



# Molecular phylogenetic analyses of lesser known colubrid snakes reveal a new species of *Herpetoreas* (Squamata: Colubridae: Natricinae), and new insights into the systematics of *Gongylosoma scriptum* and its allies from northeastern India

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**Abstract.** A new species of the genus *Herpetoreas* is described from Murlen National Park, Mizoram, northeastern India, based on morphological differences and molecular evidence inferred from the mitochondrial cytochrome b and 16S rRNA genes. The new taxon represents the seventh nominal species in the genus *Herpetoreas*, out of which three species, i.e., *H. pealii*, *H. platyceps* and *H. xenura*, have been recorded from northeastern India as well. An updated taxonomic key to the species of *Herpetoreas* is provided. Our phylogenetic reconstructions of selected natricine and colubrine snakes from Mizoram state, northeastern India, also contribute to the systematics and known distribution of the little known species *Gongylosoma scriptum*, and corroborate its taxonomic placement into the subfamily Colubrinae. Moreover, the first molecular based identifications for *Liopeltis stoliczkae* and *Sibynophis collaris* from Mizoram are presented.

Key words. Serpentes, *Amphiesma*, *Hebius*, *Herpetoreas* sp. n., *Liopeltis*, Mizoram, Murlen National Park, *Sibynophis*, taxonomy.

## Introduction

The taxonomy of the natricine snake genus *Amphiesma* sensu lato DUMÉRIL, BIBRON & DUMÉRIL, 1854 was recently revised by GUO et al. (2014), resulting in the revalidation of the genus *Herpetoreas* GÜNTHER, 1860 along with *Hebius* THOMPSON, 1913 and *Amphiesma* sensu stricto. The genus *Herpetoreas* currently comprises six nominal taxa, namely *H. burbrinki* GUO, ZHU, LIU, ZHANG, LI, HUANG & PYRON, 2014, *H. pealii* (SCLATER, 1891), *H. platyceps* (BLYTH, 1854), *H. sieboldii* GÜNTHER, 1860, *H. xenura* (WALL, 1907), and *H. tpser* REN, JIANG, HUANG, DAVID & LI, 2022; while the latter two genera contain 46 recognized species of *Hebius* and one species, *A. stolatum* DUMÉRIL, BIBRON & DUMÉRIL, 1854, respectively. Taxonomic studies of natricid snakes from the last decades have yielded the discovery of several new species of *Hebius* (see DAVID & DAS 2003, DAVID & VOGEL 2010, DAVID et al. 2007, GUO et al. 2014, LIU et al. 2018, PURKAYASTHA & DAVID 2019, ZHOU et al. 2019, ZIEGLER & LE 2006). However, numerous instances of misidentification or synonymous treatment of valid taxa have been afflicting members of these natricine snakes, of-

ten attributable to their morphological resemblance and high degree of intraspecific variability (LIU et al. 2018). Although the true diversity of this large and complex group remains poorly investigated, the existence of multiple cryptic lineages within these genera seems plausible because paraphyly among several taxa of these groups have been demonstrated in a few recent studies (GUO et al. 2014, PURKAYASTHA & DAVID 2019). Consequently, phylogenetic reconstructions based both upon morphological characters and mitochondrial (mt) cytochrome b (Cytb) and 16S rRNA (16S) genes have indicated that one of the studied specimens from Mizoram belongs to the genus *Herpetoreas*, but it could not be assigned to any of the described species. We consider this specimen to represent a new species, and thus formally describe it herein.

In this study, we also investigated the systematic status of the poorly known colubrid snake species *Gongylosoma scriptum* (THEOBALD, 1868). Currently, the genus *Gongylosoma* FITZINGER, 1843 accommodates five nominal species, namely *G. baliodeira* (BOIE, 1827), *G. scriptum* (THEOBALD, 1868), *G. nicobariensis* (STOLICZKA, 1870), *G. longicauda* (PETERS, 1871), and *G. mukutense* GRISMER, DAS & LEONG,

2003. Although it was speculated to be a genus closely related to *Liopeltis* based on morphology (e.g., GRISMER et al. 2003, LEVITON 1964, POYARKOV et al. 2019), there is no published evidence that would resolve the precise systematic position of this genus, and it thus remained *incertae sedis* as of now (UETZ et al. 2022). Nevertheless, *Gongylosoma scriptum* is one of the least known species among the congeners, and is the only *Gongylosoma* species known from India so far. Altogether, it is known from India (Mizoram) (LALREMSANGA et al. 2018), Cambodia (NEANG et al. 2015), Myanmar (DOWLING & JENNER 1988, THEOBALD 1868), and Thailand (GRISMER et al. 2003, INGER & COLWELL 1977, SMITH 1930). Earlier works suggest this species to be diurnal and secretive in its habits, as all specimens were encountered during the day, usually below the soil surface, under rocks, bushes and leaves, and sometimes exposed on leaf litter, rocks or soil next to forest paths in evergreen forest, semi-evergreen mixed with bamboo, tropical wet evergreen forest, and in montane sub-tropical forest at approximate altitudes between 200 and 1,072 m asl. (INGER & COLWELL 1977, LALREMSANGA et al. 2018, NEANG et al. 2015). In addition, the species is poorly studied and only few specimens are available in museum collections globally (LALREMSANGA et al. 2018). Therefore, we here attempt to fill some knowledge gaps for the genus as well as to provide new insights into the morphology, distributional records, and we reassess the phylogenetic status of *G. scriptum*. In addition, we provide molecular based identifications for morphologically allied species of *G. scriptum*, such as *Liopeltis stoliczkae* (SCLATER, 1891) and *Sibynophis collaris* (GRAY, 1853) based on mt 16S and Cytb gene sequences generated from new materials from Mizoram, northeastern India.

## Material and methods

### Sampling

Specimens analysed in this study were obtained during fieldwork carried out between 2018 and 2021 in the state of Mizoram, India. Collected specimens were euthanized with MS-222, following CONROY et al. (2009); liver tissues were subsequently recovered by means of dissections and stored in 95% ethanol for genetic analysis. Specimens were then fixed in 10% formalin, subsequently preserved in 70% ethanol, and deposited in the reptile section of the Departmental Museum of Zoology, Mizoram University. The sampling sites' geographical coordinates and altitudes were recorded using a Garmin Montana-650 GPS unit, and the map (Fig. 1) was produced using QGIS version 3.16.2.

### Morphology

Morphological measurements were taken with dial callipers accurate to 0.02 mm (Mitutoyo 505–671). Snout–vent (SVL), tail (TaL) and total lengths (TL) were taken to the nearest millimetre using a measuring tape. The following

morphometrics and meristics were taken: SVL; TaL; TL; HL, head length; HW, head width; HD, head depth; ED, eye diameter; E–Sn, eye to snout distance; E–Ns, eye to nostril distance; SW, snout width; INL, length of internarial scales; PFL, length of prefrontals; FL, length of frontal; PL, length of parietals; DSR, dorsal scale rows; PVe, pre-ventrals; Ve, ventrals; Sc, subcaudals; As, condition of anal scute; SL, supralabials; IL, infralabials; SLe, supralabials contacting the eye; AG, anterior genials; PG, posterior genials; Tem, temporals; PrO, preoculars; PoO, postoculars; and Lor, loreal. Ventral scales were counted following DOWLING (1951). Dorsal scales were counted at one head length posterior to the neck, at the midpoint of snout–vent length, and at one head length anterior to the As. Paired Sc were counted from immediately posterior to the anal scute to the tail tip, but excluding the terminal scute.

