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continued on the back inside cover

Cover: Emperor Tamarin *Saguinus imperator*: a look into a better world through the mustache lens – mixed media illustration. © Maya Santhanakrishnan.

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ARTICLE

First record of two species of venomous snakes *Bungarus suzhenae* and *Ovophis zayuensis* (Serpentes: Elapidae, Viperidae) from India

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Abstract: We report *Bungarus suzhenae* Chen, Shi, Vogel, Ding & Shi, 2021 and *Ovophis zayuensis* (Jiang, 1977) for the first time from India. Specimens of *B. suzhenae* and *O. zayuensis* were collected during our field surveys in north (Arunachal Pradesh) and south (Nagaland-Manipur border) of the river Brahmaputra. Species identity was supported by partial cytochrome *b* (cyt *b*), and 16s mitochondrial gene. We provide a detailed morphological description and a key to the two genera of this region. This report extends the westernmost distribution of *B. suzhenae* by ca. 300 km from Myanmar, and the southernmost range of *O. zayuensis* by 170 km from Tibet. Until now eight species of *Bungarus* and only one *Ovophis* species have been reported from India. *Ovophis* species are recently reported to be medically important venomous snakes whose venom properties have not been investigated in depth.

Keywords: Krait, northeastern India, pit viper, range extension, taxonomy.

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Author details: Jason D. Gerard is a researcher with interest in taxonomy and ecology of reptiles. Bitupan Boruah is a PhD scholar whose interests are systematics and biogeography of lesser-known fauna such as amphibians and reptiles. V. Deepak is a researcher whose work predominantly focuses on the evolution and systematics of lizards, snakes and turtles in southern Asia. Abhijit Das is a scientist and faculty involved in teaching, training and research in Herpetology.

Author contributions: JDG and BB equally contributed to this work. BB, AD and JDG carried out field work for this study. JDG and BB examined the specimens. AD and BB conceptualized the study. BB and DV contributed to the phylogenetic analyses and data verification. All authors contributed equally to the writing and editing of this manuscript.

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INTRODUCTION

Northeastern India is part of the Indo-Burma biodiversity hotspot (Tripathi et al. 2016) and home to approximately 21 species of venomous snakes from the families Viperidae and Elapidae (Ahmed et al. 2009; Captain et al. 2019; Mirza et al. 2020; Rathee et al. 2022; Biakzuala et al. 2023 and 2024). Biodiversity explorations are continuing to reveal new information on snake diversity (Elangbam et al. 2023; Biakzuala et al. 2024). The Elapid genus *Bungarus* Daudin, 1803 consists of 18 species (Uetz et al. 2024), distributed from Iran and Pakistan eastwards to China and Indonesia (Chen et al. 2021). Eight species of *Bungarus* have been reported from India, namely, *B. andamanensis* Biswas & Sanyal, 1978, *B. caeruleus* Schneider, 1801, *B. sindanus* Boulenger, 1897, *B. walli* Wall, 1907, *B. lividus* Cantor, 1839, *B. fasciatus* Schneider, 1801, *B. niger* Wall, 1908, and *B. bungaroides* Cantor, 1839, of which the latter four are found in northeastern India (Ahmed et al. 2009; Das & Das 2017; Das 2018; Biakzuala et al. 2021). Recently, Chen et al. (2021) described *B. suzhenae* from China that is currently known from the type locality Yingjiang County, Yunnan Province, China, and the adjacent Kachin State of Myanmar.

There are eight species in the viperid genus *Ovophis* (Burger, 1981), namely: *O. makazayazaya* (Takahashi, 1922); *O. jenkinsi* Qiu et al., 2024; *O. malhotrae* Zeng, Li, Liu, Wu, Hou, Zhao, Nguyen, Guo & Shi, 2023; *O. monticola* (Gunther, 1864); *O. okinavensis* (Boulenger, 1892); *O. tonkinensis* (Bourret, 1934); and *O. zayuensis* (Jiang, 1977) (Malhotra et al. 2011; Zeng et al. 2023; Qiu et al. 2024; Uetz et al. 2024). The southernmost record of *O. zayuensis* is from Zayu, Motuo, Xizang province, China. During a herpetological field survey in northeastern India in 2012, 2022, and 2023, we came across one individual of *Bungarus* and two individuals of *Ovophis.* They were collected and based on morphological evaluation we identified them as *B. suzhenae* and *O. zayuensis*. Additionally, we generated new DNA sequences and compared them with published sequences of these species, including their types (*B. suzhanae* CIB 116088 from Yingjiang County, Yunnan Province, China, and *O. zayuensis* CIB 013375 from Chayu Co., Xizang, China), based on which we report here the first country records for India.

