



New data on the distribution, morphology, and molecular systematics of two venomous snakes, *Bungarus niger* and *Bungarus lividus* (Serpentes: Elapidae), from north-east India

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Abstract. This paper provides new information on the two medically important snakes, *Bungarus niger* and *B. lividus* from northeastern India. Included are morphological data on both the species and for the first time, genetic data (cytb) on *B. lividus* and establishing the genetic relation of the species to its congeners. We also provide brief descriptions of hemipenial morphology and new distributional records for both the species, along with notes on their natural history.

Key words. Squamata, Assam, greater black krait, lesser black krait, Meghalaya, Mizoram, natural history, phylogeny.

Introduction

Elapid snakes belonging to the genus *Bungarus* DAUDIN, 1803 are represented by 17 species known to occur throughout most of the Oriental region (KUCH et al. 2005, ABTIN et al. 2014, WALLACH et al. 2014, SUNAGAR et al. 2021). India is home to eight species of *Bungarus* (Kraits) and north-east (NE) India harbours four of them, namely, *B. bungaroides* (CANTOR, 1839), *B. fasciatus* (SCHNEIDER, 1801), *B. lividus* (CANTOR, 1839) and *B. niger* (WALL, 1908). Throughout their respective ranges, kraits are nocturnal and active predators, and are among the most medically important snakes (WARRELL 1999). Brahmaputra Basin, south of the Himalayas was noted as part of the ranges of both *B. lividus* and *B. niger* (WALL 1908). SMITH (1943) agrees to WALL (1908) in recognizing *B. lividus* as a species distinct from *B. niger* but added that the ventrals of both the species to be white with distinct dark mottling at the base of the ventral and subcaudal scales. Furthermore, SMITH (1943) stated the total maximum size of *B. lividus* and *B. niger* to be 1,020 mm and 1,200 mm, respectively. According to SMITH (1943), *B. lividus* is recorded from Rangpore (=Rangpur, in the Republic of Bangladesh), Jalpaiguri and Darjeeling (West Bengal State, India), and Dibrugarh (Assam State, India), and *B. niger* from Darjeeling (West Bengal State, India), Dibrugarh, Sadiya and Sibsagar (Assam State, India), Garo Hills (Meghalaya State, India).

A morphology-based phylogenetic analysis of *Bungarus* species by SLOWINSKI (1994) included *B. andamanensis* BISWAS & SANYAL, 1978, *B. bungaroides*, *B. caeruleus* (SCHNEIDER, 1801), *B. candidus* (LINNAEUS, 1758), *B. ceylonicus* GÜNTHER, 1864, *B. fasciatus*, *B. flaviceps* REINHARDT, 1843, *B. lividus*, *B. magnimaculatus* WALL & EVANS, 1901, *B. multicinctus* BLYTH, 1861, *B. niger*, and *B. sindanus* BOULENGER, 1897. SLOWINSKI (1994) used six parameters, namely, relative size of the vertebral scales, presence or absence of postzygapophysial processes, structure of choanal process of the palatine, subcaudals structure (divided or entire), demarcation between calyculate and spinose zone of hemipenis, and colour pattern. According to his model, *B. lividus* and *B. niger* were found to be sisters to each other sharing five of the six characters considered for the analysis. Both the species differed from each other in only relative size of the vertebral scales: *B. niger* has vertebral scales which are strongly enlarged compared to other dorsal scales, whereas in *B. lividus* the posterior vertebral scales are only slightly enlarged. Both the species together were placed as the sister group to a clade comprising *B. andamanensis*, *B. caeruleus*, *B. candidus*, *B. ceylonicus*, *B. magnimaculatus*, *B. multicinctus* and *B. sindanus*. Although the morphology-based taxonomic procedure is considered as an effective method for identifying snakes (BURBRINK & CROTHER 2011, WALLACH et al. 2014), differences between life stages and sexes can lead to misidentification (LAO-PICHENPONG et al. 2016). Consequently, the use of molec-

ular tools are valuable in assisting rapid species identification, phylogenetic reconstruction, biodiversity research, and population genetics (BURBRINK & LAWSON 2007, CASTOE et al. 2012). There has been rather limited molecular studies on Indian snakes, especially of those found in northeastern India. Despite the relative abundance in the region of the two closely related sympatric species, *B. niger* and *B. lividus*, their conservation status and distribution pattern in the country are poorly documented (AHMED et al. 2009). Herein, we attempt to provide additional data on their morphology, distributional records and natural history of the two species of black kraits in northeastern India, and also establish their phylogenetic relationship with the congeners using mitochondrial cytochrome *b* (*cytb*) marker gene.