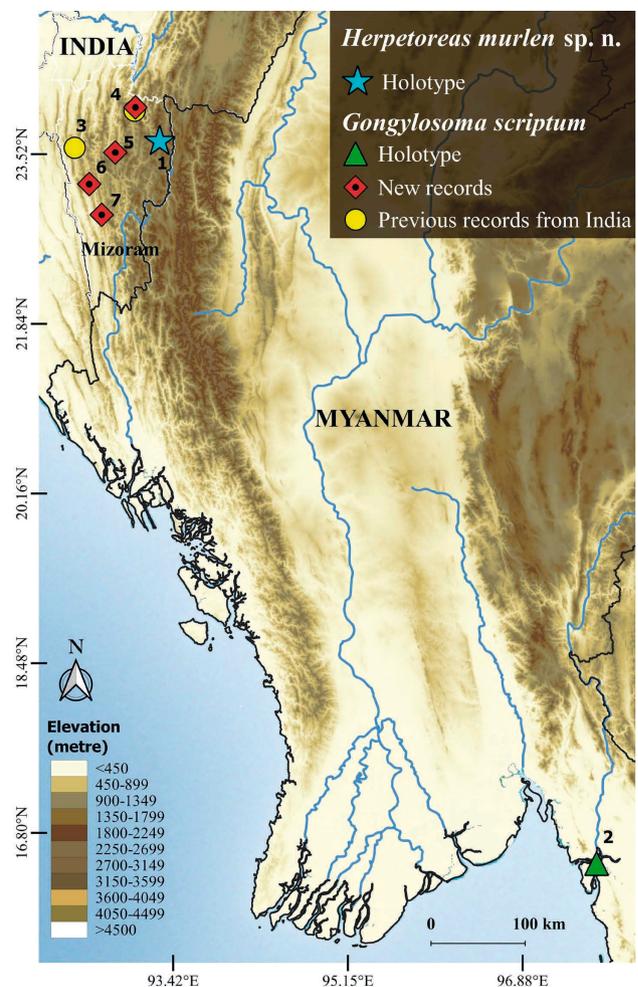


Figure 1. Digital topographic map of the Indo-Myanmar region: Type locality of *Herpetoreas murlen* sp. n. in the Murlen National Park, Mizoram, India (1); type locality of *Gongylosoma scriptum* at Mottama, Mon State, Myanmar (2); previous records of *G. scriptum* from India, at Saithah village (3) and Suangpuilawn village (4); new records (this study) at Suangpuilawn village (4), Baktawng village (5), Dampui village (6), and Vanhne village (7).

Table 1. Partitions and models of sequential evolutionary models used in the Bayesian Inference (BI) and Maximum Likelihood (ML) phylogenetic analyses.

Datasets	Partitions	Models	
		BI (PartitionFinder)	ML (ModelFinder)
Natricine	16S	GTR+I+G	TIM2+F+I+G4
	Codon 1 <sup>st</sup> pos of Cytb	TRN+I+G	TIM2+F+I+G4
	Codon 2 <sup>nd</sup> pos of Cytb	K81UF+I+G	TPM2u+F+I+G4
	Codon 3 <sup>rd</sup> pos of Cytb	TIM+G	TIM+F+G4
Colubrine	16S, Codon 1 <sup>st</sup> pos of Cytb	GTR+G	TIM2+F+I
	Codon 2 <sup>nd</sup> pos of Cytb	HKY+I	HKY+F+I
	Codon 3 <sup>rd</sup> pos of Cytb	TIM+G	TIM+F

### Museum acronyms

Abbreviations used for natural history collections are: AMNH, American Museum of Natural History (USA); BMNH, British Museum of Natural History (Great Britain); CAS, California Academy of Science (USA); CBC, Centre for Biodiversity Conservation (Cambodia); CHS, Collection Huang Song (China); DTU, Duy Tan University, Da Nang (Vietnam); DL, private catalogue of Ding Li (China); GP, private catalogue of Guo Peng (China); KU, Biodiversity Institute, University of Kansas (USA); KUZ, Kyoto University, Department of Zoology Museum (Japan); LSUHC, La Sierra University Herpetological Collection (USA); MNHN, Muséum national d'Histoire naturelle, Paris (France) MZMU, Departmental Museum of Zoology, Mizoram University (India); NCBS, National Centre for Biological Sciences (India); NCSM, North Carolina Museum of Natural Sciences (USA); NMBE, Naturhistorisches Museum Bern (Switzerland); NMW, Naturhistorisches Museum Wien (Austria); ROM, Royal Ontario Museum (Canada); WII, Wildlife Institute of India (India); YBU, Yibin University (China); ZFMK, Zoologisches Forschungsmuseum Alexander Koenig (Germany), ZMB, Zoologisches Museum für Naturkunde der Humboldt-Universität zu Berlin (Germany); ZMMU, Zoological Museum of Moscow (Russia); ZSM, Zoologische Staatssammlung München (Germany).

### Molecular analyses

Genomic DNA was extracted from the liver tissues using the QIAamp DNA Mini Kit following the manufacturer's protocol. The fragment of 16S was amplified using forward L02510 (PALUMBI 1996) and reverse H03063 primers (RASSMANN 1997) at thermal conditions of 95°C for 5 min., followed by 35 cycles of 95°C for 1 min., 50.3°C for 30 sec., 72°C for 1 min., and a final extension step at 72°C for 5 min.; and Cytb using forward and reverse primers (Snk) (DUBEY et al. 2009) at thermal conditions of 94°C for 3 min., followed by 35 cycles of 94°C for 30 sec., 49°C for 40 sec., 72°C for 30 sec., and a final extension at 72°C for 5 min. The amplified products were purified and se-

quenced using Sanger's dideoxy method at Barcode Bio-Sciences, Bangalore, India.

The datasets of natricine and colubrine snakes comprised the newly generated sequences of 16S and Cytb along with congeneric sequences and outgroups (*Amphiesma stolatum* for natricines; *Elaphe cantoris* for colubrines) obtained from the NCBI database (see Supplementary Material for sequences utilized). Both datasets were aligned with the MUSCLE algorithm (EDGAR 2004) using default parameters in MEGA X (KUMAR et al. 2018). Both datasets were concatenated in SequenceMatrix v1.7.8 (VAIDYA et al. 2011), and were partitioned by gene and by codon positions. PartitionFinder v2 (LANFEAR et al. 2016) was employed for selecting the best partitioning schemes and for evolutionary model searching under the Bayesian Information Criterion (Table 1). For both datasets, Bayesian Inference (BI) and Maximum Likelihood (ML) phylogenies were performed in Mr.Bayes v2.3.5 (RONQUIST et al. 2012) and in IQ-TREE (NGUYEN et al. 2015), respectively. In the BI analyses, four independent runs with one cold and three hot chains were conducted for 20 million generations and sampled every 5000 generations after discarding the first 25% of samples as burn-in. The trace plots generated by the MCMC runs were viewed in Tracer v1.7 (RAMBAUT et al. 2018). Since some of the nucleotide evolutionary models selected by PartitionFinder v2 (LANFEAR et al. 2016) were unavailable in IQ-TREE (NGUYEN et al. 2015), the ML analyses were performed using the previously selected partitioning schemes with the models selected under BIC scores by ModelFinder (KALYAANAMOORTHY et al. 2017) implemented in the IQ-TREE (NGUYEN et al. 2015) at 10,000 Ultrafast Bootstrap (UFB) (MINH et al. 2013). The uncorrected p-distances were estimated in MEGA X (KUMAR et al. 2018).