MATERIALS AND METHODS

We carried out field surveys during October 2012 in the Nagaland-Manipur border, between June and July 2022–2023 in Arunachal Pradesh, northeastern India (Figure 1). Collected specimens were fixed in formalin, washed, stored in 70% ethanol, and housed in the repository at the Wildlife Institute of India, Dehradun (WII-ADR1241, WII-ADR3316 and WII-ADR3491). Before fixation, live snakes were photographed, and liver tissues were collected and stored in absolute ethanol at -20°C.

Molecular phylogenetic analysis

Genomic DNA was extracted from liver tissue samples using DNeasy Blood and Tissue Kit (Qiagen™, Germany). For the *Bungarus* specimen (WII-ADR1241), we amplified and sequenced fragments of one mitochondrial gene, cytochrome *b* (cyt *b*) using the primers L14910 (5’-GACCTGTGATMTGAAAACCAYCGTTGT-3’) and H16064 (5’-CTTTGGTTTACAAGAACAATGCTTTA) (Burbrink et al. 2000). Polymerase Chain Reaction (PCR) conditions followed was initial denaturation at 95°C for five minutes, followed by 35 cycles of denaturation at 95°C for 45 sec, annealing at 54°C for 45 sec, and extension at 72°C for 55 sec. The final extension was at 72°C for 10 min. For the *Ovophis* sample (WII-ADR3491) we amplified and sequenced fragments of 16s gene, using the primers 16Sar (5’-CGCCTGTTTATCAAAAACAT-3’) + 16Sbr (5’-CCGGTCTGAACTCAGATCACGT-3’) (Palumbi et al. 1991). Polymerase chain reaction (PCR) condition followed was initial denaturation at 95°C for five minutes, followed by 35 cycles of denaturation at 95°C for 35 sec, annealing at 55°C for 45 sec, and extension at 72°C for one minute. The final extension was at 72°C for 10 min. Amplified PCR products were run on a 2% agarose gel and viewed under a UV transilluminator. The purified PCR product was sequenced directly in an Applied Biosystems Genetic Analyzer 3500 XL in both directions using BigDye v3.1 kit.

We manually checked bidirectional sequences using the CHROMAS v2.6.6 software (http://technelysium.com.au/wp/chromas/) and aligned using ClustalW (Thompson et al. 199) with default prior settings implemented in MEGA v7.1 (Kumar et al. 2016). For the protein-coding gene (cyt *b*), we checked for unexpected stop codons by translating the sequence to amino acids in MEGA v7.1 (Kumar et al. 2016). We used *Naja atra* and *Protobothrops mucrosquamatus* as outgroup for phylogenetic analyses of *Bungarus* and *Ovophis*, respectively. The newly generated sequences were aligned with the sequences downloaded from GenBank