Materials and methods

Field surveys and sampling were conducted in Mizoram State, northeastern India, with permission (No.A.33011/2/99-CWLW/225) from the Chief Wildlife Warden of Environment, Forests and Climate Change Department, Government of Mizoram, and in Meghalaya State after obtaining the permission (No. FWC/G/173/Pt-V/2377-87) from the Forest Department, Meghalaya State Government. Tissue samples were stored in 95% ethanol at -20°C for molecular-based investigation. The voucher specimens were fixed in 10% formalin, subsequently transferred to 70% ethanol, and deposited in the Departmental Museum of Zoology, Mizoram University, India (MZMU). The localities were recorded with a Garmin, Montana 650 GPS unit, and maps created using QGIS 3.10.8.

Morphometric measurements were taken with a Mitutoyo™ slide-calliper (505–671) to the nearest 0.01 mm. We followed the scalation terminology of CAMPBELL & LAMAR (2004), DOWLING (1951) for counting ventrals (Ve), and the hemipenis terminology by DOWLING & SAVAGE (1960). The terminal scute is excluded from the number of subcaudals (Sc). Snout–vent length (SVL) and tail lengths (TaL) were measured to the nearest millimetre. The numbers of dorsal scale rows (DSR) are given at one head length behind head, at midbody (i.e., at half of SVL), and at one head length before vent, respectively. Values for symmetric head characters are given in left/right order. Sex was determined by using a metal sexing probe in live specimens, whereas in preserved specimens, it was determined by making an incision at the base of the tail followed by establishing the presence or absence of hemipenes. Other abbreviations used in the text are as follows: MZMU (Departmental Museum of Zoology, Mizoram University), YSR (collection of Yashpal Singh Rathee), TL (total length), RTaL (relative tail length), ED (eye diameter), END (eye–nostril distance), IOD (inter–orbital distance), IND (inter–narial distance), SW (snout width), SL (snout length), HL (head length), HW (head width), SL (supralabials), SLE (supralabials touching eye), IF (infralabials), Tem (temporals), ATem (anterior temporal), PTem (posterior temporal),

PoO (postoculars), PrO (preoculars), As (anal shield), a.s.l. (above sea level), WL (Wildlife Sanctuary), NP (National Park).

Genomic DNA was extracted from the tissue samples using a DNeasy Blood and Tissue Kit (Qiagen™, Valencia, California, USA) following the standard protocol provided by the manufacturer. We amplified and sequenced the partial *cytb* gene using primers L14910 and H16064 (BURBRINK et al. 2000). The newly generated sequence data was added to a dataset of previously published sequence data (KUCH 2003, KUCH 2007, PYRON et al. 2013). Sequences (maximum of 768 base pairs) were aligned in MEGA X software (KUMAR et al. 2018) using the MUSCLE algorithm with default parameter settings (EDGAR 2004). Maximum Likelihood (ML) phylogenetic reconstruction was performed in MEGA X software (KUMAR et al. 2018) with 2,000 bootstrap replicates using the model GTR+I+gamma, which was selected based on the lowest Bayesian Information Criterion (NEI & KUMAR 2000). For the Bayesian inference (BA) phylogeny, GTR+I+gamma was also selected as the optimal model of nucleotide evolution using Mr.Modeltest 2.4 (NYLANDAR 2004) under the Akaike Information Criterion. Bayesian analysis was run for 20 million generations sampling one tree each 1,000 generations using Mr.Bayes 3.2.5 (RONQUIST & HUELSENBECK 2003). Burn-in was set to 25%, and stationarity was considered to be reached when the average standard deviation of split frequencies was less than 0.01. Uncorrected p-distance was calculated in MEGA X (KUMAR et al. 2018).

Results and discussion

Bungarus niger WALL, 1908

(Type locality: Tindharia, eastern Himalayas, India)

Morphology. *Bungarus niger* commonly known as greater black krait, is a species morphologically similar to *B. lividus*. It was originally described from Tindharia, Darjeeling District of West Bengal in India by WALL (1908). According to the original diagnosis by WALL (1908), the species is distinguished from *B. lividus* in the vertebral row of dorsal scales, where they were much enlarged and were broader than long (vs. vertebral row of dorsal scales feebly enlarged and not broader than long in *B. lividus*); greater number of Ve (216–231 vs. 209–221 in *B. lividus*) and Sc (49–56 vs. 35–43 in *B. lividus*) and larger body size i.e 1,200 mm in *B. niger* vs. 1,020mm in *B. lividus* (SMITH 1943).