### Nomenclatural acts

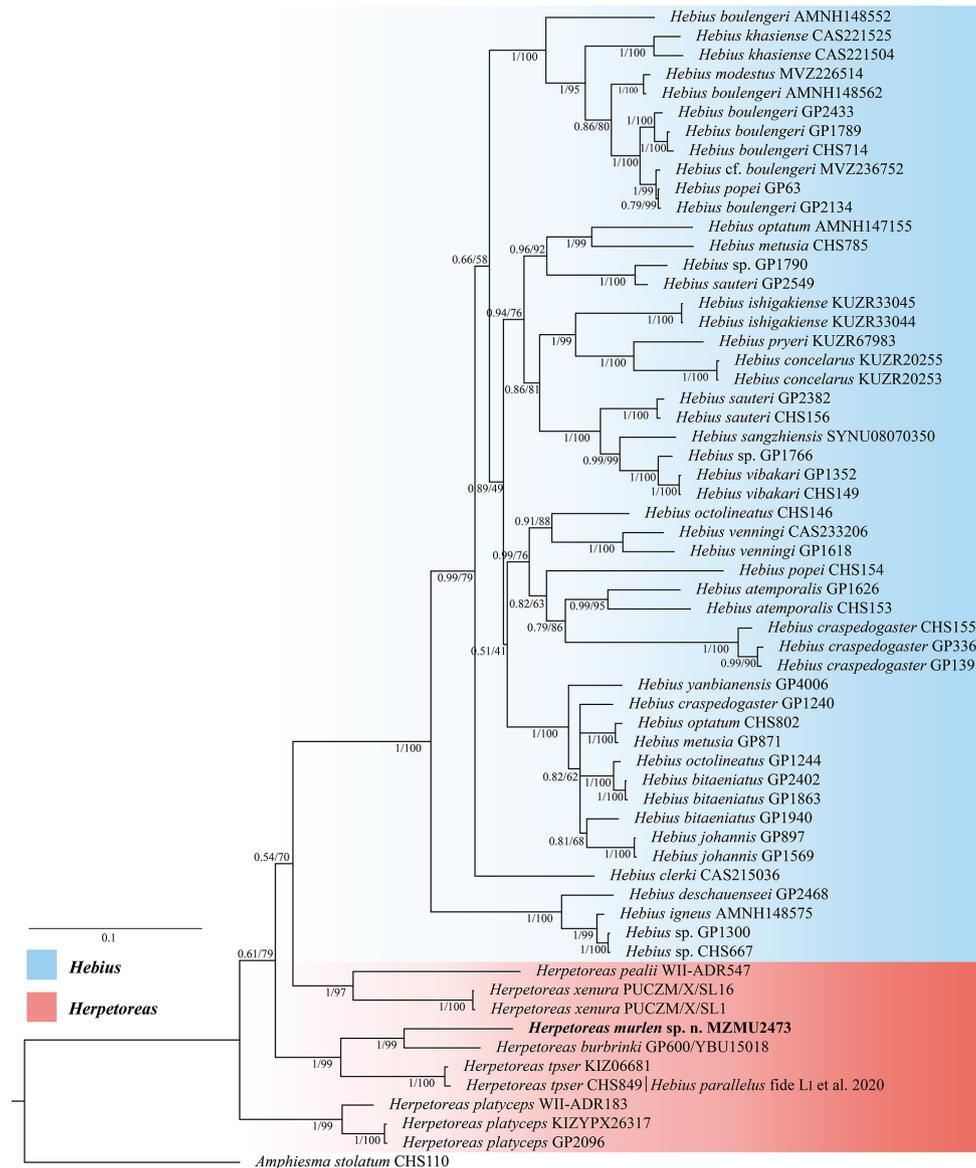
The electronic edition of this article conforms to the requirements of the amended International Code of Zoological Nomenclature, and hence the new names contained herein, are available under that Code from the electronic edition of this article. This published work and the nomen-

clatural acts it contains have been registered in ZooBank, the online registration system for the ICZN. The LSID (Life Science Identifier) for this publication is: urn:lsid:zoobank.org:pub: F65F856D-1D0A-415A-BCDB-BF9DAD940F47. The electronic edition of this work was published in a journal with an ISSN, has been archived, and is available from the following digital repositories: www.salamandra-journal.com, zenodo.org.

**Results**

The concatenated datasets (16S and Cytb) of the naticine and the colubrine groups contained 1117 and 2437 bp

aligned characters, respectively. Two types of phylogenetic analyses (BI and ML) were performed, which inferred consistent tree topologies (Fig. 2), with the Cytb gene tree (BI) also being congruent with the concatenated trees (see Supplementary Figure S1). In our phylogenetic analyses of the naticine group, the unnamed individual from Mizoram, India, is nested with the putative *Herpetoreas* clade and forms a sister species to *H. burbrinki* with well-supported Bayesian posterior probabilities (PP) and UFB values. It is distinct from the other *Herpetoreas* species by considerable genetic divergences of 8.3% (to *H. burbrinki*) to 13.7% (to *H. pealii*), while the genetic distances to *Hebius* species ranged from 9.9% (to *H. parallelus* CHS849 fide Li et al. (2020)) to 17.9% (to *H. conelarus*), and 16.6% to the



outgroup (*A. stolatum*). The morphological features of the specimen agree with the generic characters of *Herpetoreas* provided by GUO et al. (2014), but exhibit strong genetic divergence from the five nominal species of *Herpetoreas*. Therefore, based on morphological and molecular data, the specimen from Mizoram is considered a distinct evolutionary lineage of *Herpetoreas*, and is described as follows.

***Herpetoreas murlen* sp. n.**

ZooBank LSID: [zoobank.org/pub:F65F856D-1D0A-415A-BCDB-BF9DAD940F47](https://zoobank.org/pub:F65F856D-1D0A-415A-BCDB-BF9DAD940F47)

Holotype. MZMU2041, adult male, from Murlen National Park (coordinates: 23.62627° N, 93.28936° E, 1,763 m asl.), Champhai District, Mizoram, northeastern India, collected at ca. 1700 hrs on 11 August 2021, by Amit Kumar Bal.

Etymology. The specific epithet refers to the type locality, Murlen National park, Champhai District, Mizoram, India. We propose as common names, Murlen Keelback Snake (English) and Murlen-Wassernatter (German).

Diagnosis. *Herpetoreas murlen* sp. n. is diagnosable by the following morphological characters (based on the holotype, male; Figs. 3–6): 1) TaL/TL 0.23; 2) two PVe, 179 Ve,

and 78 paired Sc; 3) As divided; 4) nine IL, with the first four contacting the AG, and the fourth and fifth contacting the PG; 5) eight SL, the third to fifth contacting the eye, the seventh largest; 6) Tem 1+1; 7) two PrO, and three PoO; 8) dorsal scales in 19:19:17 rows, distinctly keeled, those in the first row feebly keeled; 9) internasal scales sub-triangular; 10) scales on posterior part of head and temporal region smooth; 11) the everted hemipenes bilobate near the tip; sulcus spermaticus bifurcated just beneath the crotch; weakly developed apical naked area at the crotch and invisible from the asulcate face; numerous small spines present, increasing in size distally, and a distinct basal hook present (Fig. 6).

Description of the holotype. Body elongated and slender; SVL 355 mm; TaL 106 mm; TaL/TL 0.23; head distinct from neck, longer than wide (3.9% of the SVL); snout modestly long (23% of HL); nostrils small; eyes rather large (33% of HL), pupils round; a single loreal, wider than long; prefrontals wider than long, extending laterally in contact with internasals, nasals, loreal, preoculars, and frontal; frontal pentagonal, anterior part a bit wider; parietals longer than wide; two PrO, and three PoO; maxillary teeth 13 on one side, the last two distinctly enlarged without diastema between the last two and the anterior teeth.

In life, body dark olive-grey, most scales randomly speckled with black on the margins; inter-scales sparse-



Figure 3. Holotype of *Herpetoreas murlen* sp. n. (MZMU2041) in life (A–C). Head of an uncollected individual in dorsolateral view (D).

ly speckled with white; a dorsolateral stripe extending from the neck to the tail, covering the upper part of the 5<sup>th</sup> row along the anterior part of the body (where there are 19 DSR), the whole of the 6<sup>th</sup> row, and the lower part of the 7<sup>th</sup> row, covering the upper part of the 4<sup>th</sup> row along the posterior part of body (where there are 17 DSR), the whole of the 5<sup>th</sup> row, and the lower part of 6<sup>th</sup> row, conspicuous maroon, lighter in the inter-scales, with dark speckles on the margins of the lower part of the 5<sup>th</sup> row and the upper part of the 7<sup>th</sup> row along the anterior part and in the lower part of the 4<sup>th</sup> row and the upper part of the 6<sup>th</sup> row along the posterior contrast stripe; tail colored and patterned as the posterior part of the body, with the maroon dorsolateral stripe progressively vanishing towards half the length of the tail, ill-defined and diffuse towards the tail tip.

