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A new species of Mud Snake (Serpentes, Homalopsidae, *Gyiophis* Murphy & Voris, 2014) from Myanmar with a first molecular phylogenetic assessment of the genus

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Abstract

A newly discovered species of homalopsid snake from the genus *Gyiophis* Murphy & Voris is described from the lowlands of Mawlamyine District in Mon state, southeastern Myanmar. *Gyiophis salweenensis* sp. nov. is presumed to be closely related to *G. maculosa* Blanford and *G. vorisi* Murphy based on the similarities in pholidosis and patterning but can be separated from *G. maculosa* by the shape of its first three dorsal scale rows that are square, ventral scale pattern that lacks a central spot, and a faint stripe on dorsal scale rows 1–4. It can be further distinguished from *G. vorisi* by its lower number of ventral scales (129 vs. 142–152), lower number of subcaudals (30/29 vs. 41–58), narrow rostral scale, and having more rows of spots on the dorsum (four vs. three). A preliminary molecular analysis using 1050 base pairs of cytochrome b (cytb) recovered *G. salweenensis* sp. nov. as the sister species to the Chinese Mud Snake (*Myrophis chinensis*). *G. maculosa* and *G. vorisi* were unavailable for the analysis. The discovery of *G. salweenensis* sp. nov. highlights the need for more surveys into the herpetological diversity of eastern Myanmar which remains very much underestimated.

Key words: phylogeny, *Enhydryis*, homalopsid, conservation, endemic biodiversity, Burma

Introduction

At the turn of the 19th century, Myanmar proved a treasure trove of herpetological discoveries with many new species of reptiles and amphibians being collected and described by early explorers and naturalists including a number of interesting snake species such as *Azemiops fea* Boulenger, 1888, *Ahaetulla fronticinta* (Günther, 1858), *Bungarus magnimaculatus* Walls & Evans, 1901, and *Cylindrophis burmanus* Smith, 1943. More recent herpetological research in Myanmar has continued to discover additional new species of snakes such as *Lycodon zawi* Slowinski, Pawar, Win, Thin, Gyi, Oo & Tun, 2001, *Naja mandalayensis* Slowinski & Wüster, 2000, *Pareas vindumi* Vogel, 2015 and *Python kyaiktiyo* Zug, Gotte & Jacobs, 2011.

Currently, approximately 176 species of snakes have been recorded from Myanmar (Uetz *et al.* 2016) and one of the families recorded are the mud snakes Homalopsidae. Snakes of the family homalopsidae have been widely studied since the 1970s but careful taxonomic reappraisal of various species groups have resulted in the continued discovery of new species (Gyi 1970; Murphy *et al.* 2012a, b; Murphy & Voris 2014). To date 11 species of homalopsid snakes have been reported from Myanmar, namely *Bitia hydroides* Gray, 1842, *Cantoria violacea*

Girard, 1858, *Cerberus rhynchops* (Schneider, 1799), *Enhydris enhydris* (Schneider, 1799), *Ferania sieboldii* (Schlegel, 1837), *Fordonia leucobalia* (Schlegel, 1837), *Gerarda prevostiana* (Eydoux & Gervais, 1837), *Gyiophis maculosa* (Blandford, 1879), *G. vorisi* (Murphy, 2007b), *Homalopsis semizonata* Blyth, 1855 and *Hypsiscopus plumbea* (Boie, 1827) (Murphy & Voris 2014). A recent herpetological survey in Myanmar resulted in the collection of a single individual of homalopsid snake that we determined belonged to the genus *Gyiophis* owing to its lack of rostral appendages and having ventral scales wider than dorsal scales; nasals in contact; smooth dorsal scales; 25 dorsal scale rows at mid-body; no horizontally divided supralabials; and the first upper labial in contact with the loreal (Murphy & Voris 2014)—character states that diagnose *Gyiophis* from all other homalopsid genera. However, this specimen differed from the two other species known from Myanmar, *G. maculosa* and *G. vorisi*, by a suite of unique morphological and colour pattern characters. We therefore consider it a new species and describe it below. The specimen was added to the molecular phylogenetic dataset of Kumar *et al.* (2012).

Material and methods

Morphological analysis. Morphological and colour pattern data were taken from the specimen collected near Sanpel Cave, Mon State, Myanmar and compared with the data reported for the neotype of *G. maculosa* and the type series of *G. vorisi* (Murphy 2007b: Table 1). Scale counts and scale nomenclature follow Murphy (2007b) and Murphy & Voris (2014). All body measurements were made to the nearest millimeter. The number of ventral scales was counted according to Dowling (1951). The terminal scute (anal plate) was not included in the number of ventrals. Dorsal scale row counts are given at one head length behind the head, at mid-body (i.e., at the level of the ventral scale corresponding to one-half of the total number of ventrals), and at one head length anterior to the vent. We considered chin shields as those scales that had more than one-half their length below a supralabial. The values for paired head scales are listed in left/right order. Character abbreviations are adapted from Grismer *et al.* (2014) and Murphy (2007b) and include SVL—Snout-vent length (mm), TaL—tail length (mm), TL—total length (mm), ASR—dorsal scale rows at neck, MSR—dorsal scale rows at mid-body, PSR—dorsal scale rows before vent, VEN—number of ventral plates, SC—number of subcaudal scales, cloacal plate single or divided, L—presence of loreal scales, SL—number of supralabials, SL/Eye—numbers of supralabials entering the orbit, Larg SL—largest supralabial, IL—number of infralabials, IL/1st chin shield—number of infralabials in contact with the anterior chin shield, PreOc—number of preoculars, and PostOc—number of postoculars. The museum abbreviation LSUHC refers to La Sierra University Herpetological Collection, La Sierra University, Riverside, California, USA.

