral surface from the posterior surface of the knee while flexed 90 to the base of the heel; axilla to groin length (AG), taken from the posterior margin of the forelimb at its

TABLE 1. Specimens used for the molecular phylogenetic analyses. Voucher number abbreviations are as follows: HC, Herpetological Collection of the Universiti Kebangsaan Malaysia, Bangi, Selangor; LSUHC, La Sierra University Herpetological Collection; USMHC, Universiti Sains Malaysia Herpetological Collection at the Universiti Sains Malaysia, Penang, Malaysia. – Indicates missing data

Voucher number	Species	Locality	GenBank accession nos. for
LSUHC 6757	*Cnemaspis affinis*	Malaysia: Penang, Pulau Pinang	KM024684
LSUHC 6774	*Cnemaspis affinis*	Malaysia: Penang, Pulau Pinang	KM024681
LSUHC 6787	*Cnemaspis affinis*	Malaysia: Penang, Pulau Pinang	KM024682
LSUHC 6788	*Cnemaspis affinis*	Malaysia: Penang, Pulau Pinang	KM024683
LSUHC 6758	*Cnemaspis affinis*	Malaysia: Penang, Pulau Pinang	KM024685
LSUHC 6759	*Cnemaspis affinis*	Malaysia: Penang, Pulau Pinang	KM024686
LSUHC 8304	*Cnemaspis argus*	Malaysia: Terengganu, Gunung Lawit	KM024687
LSUHC 10834	*Cnemaspis argus*	Malaysia: Terengganu, Gunung Tebu	KM024688
LSUHC 10835	*Cnemaspis argus*	Malaysia: Terengganu, Gunung Tebu	KM024689
LSUHC 10858	*Cnemaspis argus*	Malaysia: Terengganu, Gunung Tebu	KM024690
LSUHC 10859	*Cnemaspis argus*	Malaysia: Terengganu, Gunung Tebu	KM024691
LSUHC 9070	*Cnemaspis bayuensis*	Malaysia: Kelantan, Kampung Bayu	KM024700
LSUHC 9071	*Cnemaspis bayuensis*	Malaysia: Kelantan, Kampung Bayu	KM024701
LSUHC 9072	*Cnemaspis bayuensis*	Malaysia: Kelantan, Kampung Bayu	KM024702
LSUHC 6562	*Cnemaspis flavigaster*	Malaysia: Selangor, Kepong	KM024717
LSUHC 8835	*Cnemaspis flavigaster*	Malaysia: Selangor, Kepong	KM024718
LSUHC 8836	*Cnemaspis flavigaster*	Malaysia: Selangor, Kepong	KM024719
LSUHC 10380	*Cnemaspis flavigaster*	Malaysia: Selangor, Ulu Gombak	KM024720
LSUHC 8079	*Cnemaspis flavolineata*	Malaysia: Pahang, Fraser's Hill, The Gap	KM024721
LSUHC 9969	*Cnemaspis grismeri*	Malaysia: Perak, Lenggong	KM024722
LSUHC 9970	*Cnemaspis grismeri*	Malaysia: Perak, Lenggong	KM024723
LSUHC 9730	*Cnemaspis grismeri*	Malaysia: Perak, Lenggong	KM024724
LSUHC 9732	*Cnemaspis grismeri*	Malaysia: Perak, Lenggong	KM024725
LSUHC 9733	*Cnemaspis grismeri*	Malaysia: Perak, Lenggong	KM024726
LSUHC 9358a	*Cnemaspis hangus*	Malaysia: Pahang, Bukit Hangus	KM024727
LSUHC 9358b	*Cnemaspis hangus*	Malaysia: Pahang, Bukit Hangus	KM024728
HC 0225	*Cnemaspis hangus*	Malaysia: Pahang, Bukit Hangus	KM024729
LSUHC 9665	*Cnemaspis harimau*	Malaysia: Kedah, Gunung Jerai	KM024730
LSUHC 9667	*Cnemaspis harimau*	Malaysia: Kedah, Gunung Jerai	KM024731

……continued on the next page

TABLE 1. (Continued)