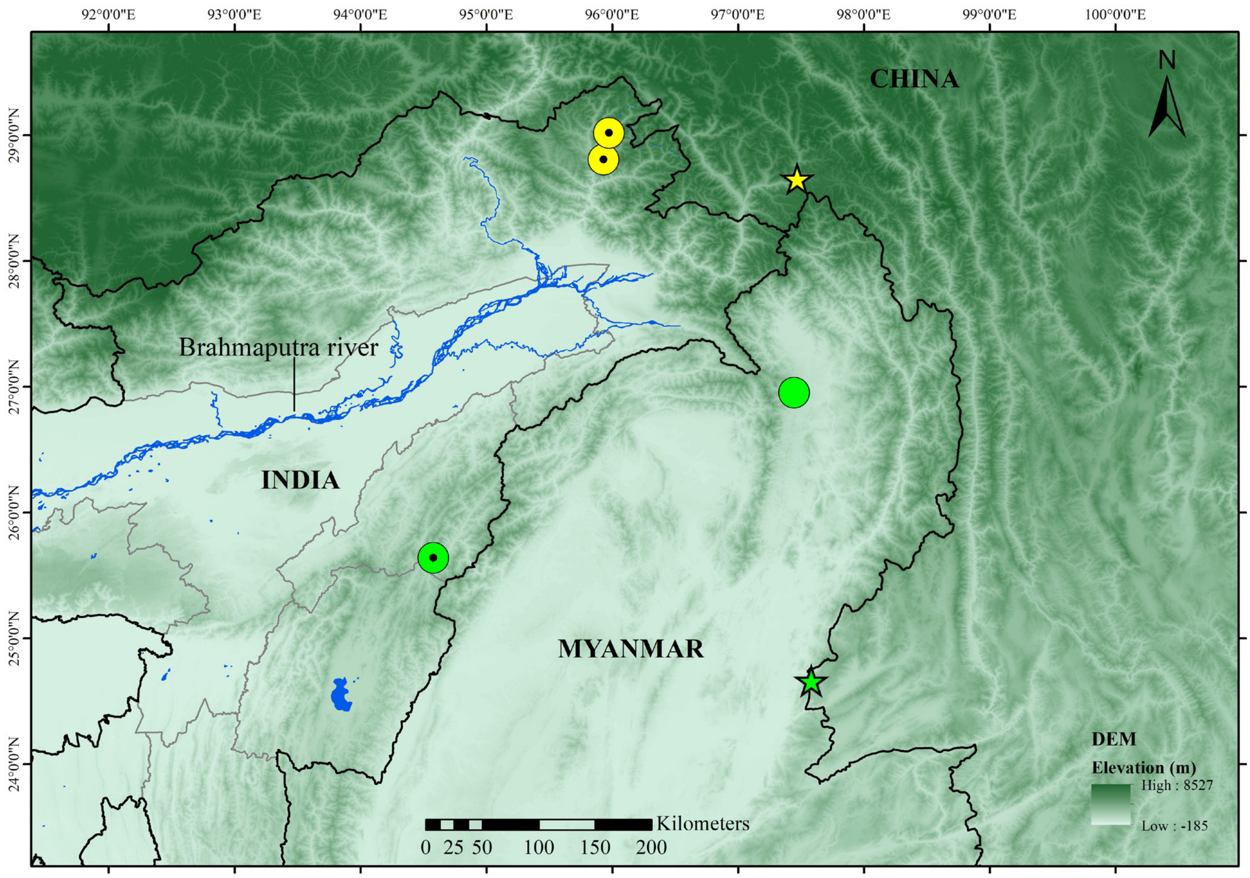

Figure 1. Map showing the locality of Indian records of *Bungarus suzhenae* (green) and *Ovophis zayuensis* (yellow). Type locality denoted by star, known locality shown as circles and new records denoted by circles with a black centre.

(Benson et al. 2009) (Appendix 1).

We performed maximum likelihood (ML) analyses using IQ-TREE (Nguyen et al. 2015), implemented in the web server version (http://iqtree.cibiv.univie.ac.at) (Trifinopoulos et al. 2016). For cyt *b*, the dataset was partitioned by codon positions using Modelfinder (Kalyaanamoorthy et al. 2017), to find the best-fit partitions and models of sequence evolution for each partition (Appendix 2). Support for internal branches was quantified using the bootstrap approximation (UFB 1000 pseudoreplicates) (Minh et al. 2013). Uncorrected P-distance was calculated in MEGA v7.1 (Kumar et al. 2016) with pairwise deletions of missing data and gaps.

Morphological character scoring and identification

Total length, snout-vent length, and tail length were measured with a thread and a metre tape in millimetre (mm). Morphometric measurements were taken with the help of a digital calliper (Mitutoyo TM) to the nearest 0.1 mm. Length and width of head scales were measured at the longest and the widest points of the respective scales. Morphological comparisons follow Das et al. (2021). All measurements were taken on the specimen's right side and scales were counted on both sides for bilateral scales. Morphometric and meristic characters were examined with the help of the Olympus SZX10 microscope. Dorsal scale rows (DSR) were counted at one head length behind the head, at midbody, and at one head length anterior to the anal scute. Ventral scales were counted following Dowling (1951). Bilateral scale counts separated by a comma are given in left, and right order. Abbreviations used are WII-ADR: Wildlife Institute of India Abhijit Das Reptile collection.