Molecular analysis. Sequence data from a 1,050 base pair fragment of the cytochrome *b* gene (*cyt b*) was obtained from specimen LSUHC 12960. Outgroup samples included 23 specimens from Kumar *et al.* (2012) comprising 22 species downloaded from GenBank. The new sequence used in this study is deposited in GenBank (Accession number KY471646).

Mitochondrial DNA was isolated from liver tissue stored in 95% ethanol and extracted using the animal tissue protocol provided by the Qiagen DNeasy™ tissue kit (Valencia, CA, USA). The gene cytochrome *b* (*cyt b*) was amplified using a double stranded Polymerase Chain Reaction (PCR) under the following conditions: 1.0 µl genomic DNA (concentration 10–30 µg of DNA), 1.0 µl light strand primer (concentration 10 µM) HI4910 5′–GACCTGTGATMTGAAAACCAAYC–3′ (Burbrink 2000), 1.0 µl heavy strand primer (concentration 10 µM) THRSN2 5′–CTTTGGTTTACAAGAACAATGCT–3′ (Burbrink 2000), 1.0 µl deoxynucleotide pairs (1.5 µM), 2.0 µl 5x buffer (1.5 µM), 1.0 MgCl 10x buffer (1.5 µM), 0.18 µl Promega Taq polymerase (5u/µl), and µl H₂O. PCR reactions were completed using an Eppendorf Mastercycler gradient thermocycler with the following reaction conditions: initial denaturation at 95°C for 2 min, second denaturation at 95°C for 35 s, annealing at 50°C for 35 s followed by an extension cycle at 72°C for 95 s + 4 s per cycle for 32 cycles. PCR products were visualized using gel electrophoresis using a 1.0% agarose gel. PCR products that had a distinct band with the correct molecular weight based on the standardized ladder were purified using vacuum MANU 30 PCR Millipore plates and sequenced through the Brigham Young University Sequencing Center (Provo, UT, USA). Sequences were analyzed from both the 3′ and 5′ ends independently to ensure congruence between the sequences. Both the forward and the reverse sequences were assembled and edited in Geneious™ version v6.1.8 (Kearse *et al.* 2012). Sequences were aligned by eye and to ensure the correct amino acid reading frame Mesquite v3.02 (Maddison and Maddison 2015) was used to check for premature stop codons.

Phylogenetic analyses. Phylogenetic trees were constructed using Bayesian Inference (BI) and Maximum Likelihood (ML). In both, the data were partitioned by codon. The ML analysis was conducted using IQTREE software on the webserver (Trifinopoulos *et al.* 2016) with a model of molecular evolution estimated for each codon position (1st codon= TPM2u+G4, 2nd codon= TN+I+G4 3rd codon= TPM3+G4). To assess nodal support, 1000 bootstrap pseudoreplicates via the ultrafast bootstrap approximation algorithm (Minh *et al.* 2013) were employed. ML ultrafast bootstrap support values (ML) of 90 and above indicate well-supported nodes (Minh *et al.* 2013). The partitioned Bayesian (BI) analysis was implemented in MrBayes v3.2.6 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003) following the default priors using the closest model of molecular evolution estimated by IQTREE. Two simultaneous runs were performed with eight chains per run, seven hot and one cold. The analysis was run for 5,000,000 generations and sampled every 500 generations from the Markov Chain Monte Carlo (MCMC). The analysis was halted after the average standard deviation split frequency fell below 0.01. The first 25% of the trees were discarded as a burn-in. A consensus tree was computed from the two parallel using the sumt function in MrBayes. Nodes that had Bayesian posterior probabilities (BPP) of 0.95 or greater were considered well-supported (Huelsenbeck & Ronquist 2001; Wilcox *et al.* 2002). Nodal support values for all analyses are reported on the tree (BPP/ML).