Dorsal face of head and nape dark olive-brown; a median lighter brown stripe on the mid-dorsal scales of the nape starting from behind the posterior interparietals, flanked by irregular dark speckling on either side, bifurcating at the 7<sup>th</sup> scale, partially interrupted by small dark speckles before becoming the dorsolateral stripes on both

sides; frontal with irregular and thin dark speckles on the lateral and posterior margins. Lower region of the snout and the lateral faces of the head pale ivory cream, demarcated from the upper olive-brown coloration by a distinct dark streak on the upper borders of the rostral and extending posteriorly through the nasal, loreal and the lower pre-ocular; a continuous streak on the middle postocular, upper part of the lower postocular, 1<sup>st</sup> temporal, upper parts of 6<sup>th</sup> and 7<sup>th</sup> SLs, and extending posteriorly as an oblique band in the 8<sup>th</sup> SL on both sides of the head; anterior supralabials pale ivory cream and edged with dark brown on their posterior borders; a dark spot on the upper edge of the 4<sup>th</sup> SL, an oblique black streak from the posterior upper margin of the 5<sup>th</sup> SL interrupted in the lower anterior part of the 6<sup>th</sup> SL; anterior IL the same colour as SL, thinly framed with darker pigment on their posterior borders.

Venter uniformly light sand-brown, the outer part of each scale brick-red, becoming darker olive-brown on the

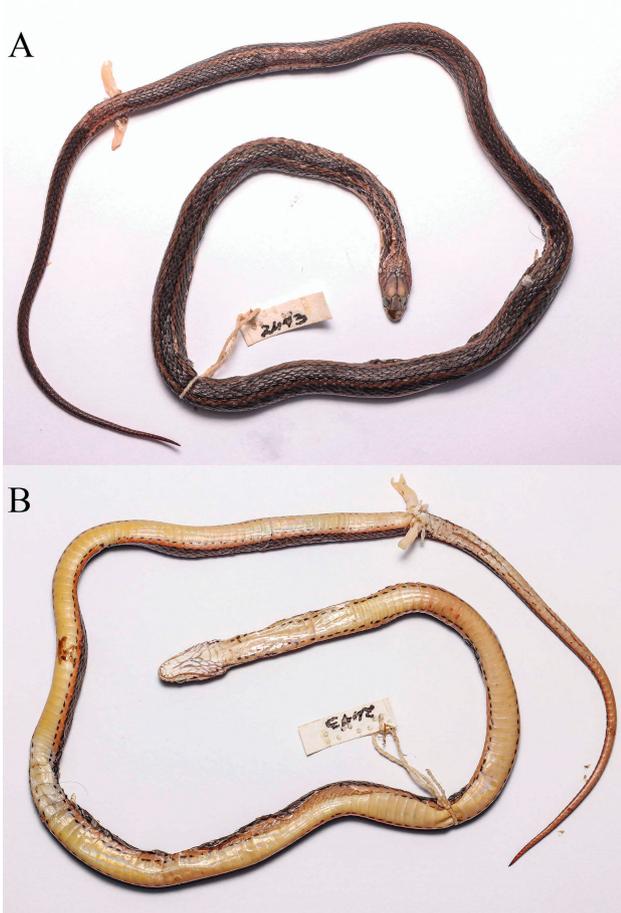


Figure 4. Dorsal (A) and ventral (B) views of the preserved holotype (MZMU2041) of *Herpetoreas murlen* sp. n.

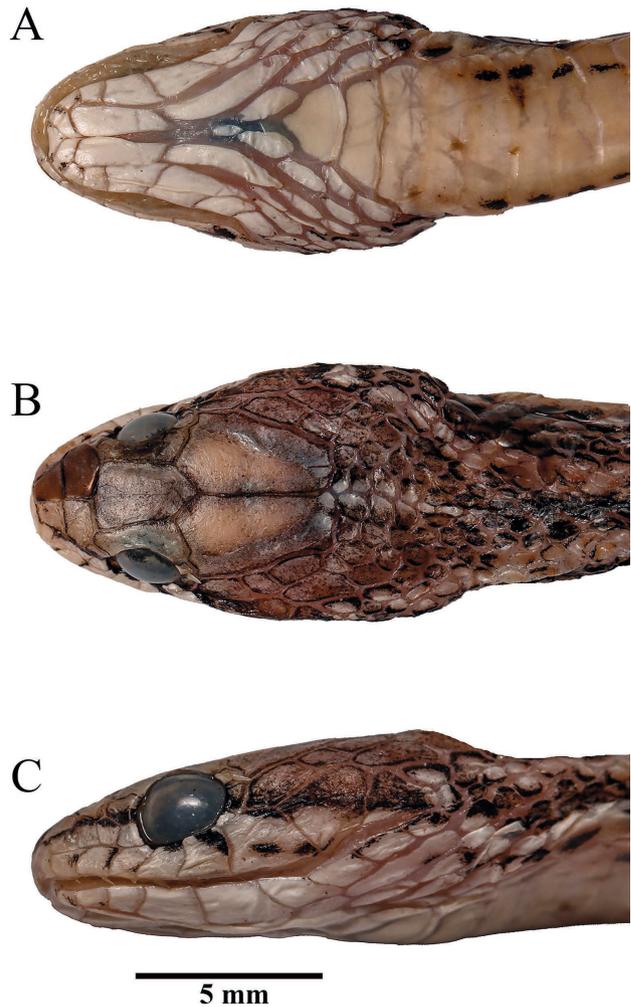


Figure 5. Dorsal (A), ventral (B), and lateral (C) views of the head of the holotype (MZMU2041) of *Herpetoreas murlen* sp. n.

scales' outer tips; each ventral with a thin, yet well defined, blackish brown spot between the brick-red and light brown parts, these spots become progressively smaller posteriorly from mid-body and do not connect with each other. Ventral part of tail same as the venter, bordered on either side by a blackish brown stripe as described above; the blackish brown ventral spots progressively vanish in the anterior half of the tail length. Chin, throat, and ventral part of the neck uniform whitish ivory cream, lighter than venter. Posterior infralabials each with a blackish spot on the rear margin (Figs 3A–C).

Comparison with other species. Among the known *Herpetoreas* species, the new species is genetically closest to *H. burbrinki* by forming a well supported sister lineage in all the phylogenetic analyses. In the Cytb gene-based genetic divergence (p-distance) estimation (Table 2), the new species likewise has the least genetic divergence from *H. burbrinki* (8.3%). However, the new species is morphologically distinct from *H. burbrinki* by having: smooth scales in the posterior part of the head and in the temporal region (vs. keeled); more Ve (179 vs. 169–172); fewer Sc (78 vs. 94–96); a lower TaL/TL ratio (0.23 vs. 0.26–0.29); fewer maxillary teeth (13 vs. 21); fewer Ate and Pte (1+1 vs. 3+2 or 2+2); lesser IL (9 vs. 10), and a lower number of IL contacting the AG (1–4 vs. 1–5) (Table 3).

*Herpetoreas murlen* sp. n. is distinguished from *H. pealii* by the following characters: higher Ve count (179 vs. 136–142); fewer SL and IL (8 vs. 9 and 9 vs. 10); bifid anal scute (vs. entire); 3–5 SLe (vs. 4–5); more PrO (2 vs. 1); the first four IL touching the AG (vs. the first five); the fourth and fifth IL contacting the PG (vs. fifth to sixth); 13.7% uncorrected p-distance between them.

*Herpetoreas murlen* sp. n. differs from *H. xenura* in the following characters: higher Ve count (179 vs. 156–165); paired and lower Sc count (78 vs. 87–114, entire); more PrO (2 vs. 1); lower numbers of SL and IL (8 and 9 vs. 9 and 10); 3–5 SL touches the eye (vs. 4–6); lower TaL/TL ratio (0.23 vs. 0.26–0.31); fewer maxillary teeth (13 vs. 22–23); uncorrected p-distance 13.4%.

*Herpetoreas murlen* sp. n. differs from *H. platyceps* by having fewer Ve (179 vs. 191–234); more PrO (2 vs. 1); a smaller number of maxillary teeth (13 vs. 18–22); interspecific genetic divergence 13.3%. The new species also differs from *Tropidonotus firthi* (WALL, 1914), a junior synonym of *H. platyceps*, by having fewer Sc (78 vs. 80–88); more PrO (2 vs. 1); fewer maxillary teeth (13 vs. 18–19).