RESULTS

Molecular phylogeny

Based on mitochondrial gene cyt *b*, the specimen of *Bungarus* from Northeastern India clustered with the type sequences of *B. suzhenae* with strong bootstrap value (100) (Figure 2). Uncorrected P-distance between

Table 1. Uncorrected P-distances (%) of *Bungarus* species based on the cyt *b* sequences.

	1	2	3	4	5	6	7	8	9	10	11	12
1. *Bungarus suzhenae* (India)												
2. *B. bungaroides* (AY973270)	0.188											
3. *B. caeruleus* (AJ749305)	0.135	0.189										
4. *B. candidus* (AJ749329, AJ749339, AJ749341, MN165133)	0.098–0.101	0.167–0.17	0.139–0.142	0.003–0.008								
5. *B. ceylonicus* (KC347457)	0.144	0.201	0.101	0.151								
6. *B. fasciatus* (AJ749350, MW596457)	0.147–0.154	0.171–0.183	0.152–0.154	0.152–0.154	0.174–0.176	0.041						
7. *B. lividus* (MW596472)	0.137	0.201	0.114	0.144	0.111	0.169						
8. *B. multicinctus* (AJ749344, MN165136, MN165137, MN165139, MN165138, MN165135)	0.086–0.090	0.169–0.171	0.143–0.145	0.026–0.031	0.147–0.148	0.153–0.154	0.136–0.139	0–0.006				
9. *B. niger* (AJ749304, MW596473)	0.091–0.095	0.177–0.181	0.135–0.14	0.101–0.106	0.144–0.146	0.152	0.14–0.143	0.102–0.104				
10. *B. sindanus* (AJ749346)	0.145	0.186	0.129	0.136	0.134	0.166	0.142	0.130	0.129			
11. *B. slowinskii* (AJ749306)	0.176	0.087	0.190	0.179	0.199	0.174	0.197	0.170	0.171	0.183		
12. *B. suzhenae* (AJ749435, MN165142, MN165140, MN165141, MN165143)	0.015–0.019	0.185–0.187	0.133–0.136	0.096–0.1	0.138–0.142	0.151–0.156	0.135–0.140	0.087–0.091	0.091–0.095	0.141–0.144	0.171–0.176	0.002–0.007
13. *B. wanghaotingi* (MN165144, KY952766, MN165146, MN165145, MN165132, AJ749336, AJ749308, MN165134, AJ749309, MN165131, AJ749331, AJ749337)	0.092–0.1	0.163–0.177	0.136–0.144	0.018–0.024	0.142–0.151	0.148–0.161	0.134–0.139	0.026–0.03	0.096–0.102	0.126–0.137	0.164–0.175	0.087–0.097

the newly collected Indian samples of *Bungarus* and the type series of *B. suzhenae* from the type locality varied 0.015–0.019 (Table 1). The inferred ML tree based on *cyt*–b showed *B. suzhenae* as a sister lineage to the cluster containing *B. caeruleus*, *B. ceylonicus*, *B. lividus,* and *B. sindarus* with low bootstrap value (48) (Figure 2). Based on 16s gene, the *Ovophis* sample from Arunachal Pradesh nested with the *Ovophis zayuensis* sequence from Xizang province, China (with strong bootstrap value, (97) (Figure 3) along with two other samples from Yunnan province, China and Chin state, Myanmar. These samples altogether form a sister relationship with the samples of *O. zayuensis* from Tongmai and Xizang provinces, China with low node support (Figure 3). Uncorrected P-distance between our newly collected samples of *Ovophis* and samples of *O. zayuensis* from China and Myanmar was minimal (Table 2).

Morphology

We confirmed the new krait specimen as *Bungarus suzhenae* based on the following set of diagnostic morphological characteristics (Chen et al. 2021): enlarged hexagonal vertebral scale rows present, dorsal scales in 15:15:15 rows, anterior chin shields are slightly larger than the posterior chin shields, dorsal body black with 34 white bands, ventral scales connected with the black bands of the dorsal body by small dark patches, the ventral surface uniform white, underside of tail white with tiny brown dots in the middle.