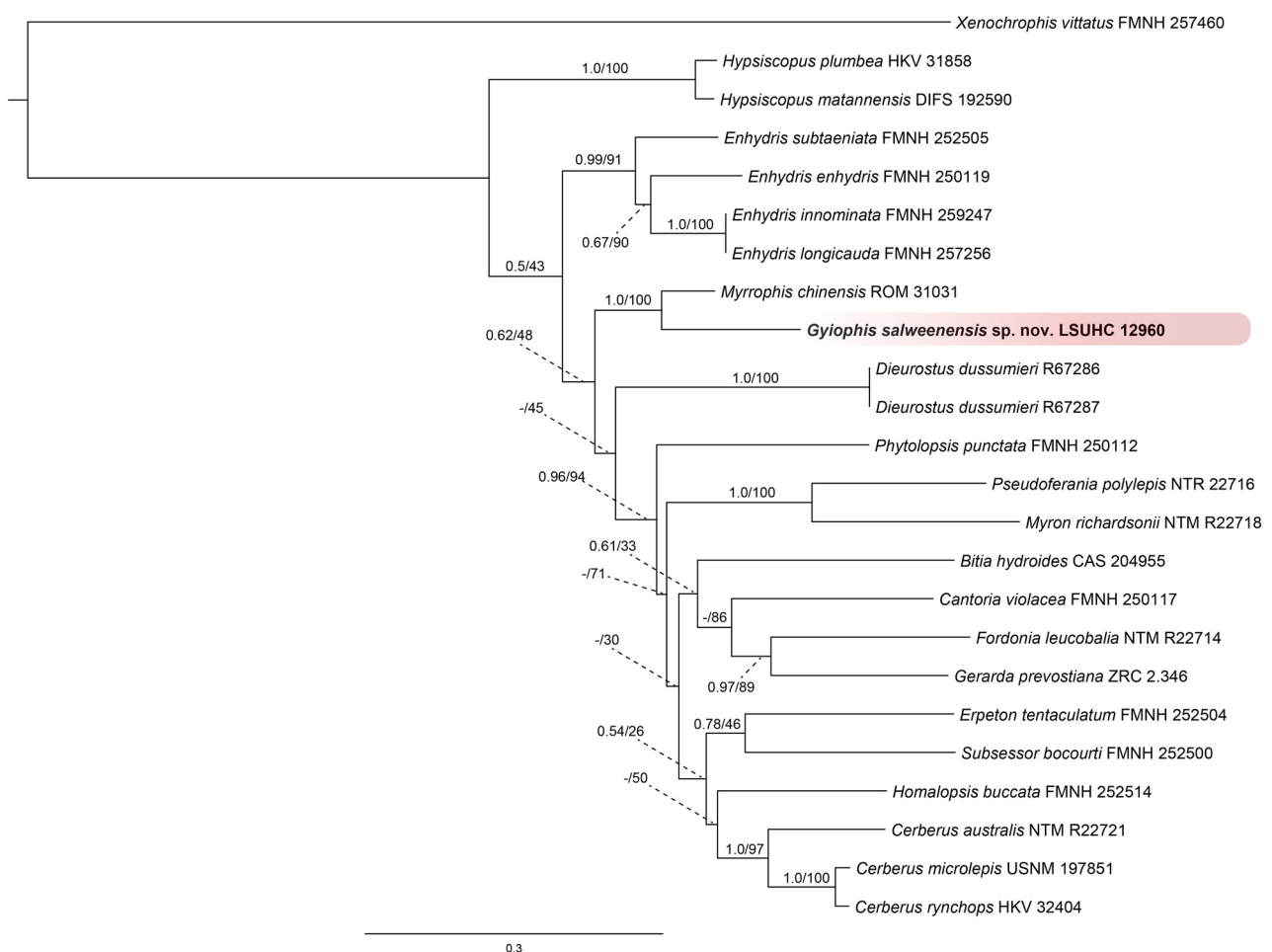


FIGURE 1. Maximum Likelihood tree of the family Homalopsidae Bonaparte, 1845 highlighting the phylogenetic position of *Gyiophis salweenensis* sp. nov. Bayesian posterior probabilities (BPP) and Maximum Likelihood (ML) bootstrap values (BPP/ML), respectively, are listed at the nodes.

Results

This preliminary molecular analysis contradicts the hypothesized phylogenetic placement of the genus *Gyiophis* in the South Asian homalopsid group along with *Ferania sieboldii*, *Dieurostus dussumieri* (Duméril, Bibron & Duméril, 1854) and *Mintonophis pakistanicus* (Mertens, 1959) based on morphology. Instead, *Gyiophis* is

recovered as sister to *Myrrophis chinensis* (Gray, 1842) of the South China group (Murphy & Voris 2014) with strong support (1.0/100: Fig. 1). Although there are no tissues available for the two other species (*G. maculosa* and *G. vorisi*), this new specimen differs from them by a suite of unique morphological and colour pattern characters. We therefore recognise it as the new species described below.

***Gyiophis salweenensis* sp. nov.**

Salween River Basin Mud Snake

Figs. 2–4.

Holotype. Adult female (LSUHC 12960) collected on 8 October 2016 by Myint Kyaw Thura, Thaw Zin, Evan S.H. Quah, L. Lee Grismer, Perry L. Wood, Jr., Marta S. Grismer, Matthew L. Murdoch and Htet Kyaw from close to Sanpel Cave, Mawlamyine, Mon State, Myanmar (N16°22.427, E97°46.388; 44 m in elevation).

Diagnosis. *Gyiophis salweenensis* sp. nov. is separated from all congeners by having a unique combination of the following characters: a narrow rostral scale; the first three dorsal scale rows square; 129 (female) ventral scales; 30/29 (female) paired subcaudals; a divided cloacal plate; eight or nine supralabials; 10 infralabials; a maximum total length of 416 mm; relative tail length ratio of 0.13; a ventral patterning lacking a central spot on each ventral scale; the presence of a faint stripe on the lower, dorsal scale rows; and four rows of dark spots on the dorsum (Table 1).