Voucher number	Species	Locality	GenBank accession nos. for
LSUHC 9668	*Cnemaspis harimau*	Malaysia: Kedah, Gunung Jerai	KM024732
LSUHC 9054	*Cnemaspis karsticola*	Malaysia: Kelantan, Gunung Reng	KM024736
LSUHC 9055	*Cnemaspis karsticola*	Malaysia: Kelantan, Gunung Reng	KM024737
LSUHC 11828	*Cnemaspis mahsuriae* sp. nov.	Malaysia: Kedah, Pulau Langkawi, Gunung Raya	KT250633
LSUHC 11829	*Cnemaspis mahsuriae* sp. nov.	Malaysia: Kedah, Pulau Langkawi, Gunung Raya	KT250634
LSUHC 8853	*Cnemaspis mcguirei*	Malaysia: Perak, Bukit Larut	KM024751
LSUHC 8854	*Cnemaspis mcguirei*	Malaysia: Perak, Bukit Larut	KM024752
LSUHC 8855	*Cnemaspis mcguirei*	Malaysia: Perak, Bukit Larut	KM024753
USMHC 1347	*Cnemaspis narathiwatensis*	Malaysia: Perak, Belum-Temengor, Sungai Enam	KM024762
USMHC 1348	*Cnemaspis narathiwatensis*	Malaysia: Perak, Belum-Temengor, Sungai Enam	KM024763
USMHC 1349	*Cnemaspis narathiwatensis*	Malaysia: Perak, Belum-Temengor, Sungai Enam	KM024764
USMHC 1350	*Cnemaspis narathiwatensis*	Malaysia: Perak, Belum-Temengor, Sungai Enam	KM024765
LSUHC 8699	*Cnemaspis perhentianensis*	Malaysia: Terengganu, Pulau Perhentian Besar	KM024820
LSUHC 8700	*Cnemaspis perhentianensis*	Malaysia: Terengganu, Pulau Perhentian Besar	KM024821
LSUHC 9060	*Cnemaspis perhentianensis*	Malaysia: Terengganu, Pulau Perhentian Besar	KM024822
LSUHC 9412	*Cnemaspis perhentianensis*	Malaysia: Terengganu, Pulau Perhentian Besar	KM024823
LSUHC 9145	*Cnemaspis pseudomcguirei*	Malaysia: Perak, Bukit Larut	KM024824
LSUHC 9146	*Cnemaspis pseudomcguirei*	Malaysia: Perak, Bukit Larut	KM024825
LSUHC 9147	*Cnemaspis pseudomcguirei*	Malaysia: Perak, Bukit Larut	KM024826
LSUHC 11015	*Cnemaspis selamatkanmerapoh*	Malaysia: Pahang, Merapoh, Gua Gunting	KM024832
LSUHC 11016	*Cnemaspis selamatkanmerapoh*	Malaysia: Pahang, Merapoh, Gua Gunting	KM024833
LSUHC 6773	*Cnemaspis shahruli*	Malaysia: Kedah, Pulau Pinang	KM024834
LSUHC 9163	*Cnemaspis shahruli*	Malaysia: Penang, Pulau Jerejak	KM024835
LSUHC 9586	*Cnemaspis shahruli*	Malaysia: Kedah, Sungai Sedim	KM024836
LSUHC 9613	*Cnemaspis shahruli*	Malaysia: Penang, Pulau Jerejak	KM024837
LSUHC 10375	*Cnemaspis shahruli*	Malaysia: Kedah, Pulau Pinang	–
LSUHC 11089	*Cnemaspis stongensis*	Malaysia: Kelantan, Gunung Stong, Kem Baha	KM024840
LSUHC 11090	*Cnemaspis stongensis*	Malaysia: Kelantan, Gunung Stong, Kem Baha	KM024841
LSUHC 11091	*Cnemaspis stongensis*	Malaysia: Kelantan, Gunung Stong, Kem Baha	KM024842
LSUHC 5314	*Cnemaspis stongensis*.	Indonesia: Riau Province, Pulau Natuna Besar	KM024843
LSUHC 9160	*Cnemaspis temiah*	Malaysia: Pahang, Cameron Highlands, Tanah Rata	KM024849
LSUHC 9739	*Cnemaspis temiah*	Malaysia: Pahang, Cameron Highlands, Tanah Rata	KM024850
LSUHC 9816	*Cnemaspis temiah*	Malaysia: Pahang, Cameron Highlands, Tanah Rata	KM024851

insertion point on the body to the anterior margin of the hind limb at its insertion point on the body; head length (HL), the distance from the posterior margin of the retroarticular process of the lower jaw to the tip of the snout; head width (HW), measured at the angle of the jaws; head depth (HD), the maximum height of head from the occiput to the throat; eye diameter (ED), the greatest horizontal diameter of the eyeball; eye to ear distance (EE), measured from the anterior edge of the ear opening to the posterior edge of the eyeball; eye to snout distance (ES), measured from anteriormost margin of the eyeball to the tip of snout; eye to nostril distance (EN), measured from the anteriormost margin of the eyeball to the posterior margin of the external nares; inner orbital distance (IO), the width of the frontal bone at the level of the anterior edges of the orbit; ear length (EL), the greatest vertical distance of the ear opening; and internarial distance (IN), measured between the medial margins of the nares across the rostrum. Additional character states evaluated were numbers of supralabial and infralabial scales counted from below the middle of the orbit to the rostral and mental scales, respectively; the texture of the scales on the anterior margin of the forearm; the number of paravertebral tubercles between limb insertions counted in a straight line immediately left of the vertebral column (where applicable); the presence or absence of a row of enlarged, widely spaced, tubercles along the ventrolateral edge of the body (flank) between the limb insertions; the degree of tuberculation (*i.e.*, strong, moderate, weak) and arrangement (i.e., random or linear) of the dorsal body tubercles; the number of subdigital lamellae beneath the fourth toe counted from the base of the first phalanx to the claw; the distribution of transverse and granular subdigital lamellae on the fourth toe; the total number of precloacal pores, their orientation and shape; the number of precloacal scales lacking pores separating the left and right series of pore-bearing precloacal scales; the degree and arrangement of body and tail tuberculation; the relative size and morphology of the subcaudal scales, subtibial scales, and submetatarsal scales beneath the first metatarsal; and the number of postcloacal tubercles on each side of the tail base. Caudal tubercles were counted as follows: paravertebral row—the dorsal row adjacent to the middorsal, caudal furrow; dorsolateral row—the row between the paravertebral row and the lateral, caudal furrow on the dorsolateral margin of the tail; lateral row—the row immediately below the lateral, caudal furrow; and ventrolateral row—the row below the lateral row on the ventrolateral margin of the tail below the lateral caudal furrow. When present, this row is usually restricted to the anterior 25% (or less) of the tail. Occasionally there may be a row of tubercles within the lateral, caudal furrow. These and 10 color pattern characters were evaluated and are presented in Table 3 for all species of the *affinis* group.

TABLE 2. Primers used for amplification and sequencing. (int)=internal used for sequencing only; cyc/temp= number of cycles/annealing temperature.