We provide updated morphological data based on 27 specimens examined in this study (male = 23, female = 4) in Fig. 1 and Supplementary Table 1. It is a moderately sized snake (SVL max: 1,170 mm), males (TaL/TL: 0.11–0.16, avg. 0.14±0.012) with slightly longer relative tail length than females (TaL/TL: 0.14–0.16, avg. 0.15±0.008); head not distinct from the neck, longer than broad (HW/HL: 0.68–0.90, avg. 0.79±0.062 in male; 0.67–0.85, avg. 0.77±0.084 in female). Eye around 14% of the HL in sex pooled (ED/HL: 0.11–0.18, avg.0.14±0.017 in male; 0.14–0.16, avg. 0.15±0.010 in female), pupil round; SL and IF 7 in number,

3rd and 4th touching the eyes; PrO1, and 2 PoO (except MZMU 1418 with single PrO); ATem 1, PTem 2. In males, Ve214–228 (avg. 220.7±3.62) and Sc 48–56 (avg. 51.9±2.09); in females, Ve 220–225 (avg. 221.8±2.22) and Sc 48–54 (avg. 51.8±2.63). Hemipenis vaguely bilobed; about one-third of the distal part is calyculate, followed by spinose from mid region with the size of spines decreasing as they approach to the proximal area with ill-defined demarcation between

calyculate and spinose region (Fig. 1E–F). We noted a peculiar nape colouration in a juvenile specimen (MZMU 1809); it was mottled with light patches at both sides from the rim of posterior temporals up to part of the first dorsal scale (Fig. 2A–B). Our data on *B. niger* extends the previously known lower limit of Ve count (214–228 vs. 216–231 in SMITH 1943), and the upper limit of the range of Sc (48–58 vs. 47–57 in PURKAYASTHA 2013).