TABLE 1. Comparison of the scalation and colour pattern in *G. maculosa*, *G. vorisi* and *G. salweenensis* sp. nov. *data obtained from Murphy 2007b, – no data available.

Characteristics	<i>Gyiophis maculosa</i> * (N=1)	<i>Gyiophis vorisi</i> * (N=11)	<i>Gyiophis salweenensis</i> sp. nov. (N=1)
Scale rows on neck (ASR)	25	26–28	26
Scale rows at mid-body (MSR)	25	25	25
Scale rows near vent (PSR)	22	21–23	20
Scale shape in first 3 rows	Ovate	Square	Square
Supralabials	8	8	9/8
Ventral scales in males	-	147–152	-
Ventral scales in females	122	142–148	129
Subcaudal scales in males	-	51–58	-
Subcaudal scales in females	32/31	41–53	30/29
Central spot on each ventral	Present	None	None
Stripe on dorsal rows 2–4	Absent	Present	Present (Faint)
Number of rows of spots on the dorsum	5–6	3	4
Width of rostral scale	Narrow	Broad	Narrow

Description of holotype (Figs. 3–4). Head depressed, distinct from neck; snout short and rounded, rostrum tapers downwards; rostral scale pentagonal, nearly as broad as tall, visible from above; eye moderate in size, pupils rounded; nasals semi-divided with nasal groove contacting first supralabial, nare in center (on left side of snout is a small, aberrant, triangular scale positioned between rostral, nasal and first supralabial); internasal small, quadrangular, not in contact with loreal; loreal 1/1, quadrangular, contacting first three supralabials on right side and supralabials 1, 2 and 4 on left side; preocular 1/1; supraocular 1/1; postoculars 2/2; prefrontals 2, in broad contact with each other, frontal, internasal, loreals, preoculars, supraoculars, and posterior tip of nasals; frontal pentagonal, 1.4 times longer than supraocular; parietals elongate; temporal scale formula 1 + 2 + 3; supralabials 9/8, largest supralabial 7/6, smallest 3/8, supralabial entering orbit 5/4 (on left side of head there is fragmentation of supralabial scales with third supralabial being small and sandwiched beneath second and fourth supralabials (Fig. 4b); infralabials 10/10, seventh elongate, first four in contact with anterior chin shield; anterior pair of chin shields largest and rounded, second pair small; 26 ASR, 25 MSR, 20 PSR; scales of first three rows of dorsal scales square;

129 ventrals; cloacal plate divided; subcaudal scales 30/29. Body short, somewhat stocky; tail short; SVL 364 mm; TaL 52mm; TL 416mm. There is a puncture wound on the right side of the dorsum at the position of ventral 63.

Colouration in life (Figs. 2–4). The colour of each ventral and subcaudal scale is uniform cream with dark edging on the anterior right and left corners of each scale. These markings merge with the dark spot on the anterior half of each scale of the first dorsal scale row and some on the second row of dorsal scales to form a zig-zag stripe along the dorsoventral edge that runs the length of the body and tail. There are no central spots on the ventral scales except for ventrals 21, 54 and 55 that are extensions of the dark edgings of the corners of the scales. The chin and throat are cream and the infralabials, chin shields, and scales on the throat are edged in dark-grey. The posterior portion of dorsal scale rows one, two, three, and four form a faint cream stripe that is most prominent on the anterior portion on the body near the jaw and neck. The ground colour of the top of the head and the dorsum is greyish-brown. On dorsal scale rows 5–7 there are a series of large black spots 3–7 scales wide along the flanks and the anterior portion of the body near the neck. Some of these spots merge to form an irregularly shaped stripe. On the back are two rows of smaller black spots approximately 2–4 scales in width and usually on dorsal scale rows 11–14 and rows 15–17. Some single, darker scales are interspersed along the body on dorsal scale rows nine or 10. The tail is greyish brown with black spots. The head is speckled with small dark-grey spots with some larger spots; one on the frontal; another beneath the eye on the lower postocular and supralabials 4/5 and six. There is a broad dark-coloured streak across the anterior temporal, lower middle temporal, and the seventh and eighth supralabials; one at the corner of the jaw; and another two-scale wide streak on the crown from the posterior tip of the parietals extending posteriorly the length of five dorsal scales. The supralabials are cream and edged in dark-grey.

Distribution (Fig. 2). *Gyiophis salweenensis* **sp. nov.** is only known from the type locality near Sanpel Cave, Mon State, Myanmar. It is expected to be wider ranging throughout the Salween River Basin and found wherever appropriate habitat occurs.

Natural history (Fig. 5). The holotype was found at approximately 1930 hours crossing a narrow dirt road between flooded fields that we presume to be its natural habitat. The weather was overcast and it rained later that night. Many other species of homalopsids are semiaquatic and commonly found in streams, rivers, ponds, and flooded rice fields (Murphy 2007a; Stuebing *et al.* 2014). *Gyiophis salweenensis* **sp. nov.** is expected to share a similar life history and the valvular nostrils located dorsally on the snout indicate this species probably spends a large part of its life in the water. Homalopsid snakes such as *Enhydryis enhydryis*, *Homalopsis buccata* (Linnaeus, 1758) and *Hypsiglossus plumbeus* have been observed crawling on land and crossing roads during wet weather (Voris & Karns 1996; Lim & D’Rozario 2009; EQSH personal obs.) and the holotype of *G. salweenensis* **sp. nov.** could have been dispersing to a new area as well. The holotype also had a puncture wound on its back which might have come from an encounter with a predator such as a heron.