Gene	Primer name	Primer reference	Sequence	cyc/temp
ND2	L4437b	(Macey & Schulte, 1999)	5'-AAGCAGTTGGGCCCATACC-3'	33/48
	L5002	(Macey & Schulte, 1999)	5'-AACCAAACCCAACTACGAAAAAT-3'	
	CYRTINTF1(int)	(Siler *et al.*, 2010)	5'-TAGCCYTCTCYTCYATYGCCC-3'	
	CYRTINTR1(int)	(Siler *et al.*, 2010)	5'-ATTGTKAGDGTRGCYAGGSTKGG-3'	

TABLE 3. Selected and applied models of molecular evolution for data partitions of the ND2 gene determined by the BIC for the Bayesian analysis and Maximum Likelihood analyses.

Bayesian analyses	Models selected	Models applied
1st pos	TN+I+G4	GTR+I+Γ
2nd pos	TN+I+G4	GTR+I+Γ
3rd pos	TN+I+G4	GTR+I+Γ
tRNAs	K3Pu+G4	HKY+I+Γ
Maximum Likelihood analyses		
1st pos	TN+I+G4	TN+I+G4
2nd pos	TN+I+G4	TN+I+G4
3rd pos	TN+I+G4	TN+I+G4
tRNAs	K3Pu+G4	K3Pu+G4

Institutional abbreviations are LSUHC for the La Sierra University Herpetological Collection, La Sierra University, Riverside, California, USA and LRCUKM for the Langkawi Research Center, Universiti Kebanngsaan Malaysia, Pulau Langkawi, Kedah, Peninsular Malaysia.

Results

The phylogenetic analyses indicate analysis that the Pulau Langkawi population is embedded within the *affinis* group (Fig. 2) and thus supports the morphological analysis. Additionally, it strongly supports (1.00/100) the new population as being most closely related to the sister species *C. harimau* and *C. affinis* from the west coast of Peninsular Malaysia (Fig.1). Given these relationships, and the fact that this new population bears a unique suite of morphological and color pattern character states that separate it from all other *affinis* group species, it is described below as the new species:

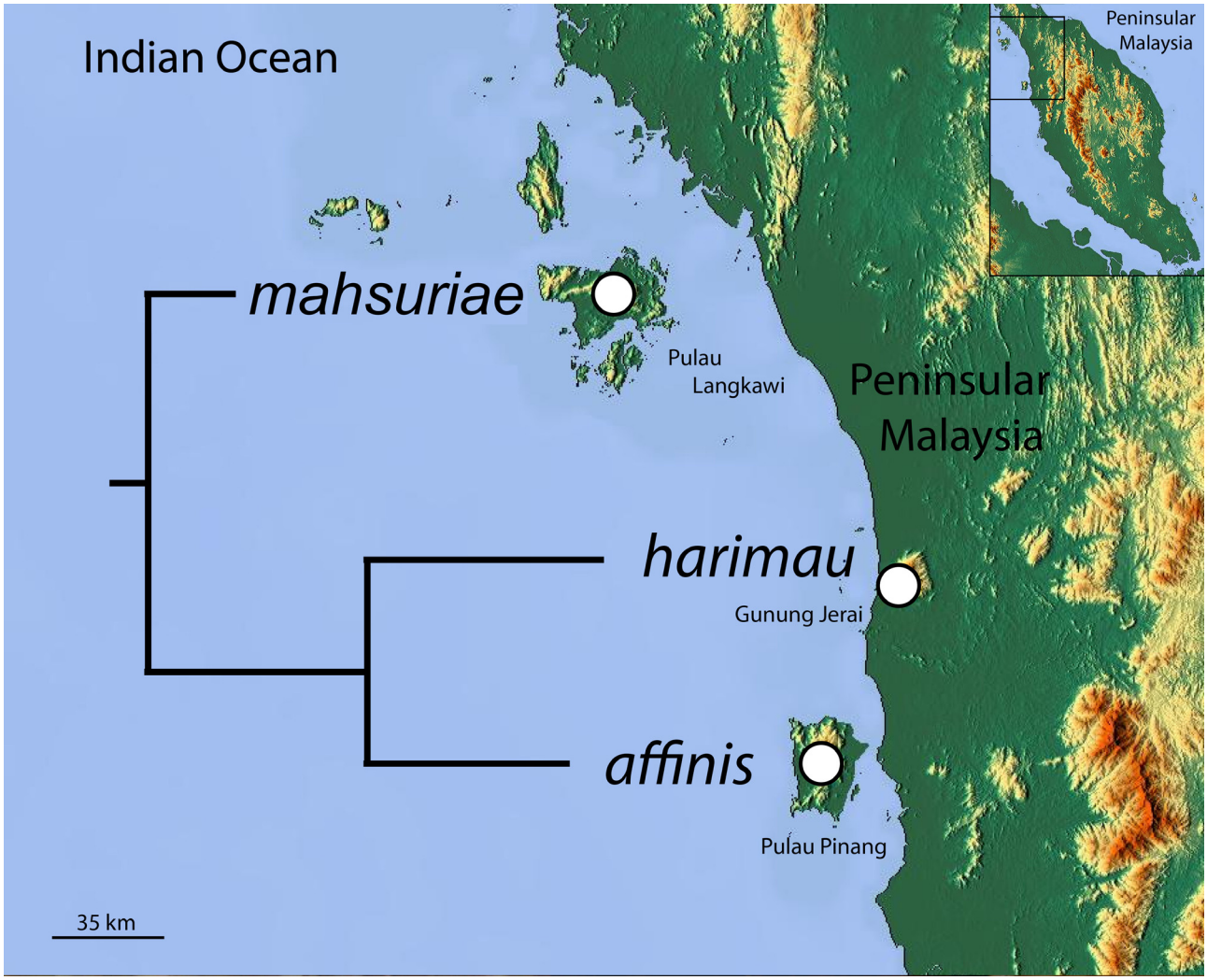

FIGURE 1. Distribution and relationships of *Cnemaspis mahsuriae* **sp. nov.**, *C. harimau,* and *C. affinis* along the northwest coast of Peninsular Malaysia. Branch lengths do not represent genetic distance.