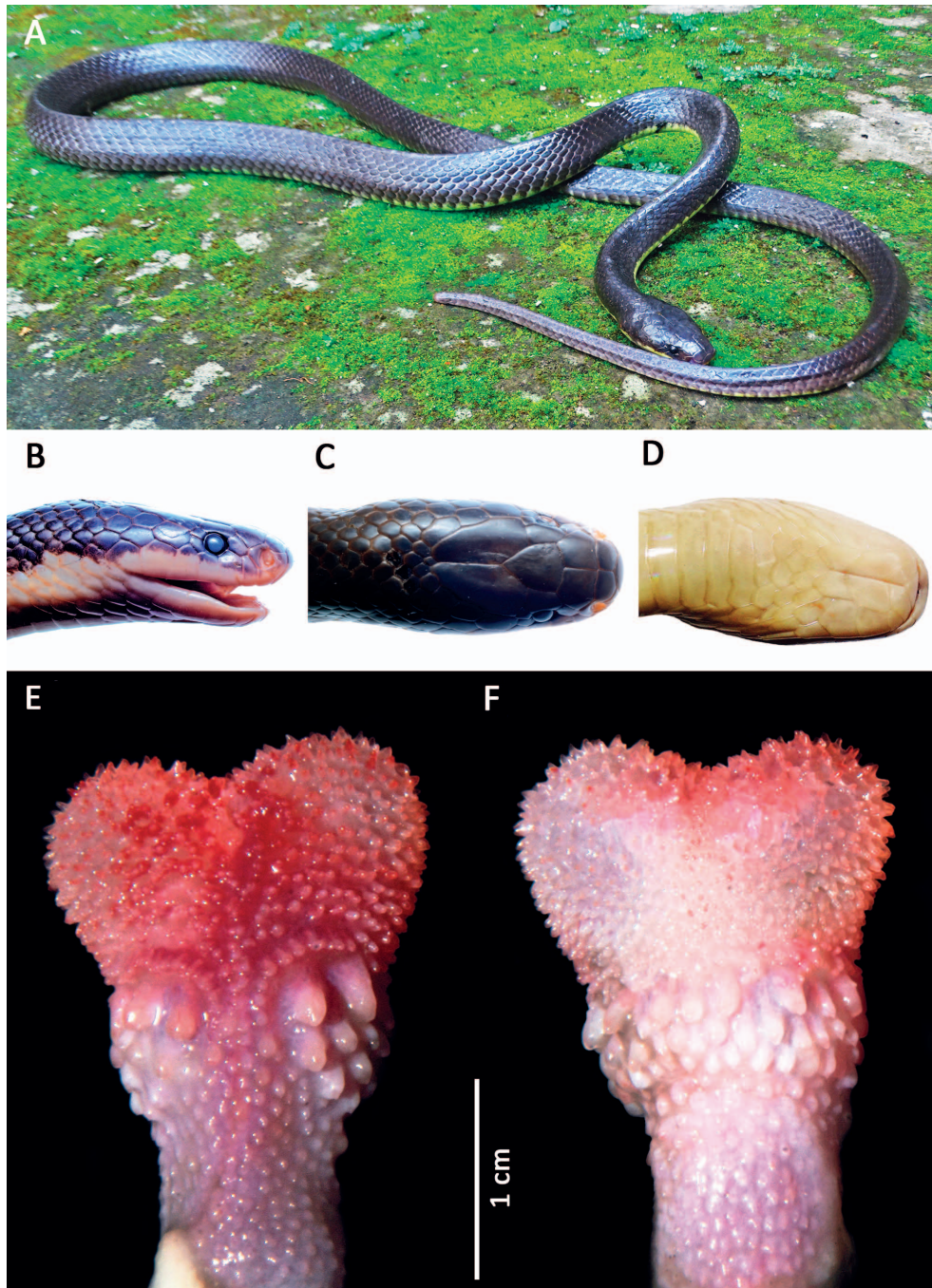


Figure 1. *Bungarus niger*. (A) Adult male from Reiek Community Reserve Forest, Mizoram, NE India; (B–D) lateral, dorsal and ventral views of the head; (E) sulcate, and (F) asulcate view of the everted hemipenis.

Distribution. In this study, we provide new distributional records (n=56) for *B. niger* from the State of Mizoram and Meghalaya, NE India at the elevation range of 50–1,433 m a.s.l. These records are represented by six individuals recorded from Umroi Military Station, Ri Bhoi District in Meghalaya State, and 55 localities from eight Districts in Mizoram State. Detailed specimens collection data is given in Supplementary Table 2. In addition, we compiled the following distributional records from published data (WALL 1908, WALL 1924, SMITH 1943, BAUER & GÜNTHER 1992, PAWAR & BIRAND 2001, TILLACK & GROSSMANN 2001, GROSSELET et al. 2004, KHAN 2004, ATHREYA 2005, BORANG et al. 2005, DASGUPTA & RAHA 2006, LEVITON et al. 2008, THEOPHILUS et al. 2008, FAIZ et al. 2010,

LALREMSANGA et al. 2011, SHARMA et al. 2013, PANDEY et al. 2016, AHSAN & RAHMAN 2017, DAS 2018, LALBIAKZUALA et al. 2019). Bangladesh: Chittagong Division–Chandanaish, Khagrachhari, Fatikchhari, Dighinala, Chittagong University, Dudpukuria-Dhopachari WS, Teknaf WS, Baraiyadhala NP, Bandarban, Rangamati, Kaptai NP, Cox’s Bazar; Mymensingh Division–Sherpur, Jamalpur; Sylhet Division–Habiganj, Moulvibazar, Lawachara NP; Dhaka Division–Savar. Bhutan: Chuka District–Phuntsholing. India: Assam–Dibrugarh, Margherita, Sadiya, Sivasagar, Guwahati, Nameri NP, Nambor WS, Borail WS, Marua-cherra, Silkuri, Assam University campus; Tripura–Dam-cherra; Arunachal Pradesh–NERIST campus, Itanagar, Mehao WS, Pakke Khellong in Eaglenest WS; Changlang,



Figure 2. *Bungarus niger*. (A) Juvenile (MZMU 1809) from Tanhril, Mizoram; (B) dorso-lateral view of the head of a juvenile *B. niger*; (C) adult male of *B. niger* preying on adult *Smithophis atemporalis* at Paikhai road, Mizoram, NE India.

Namdapha NP; Meghalaya–Garo Hill, Selbelgiri, Balpakram; Mizoram–Ngengpui WLS, Aizawl, Kolasib, Mamit and Siaha, Buhchangphai and Champhai Vengsang; Uttarakhand–Bungapani; West Bengal–Tindharia, Jalpaiguri; Nagaland (no locality record available). Nepal: Province No. 1–Golbasti, Ilam municipality; Gandaki Pradesh–Naudana, and in Kaski District. Myanmar: Chin and Rakhine States.

Natural history notes. *Bungarus niger* is known to be an ophiophagus and nocturnal species of snake, typically encountered between ca. 18:00 hrs and 02:00 hrs, and

rarely by day. It is known to inhabit evergreen and moist deciduous forests, grasslands, plantations, and human settlements (AHMED et al. 2009) at the elevation of 42–1,646 m a.s.l. (LALBIAKZUALA et al. 2019). In the wild, we observed a male individual preying on an adult *Smithophis atemporalis* on 23 September 2020 at ca. 22:00 hrs on a tarmac road at Paikhai road, Mizoram, India (23.560556°N, 92.832222°E; ca. 806 m a.s.l.; Fig. 2C). It was also reported to feed on *Coelognathus radiatus* in the wild (LALBIAKZUALA et al. 2019). In captivity, we observed the species feeding on *Argyrophis diardi*, adult *Psammodynastes pulverulentus*, sub-adult *Trimeresurus erythrurus* and *Oligodon albo-*