Etymology. The specific epithet *salweenensis* is in reference to area where the holotype was found which is close to the vicinity of the Salween River near the city of Mawlamyine. The suffix *ensis* is a Latin derivation meaning “from” or “inhabiting.” It renders the specific epithet an adjective that must be in grammatical accord with the gender of *Gyiophis*.

Comparison. *Gyiophis salweenensis* **sp. nov.** is distinguishable from *G. maculosa* by the shape of the dorsal scales of first three rows (square vs. ovate), the ventral scale pattern (absence of a central spot on each ventral scale vs. its presence), and a stripe running through the scales of the lower dorsal scale row (faint one vs. absent). It is further distinguished from *G. vorisi* by its lower number of ventrals (129 vs. 142–152), lower number of subcaudals (30/29 vs. 41–58), shape of the rostral scale (narrow vs. broad), and the number of rows of spots on the dorsum (four vs. three) (Table 1). It differs from the other species of homalopsids found in Myanmar by unique suite of characters presented in the key below.

Discussion

Although *Gyiophis salweenensis* **sp. nov.** has morphological similarities in common with *G. maculosa* and *G. vorisi*, it is found in a separate river basin. *Gyiophis maculosa* and *G. vorisi* are known from the Ayeyarwady River delta while *G. salweenensis* **sp. nov.** is found in the Salween River basin across the Gulf of Martaban (Fig. 2). At this point in time, genetic material is not available for the two other species necessary to infer their phylogenetic relationships to *G. salweenensis* **sp. nov.** but the widely separated, allopatric distribution of the latter along with the aforementioned differences in pholidosis and patterning lends support for them being different species.