***Cnemaspis mahsuriae* sp. nov.**
Mashuri's Rock Gecko
Figs. 3, 4

Holotype. Adult male (LSUHC 11828) collected on 24 August 2014 at 1900 hrs by L. L. Grismer, P. L. Wood, Jr.,

E. S. H. Quah, Jessika Vazquez at 400 m in elevation from a northwest facing slope on Gunung Raya, Pulau Langkawi, Kedah, Peninsular Malaysia (0451.715 N, 10047.993 E).

Paratypes. The paratypes were all collected from along the road to the summit of Gunung Raya on Gunung Raya. LSUHC 11829 bears the same data as the holotype. LRCUKM 0098–99 were collected on 19 March 2014 at 503m asl (0622.905 N 09948.030 E) and 657 m (0622.665 N 09949.278 E), respectively. LRCUKM 0101 was collected 20 March 2014 at 503 m (0622.905 N 09948.030 E) and LRCUKM 0104 was collected on 21 March 2014 at 657 m (0622.665 N 09949.278 E). LRCUKM 098–99, 0101, 0104 were collected by Ehwan, N.

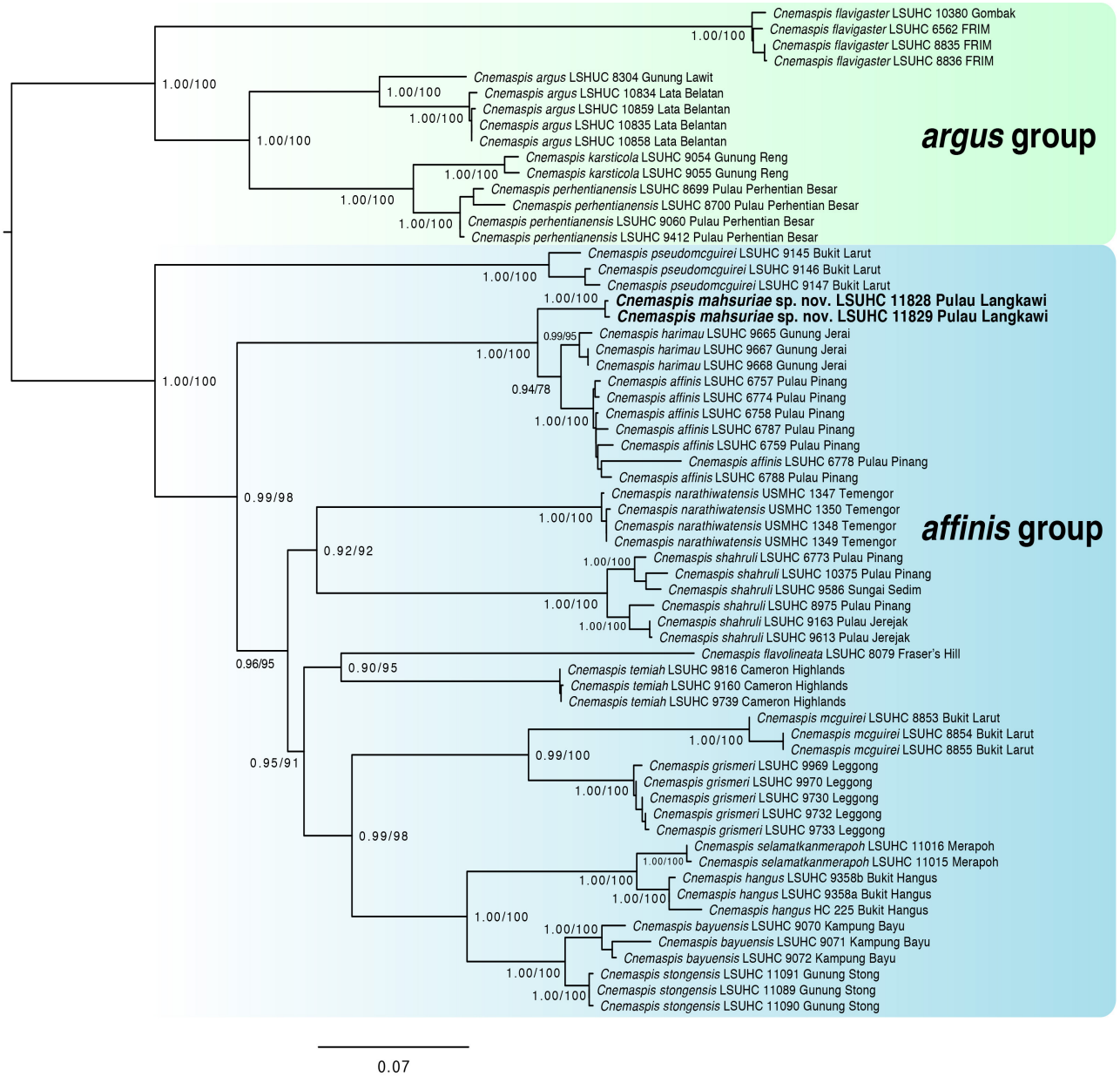

FIGURE 2. A phylogram representing the relationships of the species of the *affinis* group. The tree is a Maximum Likelihood topology (-ln L 11709.6074) with Bayesian posterior probabilities and Maximum Likelihood values, respectively.