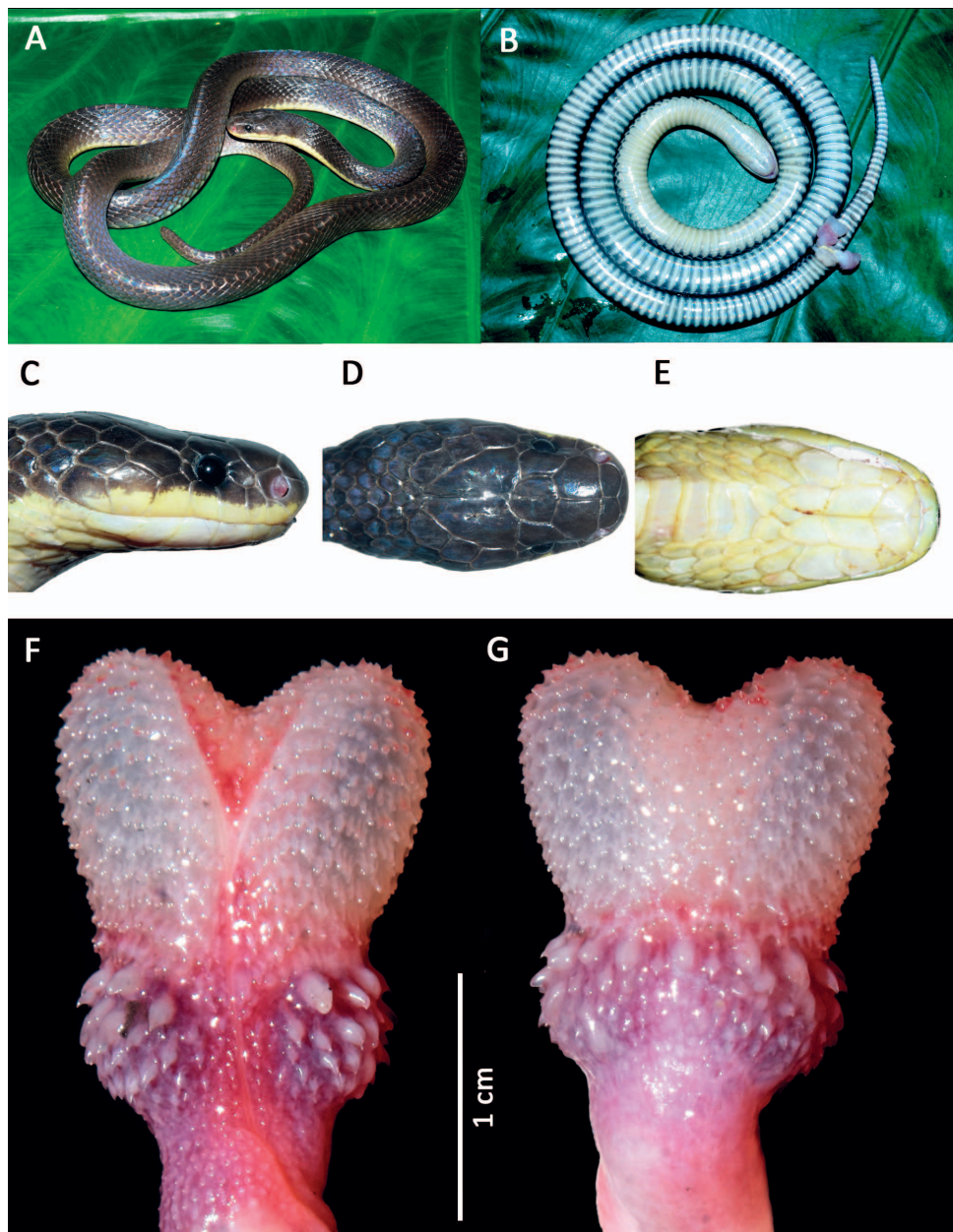


Figure 3. *Bungarus lividus*. (A) A sub-adult male (YSR 187) from Baridua, Meghalaya; (B) ventral view of the specimen; (C–D) lateral, dorsal and ventral views of the head; (E) ventral view of the head; (F) sulcate, and (G) asulcate view of the everted hemipenis.

cinctus. Another species recorded in the diet of the snake is *Trachischium tenuiceps* (WALL 1923). Moreover, we inferred that females are seemingly more secretive, or naturally rarer than the males, as only around 18% of our randomly collected specimens during this study period (2009–2020) were of the female.