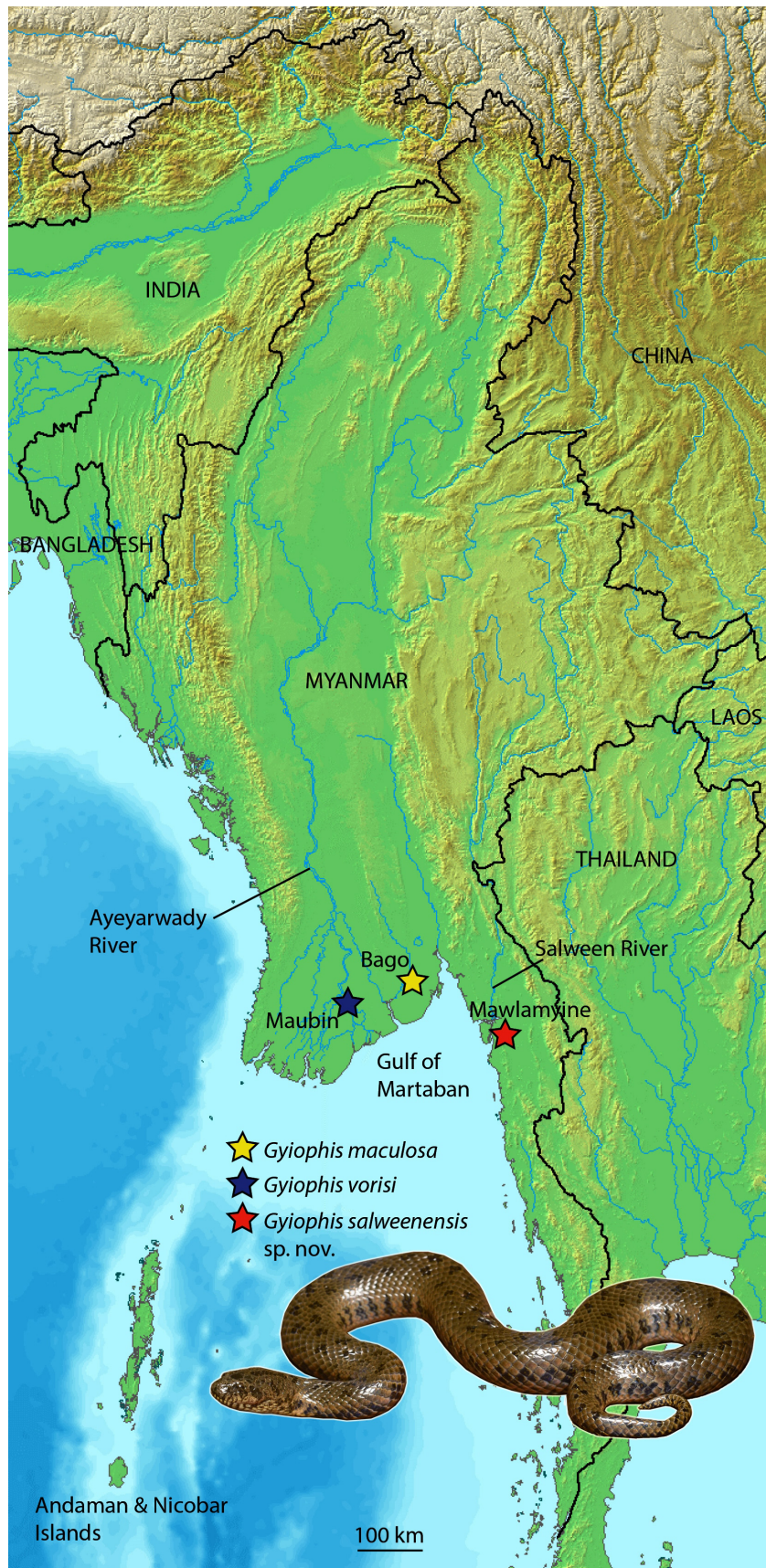


FIGURE 2. Distribution of *Gyiophis salweenensis* sp. nov. as well as *G. maculosa* and *G. vorisi* based on Murphy (2007b) in Myanmar.

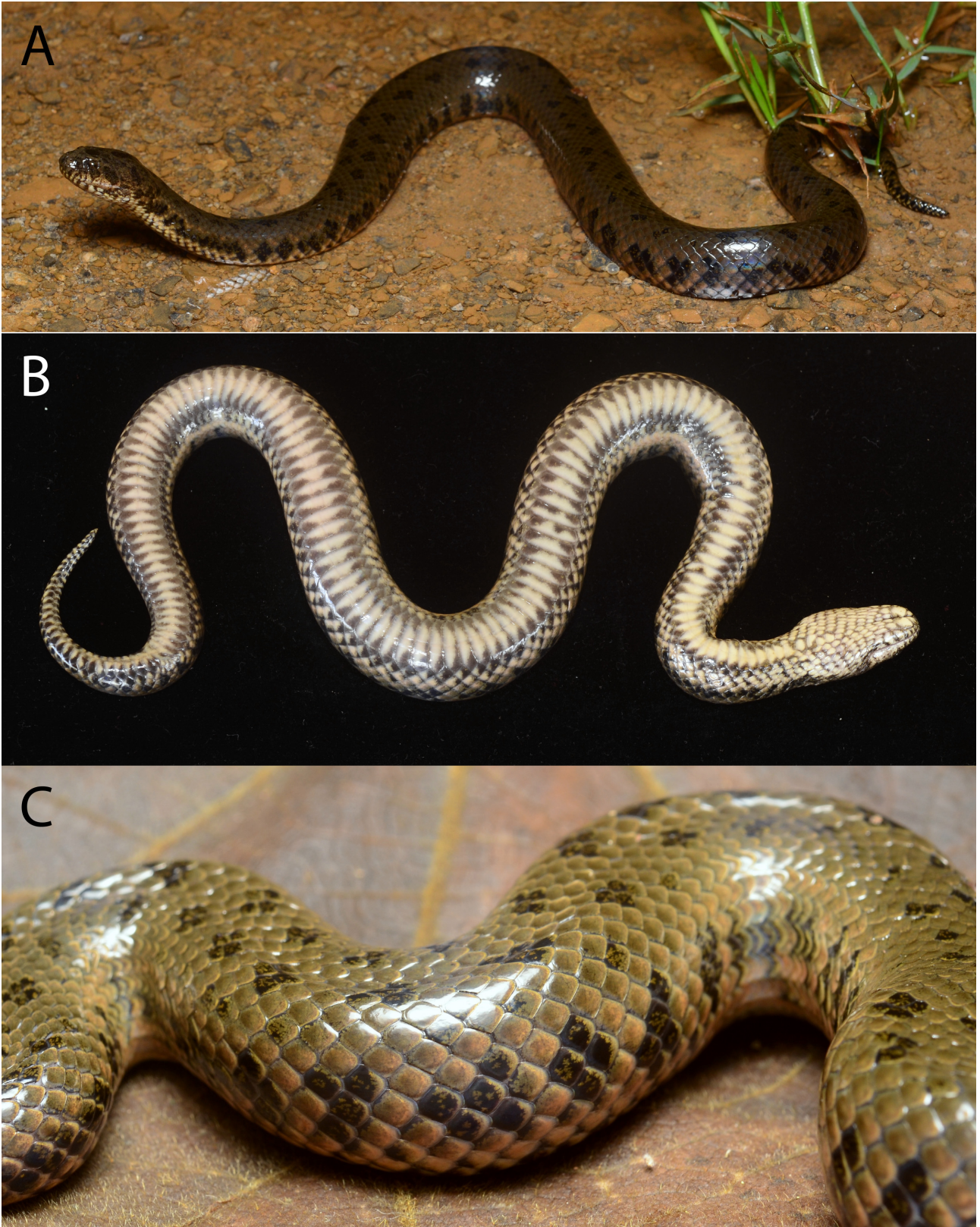


FIGURE 3. A: Holotype of *Gyiophis salweenensis* **sp. nov.** in life. B: Venter of the holotype of *Gyiophis salweenensis* **sp. nov.** C: Pattern on the dorsum of the holotype of *Gyiophis salweenensis* **sp. nov.** Photographs by Evan Quah.