Diagnosis. *Cnemaspis mahsuriae* **sp. nov.** differs from all other species of *Cnemaspis* in the *affinis* group in having the unique combination of a maximum SVL of 36.6 mm; keeled subtibials and ventrals; semi-linearly arranged body tubercles; 21–24 paravertebral tubercles; no tubercles on lower flanks; no tubercles in lateral caudal furrow; ventrolateral caudal tubercles absent; lateral row of caudal tubercles present; caudal tubercles not encircling tail; two postcloacal tubercles; no precloacal pores; 23–26 subdigital lamellae on fourth toe; dorsal color pattern sexually dimorphic; no white ocelli in shoulder region; no large, black, round spots on nape; no yellow

postscapular band; faint yellow bars on flanks; no white, dorsal, caudal tubercles or distinct black and white caudal bands; and all ventral surfaces (except for subcaudal region) beige not yellow. These differences are summarized across all *affinis* group species in Table 4.

Description of holotype. Adult male; SVL 36.6 mm; head oblong in dorsal profile, moderate in size (HL/SVL 0.27), somewhat narrow (HW/SVL 0.17), flattened (HD/HL 0.42), distinct from neck; snout short (ES/HL 0.45), slightly concave in lateral profile; postnasal region constricted medially, flat; scales of rostrum keeled, raised, larger than conical scales on occiput; weak, supraorbital ridges; no frontorostral sulcus; canthus rostralis nearly absent, smoothly rounded; eye large (ED/HL 0.21); extra-brillar, fringe scales largest anteriorly; pupil round; ear opening oval, taller than wide; rostral slightly concave, dorsal 80% divided by longitudinal groove; rostral bordered posteriorly by supranasals and one small, azygous scale and laterally by first supralabials; 8,9 (R,L) slightly raised supralabials tapering posteriorly; 7,8 (R,L) infralabials, decreasing in size posteriorly; nostrils elliptical, oriented dorsoposteriorly; bordered posteriorly by small, granular, postnasal scales; mental large, triangular, concave, bordered posteriorly by three postmentals; gular and throat scales raised, weakly keeled, conical.

FIGURE 3. Upper left: Adult male *Cnemaspis harimau* (LSUDPC 6381) from Gunung Jerai, Kedah. Lower left: Adult male *C. affinis* (LSUDPC 9078) from Penang Hill, Pulau Pinang, Penang. Upper right: Adult male holotype of *C. mahsuriae* **sp. nov.** (LSUHC 11828) from Gunung Raya, Pulau Langkawi, Kedah. Lower right: Adult female paratype of *C. mahsuriae* **sp. nov.** (LSUHC 11829) from Gunung Raya, Pulau Langkawi, Kedah.

Body slender, elongate AG/SVL 0.45); small, keeled, dorsal scales equal in size throughout body, intermixed with several large, multicarinate tubercles more or less randomly arranged; tubercles extend from occiput to base of tail; no tubercles on flanks; pectoral and abdominal scales keeled, raised, slightly elongate, not larger posteriorly; abdominal scales slightly larger than dorsals; no pore-bearing, precloacal scales or precloacal depression; forelimbs moderately long, slender; dorsal scales raised, keeled; ventral scales of brachia smooth, raised, juxtaposed; scales beneath forearm smooth, subimbricate; palmar scales smooth, juxtaposed, raised; digits long with an inflected joint; claws recurved; subdigital lamellae unnotched; lamellae beneath first phalanges granular proximally, widened distally; lamellae beneath phalanx immediately following inflection granular, lamellae of distal phalanges wide; interdigital webbing absent; fingers increase in length from first to fourth with fourth and fifth equal in length; hind limbs slightly longer and thicker than forelimbs; dorsal scales raised, keeled, juxtaposed; scales of anterior margin of thigh keeled; ventral scales of thigh keeled; subtibial scales keeled, flat, imbricate, with no enlarged anterior row; plantar scales smooth, juxtaposed, raised; no enlarged submetatarsal scales beneath first metatarsal; digits elongate with an inflected jointed; claws recurved; subdigital lamellae unnotched; lamellae

beneath first phalanges granular proximally, widened distally; lamellae beneath phalanx immediately following inflection granular, lamellae of distal phalanges wide; interdigital webbing absent; toes increase in length from first to fourth with fourth and fifth equal in length; 26,24 (R,L) subdigital lamellae on fourth toe; caudal scales arranged in segmented whorls; caudal scales keeled, juxtaposed anteriorly; shallow, middorsal furrow; deeper, single, lateral furrow; no enlarged, median, subcaudal scales; subcaudals keeled; no median row of enlarged, keeled, subcaudal scales; transverse, tubercle rows do not encircle tail; caudal tubercles absent from lateral furrow; a (R,L) enlarged, postcloacal tubercles on lateral surface of hemipenal swellings at base of tail; posterior 50% of tail regenerated.

Coloration (Fig. 3). In life, dorsal ground color of head yellow, that of body, limbs and tail grey; top of head bearing small, black markings; thin, diffuse, black postorbital stripe; thin, yellow, postorbital stripes unite on nape to form a diffuse, broken, nuchal loop; dark markings on nape anterior to yellow stripe preceded by two yellowish spots; single, light, postscapular spot just dorsal to forelimb insertion highlighting a large tubercle; faint, paravertebral blotches extend from nape to base of tail where they transform into light bands; faint, yellow, transverse markings on flanks; dark, diffuse bands on limbs on limbs; original portion of tail bearing faint grey and beige bands; all ventral surfaces except subcaudal region beige with weak stippling; subcaudal region darkly mottled.