Bungarus lividus CANTOR, 1839
(Type locality: Assam, India)

Morphology. CANTOR (1839) described *B. lividus* (Lesser Black Krait) based on a single specimen from Assam, India. According to the original description, the snake was blackish-blue dorsally, yellowish-white ventrally with 221 Ve and 56 Sc. Subsequently, BOULENGER (1890, 1896) added to the knowledge on the species and defined the species in having the rostral nearly as high as broad, visible from above; internasal shorter than prefrontal; frontal longer than broad, shorter than parietals; one PrO and two PoO; Tem 1+2; seven SL, third and fourth SLE; two pairs of chin shields, anterior longer and is in contact with three IF; DSR with 15 at the midbody; vertebral row of dorsal scales feebly enlarged and not broader than long; Ve 212–225 and Sc 37–56 in number. Uniform black or brown dorsal surface in colour, and ventral surface white or pale brown in colour.

In this study, we provide the morphological data based on three male specimens collected from Baridua, Megha-

laya (Fig. 3, Supplementary Table 1). It is a moderately sized snake (SVL max: 335 mm), Average relative tail length (Tal/TL) in male is 0.23–0.25 (avg. 0.24 ± 0.012); head not distinct from the neck, longer than broad (HW/HL: 0.68–0.76, avg. 0.72 ± 0.04). Eye around 16% of the HL (ED/HL: 0.15–0.17, avg. 0.16 ± 0.01), pupil round; SL and IF 7 in number, 3rd and 4th touching the eyes; PrO₁, PoO₂; ATem 1, PTem 2. In males, Ve 213–228 (avg. 218.3 ± 8.38) and Sc 33–36 (avg. 34.7 ± 1.53); Hemipenis extends up to 6–8 Sc, vaguely bilobed; at about one third from the base strongly spinosed rim present. Above the spinosed rim till the apex, the hemipenis is with small homogenous spines. The sulcus spermaticus bifurcates at two-third of the length of hemipenis and enters the lobe in a “V” shaped structure; the base of the organ is relatively smooth (Fig. 3F–G).

Distribution. During the study, we documented *B. lividus* from Azara in Assam State, and Baridua in Meghalaya State which were all within north-eastern India (Supplementary Table 2). We also compiled the following distributional records from published data (WALL, 1908, WALL, F. 1924, SMITH 1943, KHAN 1992, SHARMA et al. 2003, KUCH et al. 2011, AHSAN & RAHMAN 2017, BHATTARAI et al. 2018, DAS 2018, TSHEWANG & LETRO, 2018, RAY & PANDEY, 2020): Arunachal Pradesh–Pakke; West Bengal–Tindharia, Darjeeling, Jalpaiguri (Raikatpara Area); Assam–Dibrugarh, near Tezpur, Guwahati. Bangladesh: Rangpur Division–Rangpur, Carmichael University College campus,