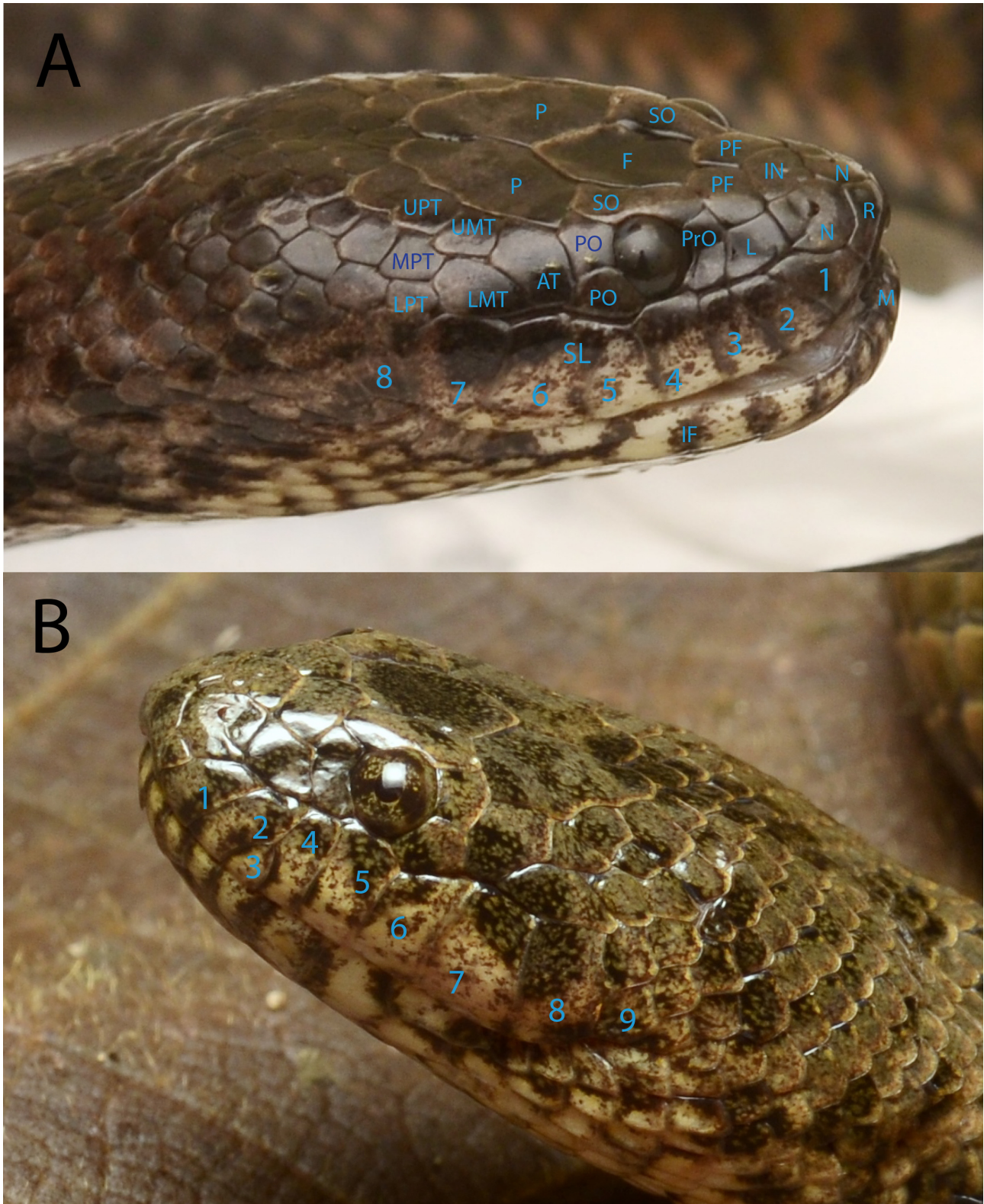


FIGURE 4. Position and number of supralabials and other head scales on the holotype of *Gyiophis salweenensis* **sp. nov.**, A: The right side of the head. B: The left side of the head. AT = anterior temporal; F = frontal; IF = infralabial; IN = internasal; L = loreal; LMT = lower middle temporal; LPT = lower posterior temporal; M = mental; MPT = middle posterior temporal; N = nasal; P = parietal; PF = prefrontal; PO = postocular; PrO = preocular; R = rostral; SL = supralabial; SO = supraocular; UMT = upper middle temporal; UPT = upper posterior temporal. Photographs by Evan Quah.



FIGURE 5. Flooded grassland habitat near where *Gyiophis salweenensis* **sp. nov.** was found. Photograph by Evan Quah.