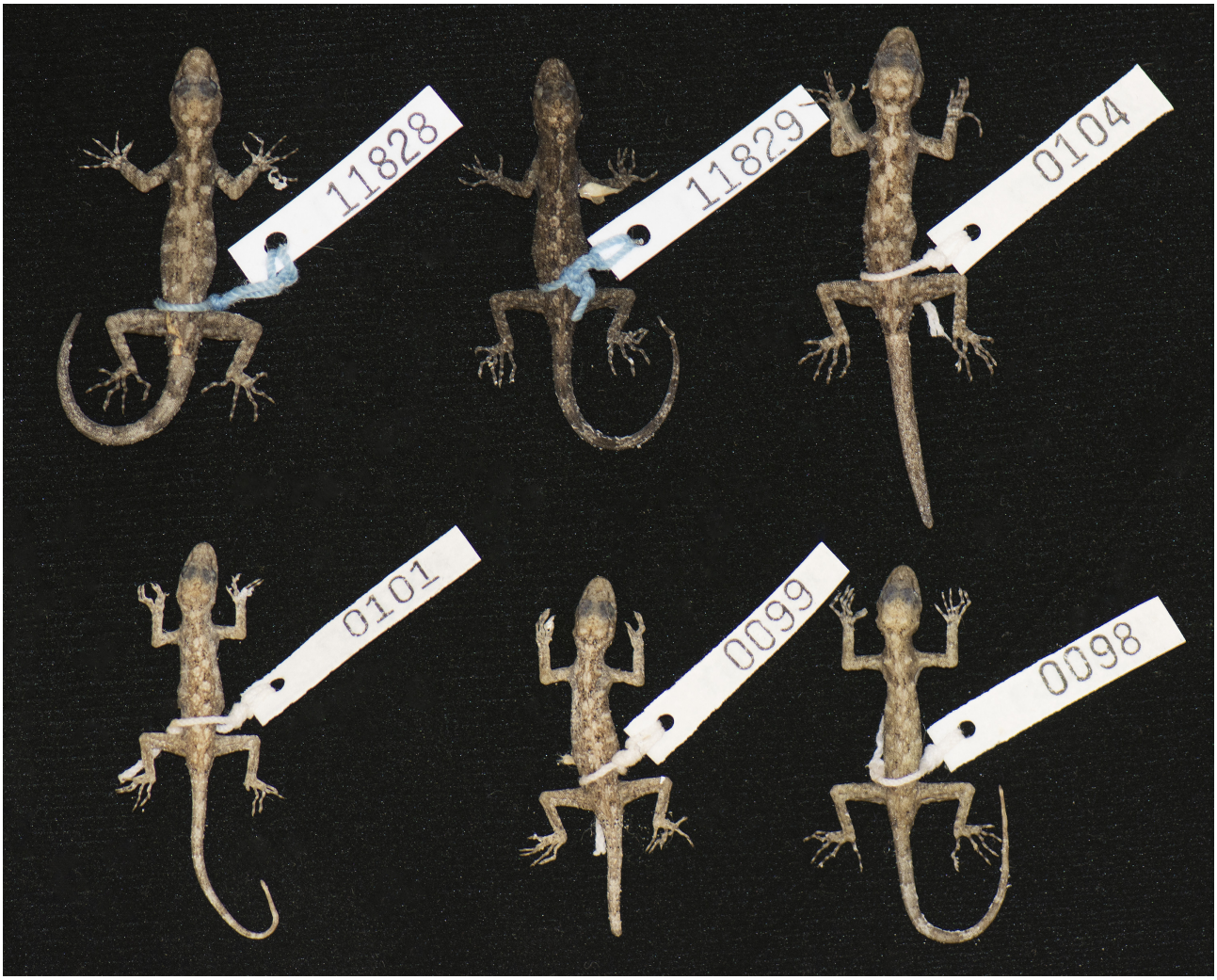

FIGURE 4. Type series of *Cnemaspis mahsuriae* **sp. nov.** from Gunung Raya, Pulau Langkawi, Kedah. Catalog numbers match those in Table 5.

Variation. Paratypes approximate the holotype (LSUHC 11828) in general aspects of coloration and pattern (Figs. 3,4), the exception being that females lack the yellowish head and the yellowish bars on the flanks found in males. Paratype LRCUKM 98 has a broken tail. The dorsal tubercles of the holotype are generally more linear in arrangement than those tubercles of the paratypes. Paratype LRCUKM 104 has a regenerated tail covered in

granular, juxtaposed scales. All LRCUKM specimens have deep incisions along the entire abdomen as a result of liver tissue extractions. Selected body measurements and variation is squamation is presented in Table 5.

Distribution. *Cnemaspis mahsuriae* is known only from the type locality at the base of Gunung Raya, Pulau Langkawi, Kedah, Peninsular Malaysia (Fig. 1).

Natural history. *Cnemaspis mahuriae* **sp. nov.** is a scansorial species known only from hill dipterocarp forest from the mid-elevation region of Gunung Raya from approximately 400–600 m (Fig. 5). All LRCUKM specimens were collected from pitfall traps at 400 m in elevation indicating that this species spends a significant amount of time on the ground. Both males and females were collected from the traps ruling out the hypothesis that only females come down to the forest floor to lay eggs. The LSUHC specimens were observed abroad at night in the forest on the trunks of large (trunk width > 1 m) and small trees ranging as high as 1.5 m above the forest floor. Another specimen (not cataloged) was observed beneath a palm frond and another (not cataloged) was found on the tire of our van. Both were at 500 m in elevation. The larger, *C. roticanai* Grismer & Chan has been collected on the same slope face of Gunung Raya at 743 m in elevation (Grismer & Chan 2010) but was found to be in syntopy with *C. mahsuriae* **sp. nov.** at approximately 500 m.

FIGURE 5. Structure of the hill dipterocarp forest on Gunung Raya, Pulau Langkawi, Kedah in which *Cnemaspis mahsuriae* **sp. nov.** occurs.