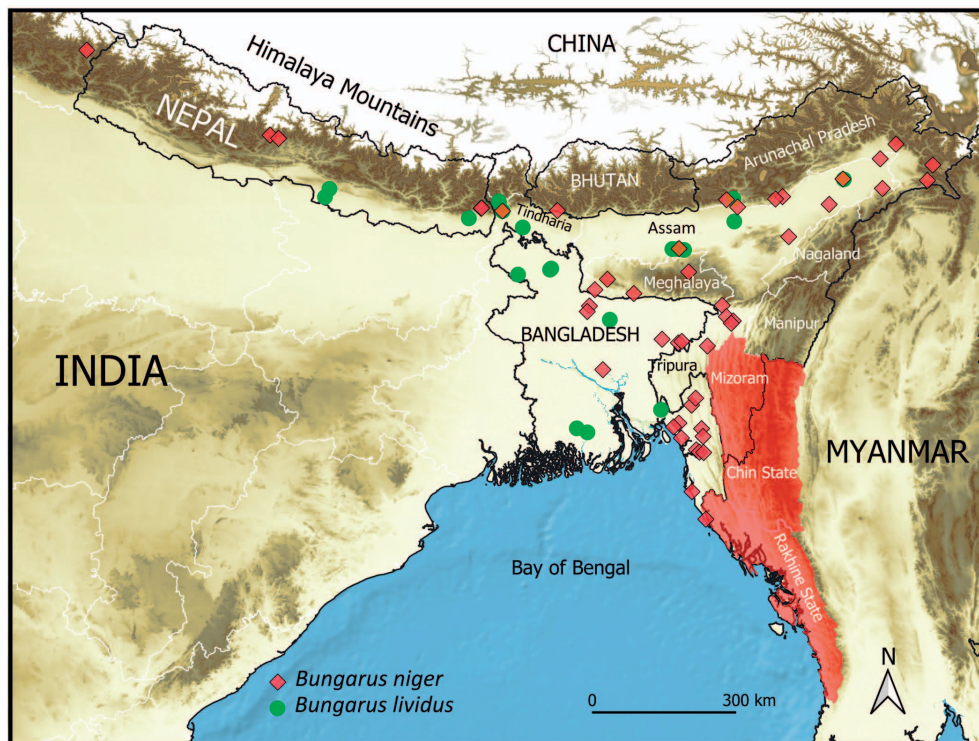


Figure 4. Distributional records of *Bungarus niger* (in red diamond and red shaded) and *Bungarus lividus* (in green dots). Distribution in Myanmar (Chin and Rakhine States), and Mizoram State, NE India is based on LEVITON et al. (2008) and LALBIAKZUALA (2019), respectively.

Dinajpur; Mymensingh division–Mymensingh district; Chittagong Division–Feni District; Barisal Division–Pirojpur; Khulna Division–Bagerhat. Nepal: Province No. 1–Beldangi I Refugee Camp near Damak in Jhapa District; Province No. 2–Amlekhganj and Bhata-Hattisar in Parsa NP. Bhutan: Langthel in Jigme Singye Wangchuck NP (Fig. 4).

Natural history notes. *Bungarus lividus* is also a night-active species, which is known to occur at an elevation range up to 340 m a.s.l. (WALLACH et al. 2014). All the individuals were encountered between 19:00 hrs and 23:00 hrs. In one occasion, an individual after being rescued from a residential area bit itself on its lower lip and soon after died (PURKAYASTHA et al. in press).

Phylogenetic relationship. For this study, the partial *cytb* gene was amplified and sequences were generated from two

individuals for *B. niger* (MZMU 975, GenBank accession no. MW596473; MZMU 1809, GenBank accession no. MW596474), and single individual each for *B. lividus* (YSR 187, GenBank accession no. MW596472) and *B. fasciatus* (MZMU 978, GenBank accession no. MW596475). The BA and ML inferred trees largely congruent except for the position of *B. flaviceps*. This species was resolved as the sister lineage to the cluster consisting of *B. bungaroides* + *B. slowinskii* in the BA analysis, but to *B. fasciatus* in the ML tree (not shown). Our generated sequence of *B. fasciatus* clustered with conspecific sequences from Thailand and Java by strong Bayesian posterior probability (BPP=1.0) and bootstrap value (100). Our analyses clearly nested *B. lividus* among the kraits of Indian subcontinent, and retrieved as a sister taxa of *B. caeruleus* and *B. ceylonicus* with a significant BPP (1.0) and bootstrap value (99), whereas *B. niger* formed a sister taxa to the clade of Southeast Asian endemic kraits (*B. multicinctus* + *B. candidus*) (BPP=0.73;