*Herpetoreas murlen* sp. n. is also distinct from *H. sieboldii* by having fewer Ve (179 vs. 190–216); a fewer number of Sc (78 vs. 81–111); a higher number of PoO (3 vs. 2); fewer IL (9 vs. 10); 13 maxillary teeth without a diastema (vs. 17–21 + 2 with a wide diastema); uncorrected p-distance 12.7–13.3%.

Taxonomic remarks. During the fieldwork for this study, another individual was encountered near the type locality within the Murlen National Park at ca. 1600 hrs on 29 November 2019. Unfortunately, this individual (approx. TL 400 mm) escaped after it was photographed (Fig. 3D). Its head scalation largely agreed with that of the holotype except that some variation was seen with regard to the left temporals, i.e., 2+2/1+1 vs. 1+1/1+1 in the holotype.

Distribution and natural history. *Herpetoreas murlen* sp. n. is as yet known only from the type locality in the Murlen National Park, located in Champhai District, Mizoram (21.95–24.5° N, 92.25–93.48° E), in the northeastern portion of Mizoram state. The holotype was collected from leaf litter along a forest trail (Fig. 7). The area is characterized by dense tropical to subtropical evergreen mixed forests, covering ca. 200 km<sup>2</sup> at an altitude of 600 to 1,800 m a.s.l. It receives an annual rainfall of 2,000–2,500 mm with temperature ranging between 5°C in winter and 35°C in summer (SHARMA et al. 2017). According to CHAMPION & SETH (1968), the area falls into the category of Assam Subtropical Pine Forest (9/C2). The vegetation is dominated by *Quercus* sp., *Schima wallichii*, *Betula* sp., *Michelia champaca*, *Pinus khasiana*, *Prunus*, *Myrica* sp., *Rhododendron* sp., *Arundinaria callosa*, canes, and a rich variety of orchids. Other snakes encountered during the survey at the type local-



Figure 6. Everted hemipenis, sulcal side (A) and asulcal side (B) of the holotype (MZMU2041) of *Herpetoreas murlen* sp. n.

Table 2. Morphometric and meristic characters of *Herpetoreas murlen* sp. n., and comparative data of its congeners obtained from published data. For *H. xenura*, a total of 18 specimens examined in this study and published data were combined. Unavailable data are indicated as “-”.

Taxa	<i>H. murlen</i> sp. n.	<i>H. burbrinki</i>	<i>H. tpser</i>	<i>H. pealii</i>	<i>H. xenura</i>	<i>H. platyceps</i>	<i>H. sieboldii</i>		
Vouchers	MZMU 2473	YBU 071128	ANU 20210006	-	BMNH 1946.1.13.43	WII ADR547	-	-	-
Sex	Male Holotype	Male Holotype	Female (n=1)	Sex pooled n=6	Male (n=1) Lectotype	Female (n=1)	Sex pooled (n=18+)	Sex pooled (n=?)	Sex pooled (n=?)
SVL	355	459	462	279-491	334	511	364-550	570-655	-
TaL	106	130	184	108-207	117	150	176-210	165- 225	-
TaL/TL	0.23	0.26	0.29	0.26-0.32	0.26	0.23	0.26-0.31	0.23-0.29	0.24-0.32
DSR	19:19:17	19:19:17	19:19:17	19:19:17	19:19:17	19:19:17	19:19:17	19:19:17	19:19:19
Ve	179	172	169	153-167	142	136	156-165	191-234	190-216
PVe	2	2	2	-	3	2	-	-	-
Sc	78 (paired)	96 (paired)	94 (paired)	79-97 (paired or Sc 7-9 single)	77 (paired)	69 (paired)	87-114 (entire)	78-98 (paired)	81-111
As	2	2	2	2	1	1	1 or 2	-	2
SL	8/8	8	9/8	8 or 9	9/9	9/9	9/9	8	8
IL	9/9	10	10/10	9-10 (8)	10/10	10/10	10/10	8 or 9	10
SLe	3-5/3-5	3-5	3-5	3-5 or 4-6	4-5/4-5	4-5/4-5	4-6/4-6	3-5	3-5
IL contacting AG	1-4/1-4	1-5	1-5	1-4 or 1-5	1-5/1-5	1-5/1-5	-	-	-
IL contacting PG	4-5/4-5	-	-	-	5-6/5-7	5-7/5-7	-	-	-
Tem	1+1/1+1	3+2/3+2	2+2/2+2	1-2 [or 1+1/1] + 2, 1-2+1 [or 1/(1+2)]	2+2/2+2	2+2/2+2	2+2 or 2+1 or 1+2 (rarely 1+1)	1+1 (rarely 2+2)	1 or 2 anterior
PrO	2/2	2/1	1/1	1 or 2	1/1	1/1	1/1	1	1 or 2
PoO	3/3	3	3/3	3 or 2	3/3	3/3	3/3	2 or 3	2
Lor	1/1	1	2/2	1/1 in holotype	1/1	1/1	1/1	1	1
HL	13.96	-	16.5	9.60-13.56	15.5	22.4	12.44-16.60	-	-
HW	6.80	-	9.2	6.91-9.54	7.3	11.9	8.50-12.98	-	-
HD	4.60	-	6.1	-	5.2	8.9	-	-	-
ED	2.48	-	3.8	-	2.5	3.3	2.44-3.32	-	-
E-Sn	3.28	-	-	-	4.1	6.1	-	-	-
E-Ns	1.70	-	-	-	2.7	3.7	2.70-4.22	-	-
INL	1.60	-	-	-	1.4	2.0	-	-	-
PFL	1.90	-	-	-	1.9	2.8	-	-	-
FL	3.72	-	-	-	3.8	5.9	-	-	-
PL	5.46	-	-	-	6.3	9.2	-	-	-
Maxillary teeth	13, gradually enlarged posteriorly, last two teeth (larger) after a small gap, but without diastema	-	21 in a continuous series, last 15 enlarged.	20-21, last two enlarged, a small gap present, with diastema	13-21, gradually enlarged posteriorly. Last two teeth after a small gap, but without diastema	22-23, gradually enlarged posteriorly. Last two teeth (large) after a small gap, but without diastema	18-22 in a continuous series, last 16 enlarged	17-21 + 2 with a wide diastema, last two enlarged	-
Hemipenes	Bilobate at tip, sulcus distinct and bifurcated just beneath the crotch area of the two lobes. Basal hook present	-	-	Sulcus single, extends to crotch	Sulcus single, bilobate	-	Sulcus single, bilobate at tip	Sulcus single, extends to tip, rarely bilobate	Sulcus single, tip, bilobate at tip
Source	This study	GUO et al. (2014)	PENG et al. (2021)	REN et al. (2022)	MALNATE (1960); DAS et al. (2020)	DAS et al. (2020); This study	SMITH (1943); MALNATE (1966); DAVID et al. (2015)	GÜNTHER (1860); MAL- NATE (1966); GUO et al. (2014); DAVID et al. (2015)	-

Table 3. Uncorrected p-distances for members of the putative *Herpetoreas* clades. GenBank accession numbers are provided after the species names.

Species	1	2	3	4	5	6	7	8	9	10
1. <i>Herpetoreas murlen</i> sp. n. ON204025										
2. <i>Herpetoreas burbrinki</i> GQ281781	0.087									
3. <i>Herpetoreas platyceps</i> MT571587	0.111	0.109								
4. <i>Herpetoreas platyceps</i> KJ685690	0.115	0.123	0.043							
5. <i>Herpetoreas platyceps</i> MW111464	0.115	0.125	0.043	0.003						
6. <i>Herpetoreas xenura</i> MN993850	0.130	0.125	0.126	0.144	0.140					
7. <i>Herpetoreas xenura</i> MN993851	0.130	0.125	0.126	0.144	0.140	0.000				
8. <i>Herpetoreas pealii</i> MT571586	0.145	0.120	0.133	0.144	0.144	0.113	0.113			
9. <i>Herpetoreas tsper</i> MW111476	0.099	0.089	0.096	0.108	0.104	0.135	0.135	0.130		
10. <i>Hebius parallelus</i> MK201567	0.099	0.092	0.099	0.111	0.108	0.135	0.135	0.133	0.003	

ity were *Ahaetulla prasina*, *Boiga ochracea*, *Dendrelaphis cyanochloris*, *Gonyosoma prasina*, *Hebius khasiense*, *Lycodon fasciatus*, *Oligodon dorsalis*, *Oreocryptophis porphyraeus*, *Orthriophis taeniurus*, *Ovophis monticola*, *Pareas andersoni*, *Pareas monticola*, *Psammodynastes pulverulentus*, *Pseudoxenodon macrops*, *Rhabdophis helleri*, *Sibynophis collaris*, *Sinomicrurus maccllellandi*, and *Trimeresurus erythrurus*. Since the two individuals of *H. murlen* sp. n. were encountered during dusk (1600–1700 hrs), we suggest the species to be crepuscular in activity. Although the park has several small seasonal and perennial streams, and is also characterized by an undulating topography and rugged mountains (SHARMA et al. 2017), there was no open water apparent in the vicinity of the collection site. It seems



Figure 7. Microhabitat at the collection site of *Herpetoreas murlen* sp. n. in the Murlen National Park, Mizoram, northeastern India.

plausible that the species may occur in the neighbouring Manipur state (India) and some parts of the adjacent Chin state (Myanmar).