Comparisons. *Cnemaspis mahsuriae* **sp. nov.** has numerous diagnostic scale and color pattern character states that separate it from all other species of the *affinis* group (see bolded character states in Table 4). The phylogeny indicates that *C. mahsuriae* **sp. nov.** is the basal species lineage of a monophyletic group containing it, *C. harimau,* and *C. affinis* (Figs. 1, 2, 3). From *C. harimau* and *C. affinis, C. mahsuriae* **sp. nov.** differs by having a smaller maximum SVL (36.6 mm versus 40.7 mm and 50.8 mm, respectively) and lacking precloacal pores, ocelli in the shoulder region and a yellow throat and gular region. *Cnemaspis mahsuriae* **sp. nov.** differs further from *C. harimau* in having 21–24 versus 18–28 paravertebral tubercles, lacking as opposed to having tubercles in the lateral caudal furrow, and lacking distinct black and white posterior caudal bands. *Cnemaspis mahsuriae* **sp. nov.** differs further from *C. affinis* in having 23–26 versus 28 or 29 subdigital lamellae on the fourth toe.

TABLE 4. Diagnostic morphological and color pattern characters (bold) separating *Cnemaspis mashuriae* **sp. nov.** from all other species of the affinis group.
w =weak; ant = anterior; post = posterior; / = data unavailable.

	***mashuriae* sp. nov.**	*harimau*	*affinis*	*pseudomcguirei*	*shahruli*	*temiah* sp. nov.	*flavolineata*	*hangus* sp. nov.	*selamatkammerapoh*	*stongensis* sp. nov.	*bayuensis*	*mcguirei*	*grismeri*	*narathiwatensis*
Maximum SVL	36.6	**40.7**	**50.8**	**42.5**	36.5	**46.7**	**39.2**	**50.5**	**43.4**	**49.3**	**46.1**	**65.0**	**50.6**	**53.2**
Ventral scales keeled (1) or smooth (0)	1	1	1	1	1	1	1	1	1	1	1	1	1	1
No. of precloacal pores	0	**4**	**5,6**	**1–5**	0	**5–7**	**5,6**	0	**1**	**5–8**	**5–9**	**5–10**	**8–10**	**3–6**
No. of paravertebral tubercles	21–24	**18–20**	20–28	23–32	19–23	22–27	23	22–24	**30**	**26–33**	23–30	**26–32**	27–32	28–34
Tubercles linearly arranged (1) or more random (0)	0,w	0	0	0	0	0,w	1	0	w	0	0	0	0	0
Tubercles present (1) or absent (0) on lower flanks	1	1	1	1	1	0,1	**0**	**w**	**w**	1	1	1	1	0,1
Lateral caudal furrows present (1) or absent (0)	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Caudal tubercles in lateral furrow (1) or not (0)	0	**1**	0	**1**	**1**	**1**	**1**	0, ant	0	0,ant	0	**1**	**1**	**1**
Ventrolateral caudal tubercles anteriorly (1) or not (0)	0	0	0	0	0	0	0	0	0	0,1	0	0	**1**	**1**
Lateral caudal tubercle row present (1) or absent (0)	1	1	1	ant	1	1	ant	1	1	ant	1	1	1	1
Caudal tubercles encircle tail (1) or not (0)	0	**1**	0	0	0	0	ant	0	0	0	0	0	0	0
No. of postcloacal tubercles in males	2	2,3	2	2,3	1–3	2,3	2	2	3	2,3	2	2–5	2,3	1–3
No. of 4th toe lamellae	23–26	25–30	**28,29**	23–26	21–30	22–26	23	**27–34**	**31–33**	**28–32**	**27–32**	**27–35**	25–31	24–30
Dorsal color pattern sexually dimorphic	yes	yes	yes	yes	yes	**no**	**no**	**no**	**no**	**no**	**no**	yes	yes	yes
Ocelli on shoulder	no	**yes**	**yes**	no	**yes**	no	no	no	no	no	no	**yes**	**yes**	**yes**
Large, black round spots on nape and anterior of body	no	no	no	no	no	no	**yes**	no	no	no	no	no	no	no
Yellow postscapular band	no	var	var	no	no	no	no	no	no	no	no	**yes**	**yes**	no
Yellow or white bars on flanks	yes	yes	yes	yes	**no**	**no**	**no**	**no**	**no**	yes	yes	yes	yes	yes
White, dorsal caudal tubercles	no	no	no	no	**yes**	no	no	no	no	no	no	no	no	no
Disticnt black and white caudal bands at least posteriorly	no	**yes**	no	no	var	no	no	no	no	**yes**	no	**yes**	**yes**	**yes**
Gular region yellow	no	**yes**	**yes**	no	**yes**	no	no	no	no	no	no	no	no	no
Throat yellow	no	**yes**	**yes**	no	**yes**	no	no	no	no	no	no	no	no	no
Pectoral region yellow	no	no	/	no	**yes**	no	no	no	no	no	no	no	no	no
Sample size	5	10	7	9	11	7	2	2	2	10	4	19	10	11

TABLE 5. Meristic and mensural character states of the type series of *Cnemaspis mahsuriae* **sp. nov.**

f = female; m = male; / = data unavaiable; H = holotype; P = paratype. Meristic abbreviations are listed in the Materials and Methods. All measurements are in milimeters.