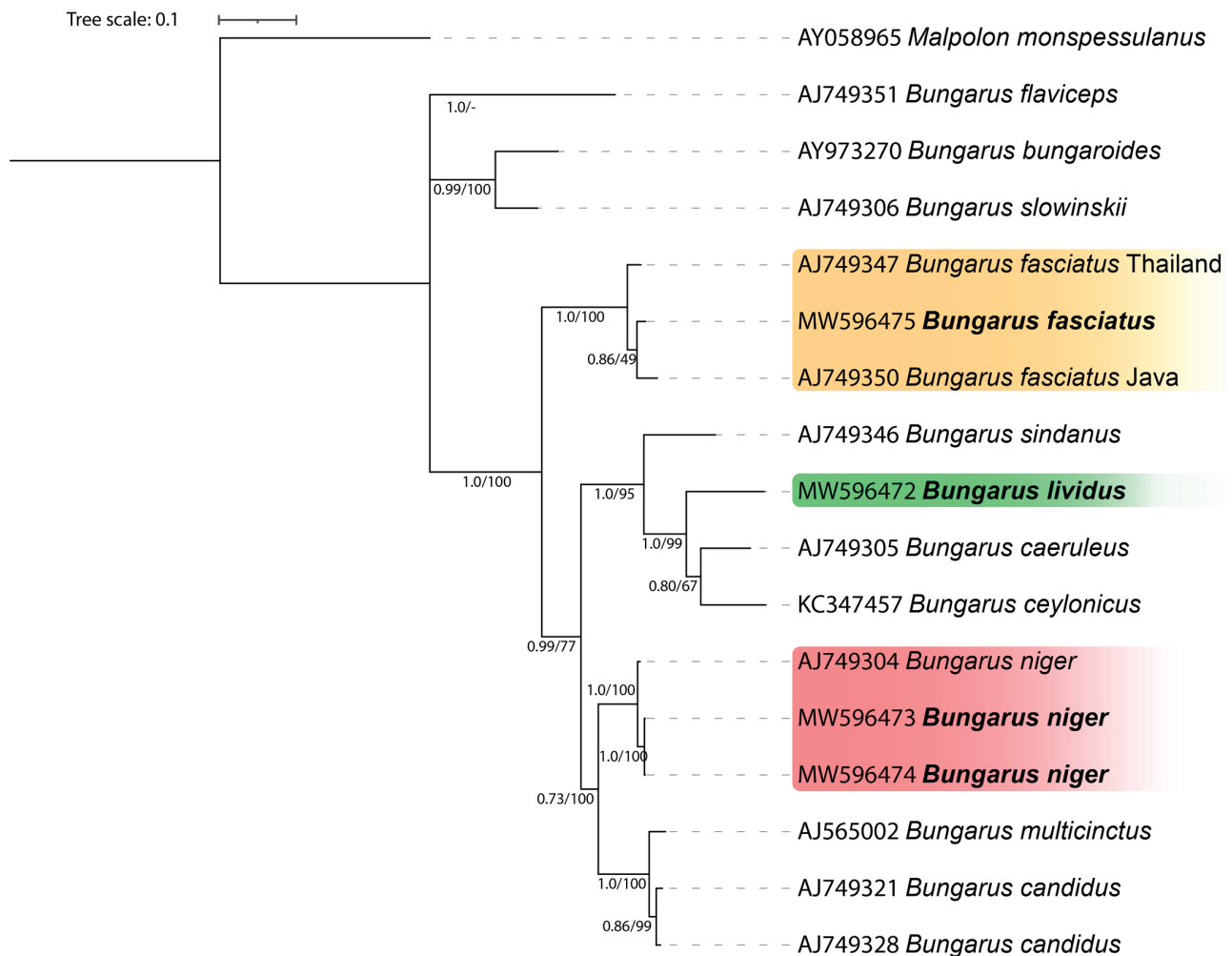


Figure 5. Bayesian inference (BA) phylogeny based on partial *cytb* gene inferred the relationship of *Bungarus lividus* and *Bungarus niger* with other congeners. Newly generated sequences are shown in bold. Numbers along internodes represent posterior probabilities from the BA phylogeny (before slashes) and bootstrap values from the Maximum Likelihood (ML) phylogeny (after slashes). (– = node not recovered in the ML analysis).

bootstrap value=100). The clade consisting of *B. sindanus* + *B. lividus* + *B. caeruleus* + *B. ceylonicus* was also inferred as sister group to *B. niger* (BPP=0.99; bootstrap value=77). Regardless of the ML bootstrap value (100), the nodal support between *B. niger* and *B. multicinctus* + *B. candidus* is not strong in the BA analysis (BPP=0.73). Likewise, with regardless of the BPP (0.99), the relationship of *B. niger* and the group containing *B. sindanus* + *B. lividus* + *B. caeruleus* + *B. ceylonicus* is also poorly supported in the ML analysis (bootstrap value=77). We therefore hinted the possibility of *B. candidus* and *B. multicinctus* as sister to *B. caeruleus*, *B. ceylonicus*, *B. lividus* and *B. sindanus*. Also, *B. niger* and *B. lividus* differ from each other by 0.151–0.154 uncorrected p-distance; the latter species differs from its closest congeners, *B. caeruleus* by 0.117 and *B. ceylonicus* by 0.120, and from its more distant congener *B. bungaroides* by 0.210 (Fig. 5, Supplementary Tables 3–4). According to the present *cytb* based phylogenetic reconstruction and genetic divergences, we argued that the two species of black kraits (*B. niger* and *B. lividus*) are possibly not sister taxa as they constituted distinct lineages. This contradicted with the morphology based phylogeny of the genus proposed by SLOWINSKI (1994). Yet, more comprehensive studies are necessary to clear up the genetic as well as morphological relationships between the two species.

As the members of this genus are known to be amongst medically important venomous snakes, accurate species identification is essential, considering the prevalence of variation in the composition of snake venom (CHIPPAUX et al. 1991) and its potential effects on the efficacy of anti-venoms (HARRISON et al. 2003). The phylogenetic study itself does not elucidate the pattern of venom composition, but contributes to the resolution of the systematics as well as provide a framework for illustrating the causes and patterns of the evolution of snake venom composition (DALTRY et al. 1996, THORPE et al. 2007, BARLOW et al. 2009). In conclusion, the present study not only contributes to the knowledge on the two krait species, but also will aid in future reference on assessing the conservation status of the species may be important for biomedical and other biological studies.

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