#### Systematic reassessment

In the scenario of the colubrine dataset, both the BI and ML phylogenetic analyses inferred ) with significant PP and UFB support the clustering of the new specimen of *G. scriptum* (MZMU2041) from Mizoram with a conspecific specimen from Cambodia (NCSM99033, and both specimens clearly nested within a clade of *Liopeltis* consisting of *L. frenatus* + *L. pallidonuchalis* + *Liopeltis* sp. (Fig. 8A). From the Cytb gene based p-distance estimation, *G. scriptum* (MZMU2041) from Mizoram has an intraspecific distance of 5.3% from the specimen (NCSM99033) from Teuk Chou, Kampot Province (Cambodia), while the smallest interspecific divergence (6.7%) is seen vis-à-vis *L. frenatus* (CAS225548) and the greatest (23.3%) vis-à-vis *S. collaris* (CHS244). The two specimens of *L. stoliczkae* (MZMU965, MZMU1420) from Mizoram exhibit 0.0% divergence between them, and 4.4% intraspecific genetic distance vis-à-vis the Chinese specimen (CHS842); with the other congeners, genetic divergences of 10.3% (*L. philippina*) to 17.4% (*L. pallidonuchalis*) are manifest. Only the 16S fragment for *S. collaris* was generated in this study so that the estimation of genetic distances was performed using the 16S dataset. *Sibynophis collaris* (MZMU1454) from Mizoram (India) showed 2.5 and 4.3% genetic distances compared with a conspecific specimen from China (CHS244) and one specimen of unknown provenance (ROM25618), respectively. Our specimen also exhibited 4.3% interspecific genetic divergences vis-à-vis the two specimens of *S. chinensis* (CHS245, CHS246). Although the present molecular phylogenetics and DNA barcoding may suggest an inclusion of *G. scriptum* in the genus *Liopeltis*, we took a conservative approach and left the generic reallocation of *G. scriptum* pending due to insufficient data. However, we contribute herein additional data for the species that may be crucial for a future nomenclatural re-evaluation of the genus.

***Gongylosoma scriptum* (THEOBALD, 1868)**

Holotype. ZSI 7207, Martaban (= Mottama), Mon State, Myanmar.

Material examined. MZMU2041, adult male, from Suangpuilawn village, (23.964530° N, 93.040957° E; 1,100 m a.s.l.; Fig. 8B) Aizawl District, Mizoram, northeastern India, collected at 1030 hrs on 30 October 2020, by J. C. LALMUANAWMA; MZMU892, subadult female, from Government Middle School Compound, Suangpuilawn village (23.949947° N, 93.037772° E, 1,072 m a.s.l.), Aizawl

District, Mizoram, northeastern India, collected on 3 June 2016, by J. C. LALMUANAWMA, H. LALTLANCHHUAHA, LALRINSANGA and H. T. LALREMSANGA (fide LALREMSANGA et al. 2018); MZMU914, adult male, from near Saithah village (23.587047° N, 92.456892° E, 730 m a.s.l.), Mamit District, Mizoram, northeastern India, collected on 27 August 2016, by LALNUNKIMA, VANLALHRIMA and H. T. LALREMSANGA (fide LALREMSANGA et al. 2018); ZMB 5286, female, from “East India”, collected by GRUBE, date unknown; ZMB 50677, adult male, from Khao Yai, Thailand, collected by W. GROSSMANN.

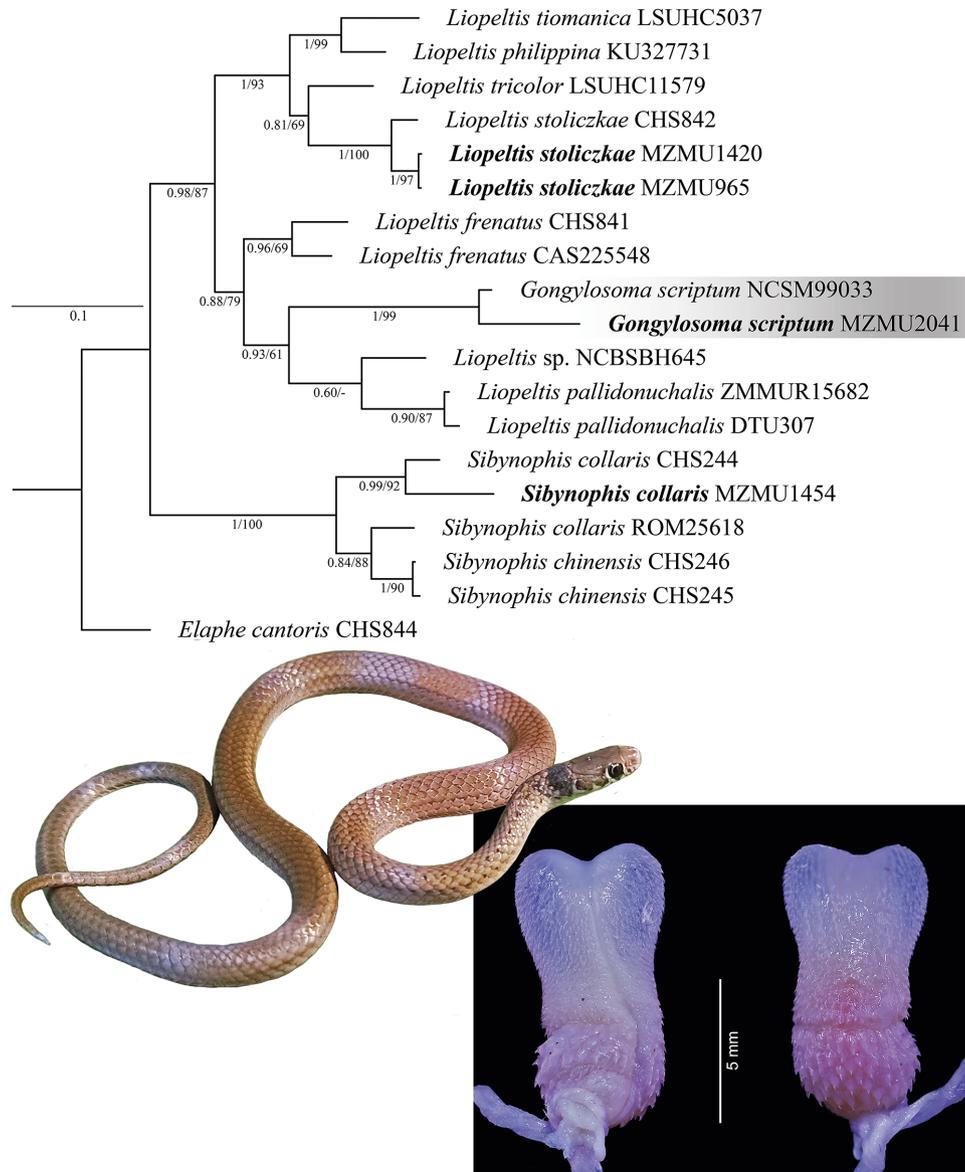


Figure 8. (A) Bayesian inference (BI) phylogenetic tree of *Gongylosoma scriptum* and allied species, based on the concatenated mitochondrial cytochrome b and 16S rRNA genes. Bayesian posterior probabilities (PP) are provided before the slash, and Ultrafast Bootstrap (UFB) values from the Maximum Likelihood (ML) analysis are given after the slash, the value for the node not recovered in the ML tree is given as “-”. Sequences generated for this study are outlined in bold; (B) The newly collected specimen of *G. scriptum* (MZMU2041) in life; (C) sulcal (left) and asulcal (right) views of the everted hemipenis of *G. scriptum* (MZMU2041).