	LSUHC 11828 (H)	LSUHC 11829 (P)	LRCUKM 98 (P)	LRCUKM 99 (P)	LRCUKM 101 (P)	LRCUKM 104 (P)
Supralabials	9	9	10	9	9	10
Infralabials	8	9	8	7	8	8
Ventral scales keeled (1) or smooth (0)	1	1	1	1	1	1
No. of precloacal pores	0	0	0	0	0	0
Precloacal pores continuous (1) or separated (0)	/	/	/	/	/	/
Precloacal pores elongate (1) or round (0)	/	/	/	/	/	/
No. of paravertebral tubercles	23	23	22	21	23	24
Tubercles linearly arranged (1) or more random (0)	1	0/1	0/1	0/1	0/1	0/1
Tubercles present (1) or absent (0) on lower flanks	0	0	0	0	0	0
Lateral caudal furrows present (1) or absent (0)	1	1	1	1	1	1
Caudal tubercles in lateral furrow (1) or not (0)	0	0	0	0	0	0
Ventrolateral caudal tubercles anteriorly (1) or not (0)	0	0	0	0	0	0
Lateral caudal tubercle row present (1) or absent (0)	1	1	1	1	1	1
Caudal tubercles restricted to a single paravertebral row on each side (1) or not (0)	0	0	0	0	0	0
Subcaudals keeled (1) or smooth (0)	1	1	1	1	1	1
Single median row of keeled subcaudals (1) or smooth (0)	0	0	0	0	0	0
Caudal tubercles encircle tail (1) or not (0)	0	0	0	0	0	0
Enlarged median subcaudal scale row (1) or not (0)	0	0	0	0	0	0
No. of postcloacal tubercles in males	2	/	/	/	/	/
Enlarged femoral scales present (1) or absent (0)	0	0	0	0	0	0
Shield-like subtibial scales present (1) or absent (0)	0	0	0	0	0	0
Subtibial scales keeled (1) or smooth (0)	1	1	1	1	1	1
Enlarged submetatarsal scales on 1st toe (1) or not (0)	0	0	0	0	0	0

…….continued on the next page

TABLE 5. (Continued)

	LSUHC 11828 (H)	LSUHC 11829 (P)	LRCUKM 98 (P)	LRCUKM 99 (P)	LRCUKM 101 (P)	LRCUKM 104 (P)
No. of 4th toe lamellae	26	23	26	25	25	26
SVL	36.6	32.1	31.2	29.5	27.5	35.6
TL	38	42	55	16.2	32.7	28.1
TW	4.1	3.7	3.3	3.3	3	3.9
FL	6.2	5.6	5	4.9	4.4	5.8
TBL	6.9	6.6	6.5	5.8	5.4	7
AG	16.6	14	13.6	13.2	10.3	15.5
HL	9.9	9.5	18.6	8.2	7.8	9.8
HW	6.3	5.7	5.3	5.1	4.8	6.2
HD	4.2	3.4	3.5	3.2	3	4.2
ED	2.1	1.9	2	1.7	1.8	2.1
EE	3.1	2.3	2.4	2.3	2.3	2.9
ES	4.5	4.0	4.1	4	3.5	4.5
EN	3.3	2.9	3.2	3	2.7	3.3
IO	2.6	1.9	2.1	2.1	1.9	2.6
EL	0.8	0.7	0.9	0.8	0.5	1.2
IN	1	0.9	0.9	0.8	0.9	0.8
Sex	m	f	f	m	m	m

Etymology. The specific epithet *mahsuriae* is a patronym honoring the legendary woman Mahsuri Binti Pandak Mayah who lived on Pulau Langkawi during the early 1800s. Her renown beauty helped to usher in her marriage to the warrior Wan Darus but it also engendered jealously in the wife of the village chief who falsely accused Mahsuri of adultery while her husband was away at war. As punishment, Mahsuri was tied to a tree and stabbed to death with her family kris and while dying she placed a curse on the island for seven generations. A tomb honoring Mahsuri rests below the type locality on Gunung Raya.

Discussion

Cnemaspis mahsuriae **sp. nov.** is the third species of *Cnemaspis* to be described from the Langkawi Archipelago. All three species are distantly related to one another, have varied geographical origins (Grismer *et al.* 2014), and at this point, are presumed to be insular endemics. *Cnemaspis monochorum* Grismer, Norhayati, Chan, Belabut, Muin, Wood & Grismer is a member of the Pattani clade centered in southern Thailand south of the Isthmus of Kra; *C. roticanai* belongs to the *siamensis* group (of the Northern Sunda clade) which occupies the northern two-thirds of the Thai-Malay Peninsula; and *C. mahsuriae* **sp. nov.** belongs to the *affinis* group (of the Northern Sunda clade) which occupies the northern two-thirds of Peninsular Malaysia (Grismer *et al.* 2014). The varied pattern of geographic origins of these three distantly related endemic Rock Geckos belies the unique geographical position of the Langkawi Archipelago along a major biogeographical transition zone. The monophyly of the three upland species *C. mahsuriae* **sp. nov.**, *C. harimau* and *C. affinis* attests to the relatively recent geographical union of upland forests along the west coast of Peninsular Malaysia during the cooler temperatures of glacial maxima which are now generally restricted to upland areas (Fig. 1).

The discovery of *Cnemaspis mahsuriae* **sp. nov.** from Gunung Raya is the third new record for lizards reported within the last year, the other two being *Bronchocela rayaensis* Grismer, Wood, Cheol, Quah, Anuar, Ehwan & Sites and *Scincella melanosticta* (Boulenger) (Grismer *et al.* 2015). To this we add *Cyrtodactylus brevipalmatus* (Smith) (LRCUKM 90) and *Eutropis novemcarinata* (Anderson) (LRCUKM 96) which were collected by Ehwan Ngadi at the type locality of *C. mahsuriae* **sp. nov.** *Cyrtodactylus brevipalmatus* also represents a new record for Peninsular Malaysia (Grismer 2008b, 2011). These new island records and the new species reported here should underscore the need for continued field studies in the Langkawi Archipelago and generate new concerns to insure that the forests on the slopes of Gunung Raya remain intact.

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