This study also provides the first molecular phylogeny of the genus *Gyiophis* and places it in the homalopsid phylogeny. Based on morphology, Kumar *et al.* (2012) hypothesized that *Gyiophis* would be related to a group of seven other species they called the Asian coastal lineage; *Dieurostus dussumierii*, *Ferania sieboldii*, *Kualatahan pahangensis* (Tweedie, 1946), *Mintonophis pakistanicus*, *Myrrophis bennettii* (Gray, 1842), *M. chinensis* and *Sumatranus albomaculatus* (Duméril, Bibron & Duméril, 1854). Murphy and Voris (2014) refined the grouping and separated the species into a number of smaller units categorized by morphological similarities and geographic proximity. *Myrrophis bennettii* and *M. chinensis* are considered part of the South China group while *D. dussumierii*, *F. sieboldii*, *M. pakistanicus*, *G. maculosa* and *G. vorisi* were considered part of the South Asian group. *Sumatranus albomaculatus* was placed in the Sunda group with *Erpeton tentaculatus* Lacépède, 1801 and *Subessor bocourti* (Jan, 1865) while *K. pahangensis* is considered monotypic. We recovered *G. salweenensis* **sp. nov.** as the sister species of *M. chinensis*, thus contradicting the hypothesized placement of *Gyiophis* in the South Asian clade with *D. dussumierii*. This is not surprising given that both genera occur in continental Indochina with *Gyiophis* in Myanmar and *Myrrophis* in northeastern Indochina but it does have implications concerning their biogeography. Kumar *et al.* (2012) suggested that the Asian coastal lineage diverged and speciated following the coastline as sea levels fluctuated between glacial and interglacial periods. They hypothesized that the ancestor of *Myrrophis* and *Dieurostus* evolved in Indochina or the adjacent Sunda Shelf before spreading along the coastline west and southwards into Southeast Asia and then dispersing eastwards into Myanmar and the Indian subcontinent. However, the recovery of *G. salweenensis* **sp. nov.** as the sister species of *M. chinensis* suggest that there may have been more than one lineage that colonized the coastal areas of Southeast and Southern Asia. The ancestral species of the South China and South Asian groups probably evolved in Indochina as suggested by Kumar *et al.* (2012) and both dispersed along the coastline and possibly overland during periods of flooding. One branch spread east to produce *M. bennettii* and *M. chinensis* in southern China and northern Vietnam while another branch spread southwest to the deltas of Myanmar to diverge into members of the genus *Gyiophis*. The closely related *D. dussumierii* is derived from another lineage that spread further westward to colonise the Indian subcontinent and evolved separately. However, we acknowledge that this hypothesis needs testing and may be refined with the addition of genetic data from *Ferania sieboldii*, *Kualatahan pahangensis*, *Myrrophis bennettii* and *Sumatranus albomaculatus* of the proposed Asian coastal lineage from intervening areas.

The discovery of *G. salweenensis* **sp. nov.** adds to a growing number of new herpetological discoveries being made in Myanmar (Bauer 2002, 2003; Lee *et al.* 2015; Mahony 2009; McMahan & Zug 2007; Zug *et al.* 2006,

2007, 2011). This emphasizes the need for further efforts to explore more regions of Myanmar in order to more accurately assess its herpetological diversity that is still greatly underestimated. Myanmar has been trailing behind many of its neighbouring countries in terms of herpetological research but is beginning to be more actively investigated. Recent surveys have already discovered approximately 12 new species of *Cyrtodactylus*, two new species of *Hemidactylus* and three new species of *Hemiphyllodactylus* (Grismer *et al.* in prep).

A key to the Homalopsid species of Myanmar based on data from Murphy (2007b) and Murphy & Voris (2014)

1.	Nasals separated from each other by a single scale	2
-	Nasals in contact	.5
2.	Loreal present	3
-	Loreal absent, second pair of chin shields in contact with each other	<i>Fordonia leucobalia</i>
3.	More than 5 supralabials	4
-	5 supralabials, none entering orbit, light cross-bands on body	<i>Cantoria violacea</i>
4.	Ventrals keeled, exposed skin between dorsal scales, body with cross bands	<i>Bitia hydroides</i>
-	Ventrals not keeled, no exposed skin between dorsal scales, no cross-bands on body	<i>Gerarda prevostiana</i>
5.	Dorsal scales keeled	6
-	Dorsal scales smooth	.7
6.	Dorsal scales in 39–44 rows, three prefrontal scales, dorsal pattern of light greyish blotches that do not completely encircle darker brown body	<i>Homalopsis semizonata</i>
-	Dorsal scales in 25 (rarely 23) rows, two prefrontal scales, dorsal pattern of narrow dark, indistinct cross-bars on greyish body, largely coastal	<i>Cerberus rynchops</i>
7.	Dorsal scales in 19 rows at mid-body	<i>Hypsicopus plumbea</i>
-	Dorsal scales in 21 or more rows at mid-body	.8
8.	Two internasals	<i>Ferania sieboldii</i>
-	One internasal	.9
9.	Dorsum with longitudinal light brown, paravertebral stripes along the sides of the body	<i>Enhydryis enhydryis</i>
-	Dorsum grey to brown with rows of spots along the flanks and back	10
10.	Scale shape of first three dorsal scale rows ovate, central spot present on each ventral scale, and stripe on lower dorsal scale rows absent	<i>Gyiophis maculosa</i>
-	Scale shape of first three dorsal scale rows square, central spot on each ventral scale absent and stripe on lower dorsal scale rows present	.11
11.	Rostral scale broad, 142–148 ventrals in females, 41–58 subcaudals, 3 rows of spots on the dorsum	<i>Gyiophis vorisi</i>
-	Rostral scale narrow, 129 ventrals in female, 30/29 subcaudals in females, 4 rows of spots on the dorsum	<i>Gyiophis salweenensis</i> sp. nov.

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