Table 4. Morphological data of *Gongylosoma scriptum* obtained in this study and published data. Asterisk indicates tail tip damaged, and unavailable data and revised data after re-examination of the same specimens are indicated as “-” and “#”, respectively.

Source	This study			LALREMSANGA et al. (2018)		NEANG et al. (2015)		SMITH (1943)
Locality	India (Mizoram)	Thailand (Khao Yai)	East India	India (Mizoram)		Cambodia (Pursat)	Cambodia (Preah Sihanouk)	-
Vouchers	MZMU 2041	ZMB 50677	ZMB 5286	MZMU 892	MZMU 914	CBC 01365	CBC 02543	-
Sex	Male	Male	Female	Female	Male	Female	Male	-
SVL	280.0	228	171	224.2#	230.0#	256.1	252.2	465 (male), 495 (female)
TaL	155.2	161	79	58.0#*	123.0#	145.6	172.2	155 (male)
TaL/TL	0.36	0.41	0.32	*	0.35	0.36	0.41	-
DSR	13:13:13	13:13:13	13:13:13	13:13:13	13:13:13	13:13:13	13:13:13	13:13:13
Ve	128	123	136	139	127	138	122	126–145
Sc	89	98	77	45*	88	93	101	87–98
As	2	2	2	2	2	2	2	2
SL	7/8	8/8	8/8	8/8	8/8	8/8	8/8	8/8
IL	8/8	8/8	8/8	8/8	8/8	8/8	8/8	-
SLe	3–4/3–5	3–5/3–5	3–5/3–5	3–5	3–5	3–5	3–5	3–5
Tem	1+2/1+2	-	-	1+2/1+2	1+2/1+2	1+2/1+2	1+2/1+2	1+2/1+2
PrO	1/1	-	-	1/1	1/1	1/1	1/1	1/1
PoO	2/2	-	-	2/2	2/2	2/2	2/2	2/2
HL	11.0	13.4	10.8	9.9	10.0	-	-	-
HW	6.8	6.7	4.8	4.6	7.2	-	-	-
ED	2.6	2.4	1.8	2.1	2.2	-	-	-
E–Ns	1.9	1.4	1.0	0.9	1.1	-	-	-
SW	3.4	-	-	2.6	3.0	-	-	-

Description. Based on the material examined, body slender and elongate; tail thin; head moderately distinct from the neck; eye rather large, pupil circular; snout blunt; rostral slightly visible from above; loreal small; precocular higher than wider. Measurements: SVL 228–280 mm in males (n=3), 171–224.2 mm in females (n=2); TaL 123–161 mm in males, 79 mm in one female (excluding the specimen with the damaged tail tip); ratio TaL/TL 0.35–0.41 in males, 0.32 in one female; HL: 10–13.4 mm in males, 9.9–10.8 mm in females; HW 6.7–7.2 mm in males, 4.6–4.8 mm in females; ratio HW/HL 0.50–0.72 in males, 0.44–0.46 in females; ED 2.2–2.6 mm in males, 1.8–2.1 mm in females; ratio ED/HL 0.18–0.24 in males, 0.17–0.21 in females. Meristics: dorsal scale rows 13:13:13, all smooth; Lor single; one nasal and two internasals; two prefrontals and a single frontal; Ve 123–128 in males, 136–139 in females; paired Sc 88–98 in males, 77 in one female; anal scutedivided; SL eight on both sides, rarely seven; eight IL on both sides; SLe 3–5, rarely 3–4. Morphological data taken from the new specimens and published values are given in Table 4.

Hemipenial morphology. The hemipenis of the newly collected specimen shows a simple cylindrical structure

with weakly differentiated apical lobes, and its medial surface is covered with smooth epithelium. The distal third of the organ is covered with fairly evenly distributed small spine-line on both faces; the remaining part in the proximal area with medium-sized spine-line, but less densely so on the sulcal face, and basal hooks are absent. Sulcus spermaticus single and running up to the crotch of the apical lobes (Fig. 8C).

Taxonomic remarks. This species is diagnosable from its congeners by having thin and light coloured vertical bars in the PrO and PoO regions, extending from the SL to the supraorbital ridge fide GRISMER et al. (2003). The morphological characters of the newly collected specimen (MZMU2041), and the two museum specimens examined for this study (ZMB50677, ZMB 5286) largely agree with the species' original description (THEOBALD 1868) and other specimens (GRISMER et al. 2003, LALREMSANGA et al. 2018, LEVITON 1964, MALKMUS et al. 2002, NEANG et al. 2015, SMITH 1943). Notably, the specimen from “East India” (ZMB 5286, female) has the lowest number of Sc, i.e., 77, compared to the known range of 87–101 (NEANG et al. 2015, SMITH 1943).

Distribution and natural history. In addition to the known distributional records from India (Mizoram) (LALREMSANGA et al. 2018), we documented three new distributional records during this study: the specimen MZMU2041 was collected at 1030 hrs on 30 October 2020, from Suangpuilawn village, Aizawl District (23.964530° N, 93.040957° E; 1,100 m a.s.l.) by J. C. LALMUANAWMA, the same locality where LALREMSANGA et al. (2018) collected one of their specimens; an uncollected individual was encountered at 1318 hrs on 16 May 2018 on the way to Dampui village from Thenhlum village, Lunglei District (23.2234504° N, 92.5891226° E; 705 m a.s.l.) by PRIYA SINGH; on 25 May 2020, one individual was observed at Baktawng village, Serchhip District (23.536526° N, 92.846490° E; 1145 m a.s.l.; and another individual was documented on 17 June 2021, at Vanhne village, Lunglei District (22.919319° N, 92.712679° E; 877 m a.s.l.) by MERLIN KHIANGTE; All specimens were encountered during daytime in habitats similar to the previous records (INGER & COLWELL 1977, LALREMSANGA et al. 2018, NEANG et al. 2015).

### Discussion

In this study, we provide molecular evidence supporting the morphology-based hypothesis of a close relationship between the genera *Gongylosoma* and *Liopeltis* (see GRISMER et al. 2003, LEVITON 1964, POYARKOV et al. 2019). Our phylogenetic reconstructions ascertain the taxonomic placement of *Gongylosoma* in the subfamily Colubrinae. Although the genus was resurrected from the synonymy of *Liopeltis* by LEVITON (1964) and most recent publications consider the genus *Gongylosoma* valid (e.g., GRISMER et al. 2003, LALREMSANGA et al. 2018, NEANG et al. 2015, POYARKOV et al. 2019, SOM et al. 2020); evidence from the present molecular phylogenies instead warrants designating its generic position to *Liopeltis* fide MANTHEY & GROSSMANN (1997), SMITH (1943), and WALL (1924). Yet, the precise determination of the generic position of *G. scriptum* must remain unresolved as of now due to the unavailability of genetic data from either the type specimen, topotypical specimens, or congeneric specimens. However, the morphology-based phylogeny proposed by GRISMER et al. (2003) suggests a probably close relationship between *G. scriptum* and *G. baliodeirum* (type species); thus, it seems plausible that the specimens of *G. scriptum* examined in this work reflect the generic position of this species to some extent. Consequently, this work has put forward a taxonomic recommendation for the genus *Gongylosoma*. Further research by sampling more genetic and morphological information is needed to resolve the nomenclatural uncertainty of this genus by and large. Nevertheless, we trust that the so far very limited knowledge of this taxon is improved to a certain degree by the newly generated molecular data, distributional records, and morphological data. Currently, the IUCN considers *G. scriptum* “least concern”, but it is also known to suffer from habitat loss and degradation in Thailand and

Myanmar (GRISMER et al. 2012). More extensive surveys are recommended to establish the exact range of distribution and the population status of this little-known snake, which will be important for implementing knowledge-based conservation strategies.

Phylogenetic analyses of natricine snakes in this study largely showed similar topologies to those arrived at by previous workers (GUO et al. 2014, LIU et al. 2018, ZHOU et al. 2019). Considering the fact that due to paucity of data many of the nominal *Hebius* species are not covered in phylogenetic studies (DAS et al. 2020), and even the plausible placement of certain species of *Hebius* in either *Amphiesma* sensu stricto or *Herpetoreas* (GUO et al. 2014), the present phylogenetic inferences, however, clearly depict a monophyletic clade of *Hebius* with well-supported rooting. On the other hand, *Herpetoreas* is recovered as paraphyletic and comprising three monophyletic sub-clades in the shapes of the *H. platyceps* lineage, the species group lineage of *H. murlen* + *H. burbrinki* + *H. tpser*, and the *H. xenura* + *H. pealii* species group lineage. In this study, although we could not examine the type species of the genus *Herpetoreas*, i.e., *H. sieboldii* (GÜNTHER, 1860), we included *H. platyceps*, which was previously synonymized with *H. sieboldii*, but later removed from synonymy and considered a closely related taxon (MALNATE 1966). In the latest review of the genus *Herpetoreas*, REN et al. (2022) mentioned misidentified specimens of *H. parallelus* from Medog, Tibet, China, including the specimen KIZO6681 fide XU et al. (2021), and subsequently re-allocated the Tibetan specimens along with KIZO6681 to their newly described *H. tpser*. Moreover, the evidence from the present phylogenetic study depict *H. parallelus* (CHS849) fide LI et al. (2020) clustering with *H. tpser* (KIZO6681), which clearly refers specimen CHS849 to *H. tpser*. The description of the new species brings the number of recognized species in the genus *Herpetoreas* to seven, of which four of them (*H. pealii*, *H. xenura*, *H. platyceps*, and *H. sieboldii*) have already been recorded from India (UETZ et al. 2022), and the remaining ones (*H. burbrinki* and *H. tpser*) are regarded as endemic to China as of now (GUO et al. 2014; REN et al. 2022). Moreover, the specimen of “*H. venningi*” recorded earlier from Mizoram by BIAKZUALA & LALREMSANGA (2019) has since been referred to an undescribed species (DAVID et al. 2021) so that the systematic status of this *Hebius* species is also waiting to be resolved in future studies. Given that the northeastern Indian *Herpetoreas*, i.e., *H. xenura* and *H. pealii*, have been recorded at altitudes from 30 m a.s.l. to mid-altitudes of 1,170 m a.s.l. (DAS et al. 2020), we consider *H. murlen* a more montane zone dweller as the only known specimens were found in the high-altitude zone of Mizoram state at 1,763 m a.s.l.

Given the lack of information on the possible threats, reproductive biology, feeding habits, population structure, distribution range, and other ecological data of the new species, we suggest *H. murlen* to be regarded as a data deficient (DD) species under the categorization of the IUCN Red List of Threatened Species (IUCN Standards and Petitions Subcommittee 2019).

Updated key to the genus *Herpetoreas*

- 1A Subcaudals single ..... *H. xenura*  
 1B Subcaudals divided ..... 2  
 2A Anal scute single ..... *H. pealii*  
 2B Anal scute divided ..... 3  
 3A Ventrals fewer than 168 ..... *H. tpser*  
 3B Ventrals no less than 168 ..... 4  
 4A Tail relatively long,  $TaL/TL > 0.300$  ..... *H. burbrinki*  
 4B Tail relatively short,  $TaL/TL \leq 0.300$  ..... 5  
 5A Ventrals  $< 190$  ..... *H. murlen* sp. n.  
 5B Ventrals  $\geq 190$  ..... 6  
 6A A high proportion of the length of the tail with 4  
 supracaudal scale rows to that with 6 supracaudal  
 scale rows high,  $SC4/SC6 = 1.43$  ..... *H. platyceps*  
 6B A low proportion of the length of the tail with 4  
 supracaudal scale rows to that with 6 supracaudal  
 scale rows high,  $SC4/SC6 = 0.53$  ..... *H. sieboldii*

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- Herpetoreas xenura*: India: Mizoram, MZMU810–820, 860, 861, 969, 1211, 1287, 1423, 1425.
- Herpetoreas platyceps*: India: Darjeeling, NMW22383.2, India: Kulu Simla, NMW18569, 18570.1, 18570.2 (syntypes *Zamenis himalayanus*).
- Herpetoreas sieboldii*: India: Darjeeling, NMW22383.1, 22383.3, 22383.4, 22383.5; India: Kulu Simla, NMW18569, 18570.1, 18570.2 (syntypes *Zamenis himalayanus*); Nepal, Kulu valley, ZSM115.1977.
- Hebius khasiense*: India: Mizoram, MZMU821, 842; India: Meghalaya, BMNH 1946.1.12.80–1946.1.12.82; Myanmar: Kachin State, “Huton, Bhamo District (30 miles north-east of Bhamo; circa 4,500 feet; Lat. circa 97° .33; Long. circa 24° .24)”, now Hutung, BMNH 1946.1.13.62 (holotype of *Natrix gilhodesi* Wall, 1925), BMNH 1946.1.13.63, BMNH 1925.4.2.10–15
- Hebius cf. venningi*: India: Mizoram: Aizawl District, Hmufang Community Reserved Forest, MZMU1092, 1117, 1464; India: Mizoram: Aizawl District, Durtlang locality, MZMU1429; India: Mizoram: Aizawl District, Tlanguam locality, MZMU1658; India: Mizoram: Mamit District, Reiek Community Reserved Forest, MZMU1313, 1355, 1357, 1463, 1536, 1556, 1580.
- Hebius* spp.: India: Mizoram: Mamit District, Dampa Tiger Reserve, MZMU2306.
- Liopeltis frenatus*: India: Mizoram, MZMU874–876; India: Meghalaya: Khasi Hills, BMNH 1946.1.1.72 (holotype); China: Yunnan: Jangcheng City, DL 2019.5.19.
- Liopeltis stoliczkae*: India: Mizoram, Aizawl District, MZMU877–881, 1420; India: Mizoram, Lunglei District, 965.
- Sibynophis collaris*: India: Mizoram, Aizawl District, Tanhril locality, MZMU1454; India: Khasi Hills, BMNH53.8.12.34A, BMNH53.8.12.34B (syntypes); India: Uttar Pradesh Bimtal, ZFMK15690; India: Darjeeling, NMW21750:2; India: Sikkim, NMW21750:1; Myanmar: Rangoon valley, NMW26031:1, 26031:2, 26031:3, 26031:4; India: Katgarh, NMW14070; Vietnam: Annam, NMW21750:4; China, Taiwan, Suishargo, NMW21749:2, 21749:34, 21749:4.
- Sibynophis chinensis*: China, MNHN-RA 1912.265; China: Szechuan: Panzihua, collection of Ding Li (no catalogue number), China: no exact locality, MNHN-RA 1912.265, China: Upper Jang Tschang Tse Kiang BMNH89.6.25.8, China: Ichang, Upper Jang Tschang Tse Kiang, BMNH1904.1.26.6 (holotype); China: Tianchuan County, Sichuan, NMW39506; China Beijing, Hairou ZFMK 61761.
- Sibynophis chinensis grahami*: China: Jang Tse Kiang, BMNH 89.6.25.8 (holotype).

### Supplementary data

The following data are available online:

Supplementary Table S1. Newly generated sequences and GenBank sequences used in this study.

Supplementary Figure S1. Bayesian inference phylogenetic tree of the genera *Herpetoreas* and *Hebius*, based on the mitochondrial cytochrome b gene.

### Appendix

#### Specimens examined

*Amphiesma stotatum*: India: Mizoram: Aizawl District, Sawleng village, MZMU823; India: Mizoram: Kolasib District, Buhchangphai village, MZMU824, 825, 962; India: Mizoram: Champhai District, Champhai vengthar, MZMU1832; China: Ning Po, NMBE1016311.