The two viper specimens we collected were confirmed as *Ovophis zayuensis* based on the following set of diagnostic morphological characteristics (Che et al. 2020): the third supralabial larger is than the fourth, the second supralabial is fused with the loreal, internasal scales are separated by two scales; the ventral scale count is 169–172, dorsal scale count is 23 or 25:23:19 rows, the subcaudal count of 34–48, mostly single and

Table 2. Uncorrected P-distances (%) of *Ovophis* species based on the 16s gene sequences.

	1	2	3	4	5	6
1. *Ovophis zayuensis* (India)						
2. *O. zayuensis* (HQ325109, HQ325111, HQ325118, HQ325089, MK193194, MK193195)	0.004–0.019	0.0–0.013				
3. *O. monticola* (HQ326117, HQ325121, HQ325078, MG995792)	0.05–0.062	0.039–0.057	0.004–0.017			
4. *O. makazayazaya* (HQ325107)	0.056	0.039–0.055	0.05–0.054			
5. *O. tonkinensis* (HQ325096, HQ325070)	0.031–0.032	0.026–0.032	0.049–0.056	0.03–0.034	0.004	
6. *O. okinavensis* (AB175670)	0.056	0.035–0.046	0.057–0.059	0.054	0.052–0.053	
7. *O. convictus* (HQ325082, HQ325083)	0.046–0.052	0.032–0.05	0.041–0.059	0.05–0.052	0.042–0.043	0.05–0.056

Table 3. Morphometric and meristic data of newly collected specimens of *Bungarus suzhenae*. All the measurements are given in millimetre. Bilateral characters are given in left, and right order separated by comma. "N" denotes sample size, "-" indicates data not provided.

Voucher ID	WIIADR1241	Chen et al. (2021)	
Sex	male	male (N = 3)	female
Snout- vent length (SVL)	664	620–1140	1310
Tail length (TL)	109	109–180	-
Head length (HL)	21.6	21–39	30.2
Head width (HW)	10.7	12.3–15.5	19.4
Head height (HH)	6.5	8.7–12.8	14.2
Eye diameter	2.3	9.3–10.5	14.6
Ventrals	219	220–229	222
Subcaudals	57	51–54	11+
Anal plate	single	single	single
Dorsal scale row	15:15:15	15:15:15	15:15:15
Supralabial	7,7	7,7	7,7
Infralabial	7,7	7,7	7,7
Preocular	1,1	1,1	1,1
Postocular	2,2	1–2	2
Temporal (anterior + posterior)	1+2	1+2	1+2
Nasal	divided	divided	divided
No. of white bands (body + tail)	34+13	26–38+9–12	34+3

some are paired, anal scale is single.

Description of *Bungarus suzhenae* (WII-ADR1241) (Image 1,2)

An adult male specimen. Body nearly triangular in cross-section, broader at midbody, more tapering posteriorly. Head slightly distinct from the neck and longer than broad (head width/head length = 0.5); head dorsally depressed at the parietal region, frontal area flat, gradually sloping towards snout from prefrontals; loreal region concave; supralabial sloping towards outer margin; snout rounded in dorsal and lateral view; eyes with rounded pupil; external nares oval, smaller than eye diameter; nasal large and divided; prenasal touches first supralabial, rostral and internasal; postnasal touches first and second supralabial, preocular, internasal and prefrontal; postnasal-preocular suture short and straight; preocular one, hexagonal on right side and pentagonal left side, bordered by second and third supralabials, postnasal, prefrontal and supraocular; internasals two, wider than long, in contact with rostral, nasals and prefrontals; prefrontals large, slightly wider than long; internasal suture shorter than prefrontal suture length and not aligned with latter; frontal shield-shaped, pointing posteriorly, 1.3 times longer than wide, bordered by prefrontals, supraoculars and parietals; supraoculars small, 1.5 times longer than wide, in contact with preoculars, upper postoculars, prefrontals, frontal and parietals; parietals large, longer than broad, bordered by frontal, supraoculars, upper postoculars, anterior temporal and upper posterior temporal on each side, and three smalls nuchal scales on posterior margins, posterolateral margins of parietals bordered by one enlarged elongate scales that anteriorly contact upper posterior temporals on each side; postoculars two on each side; temporals 1+2; supralabial seven on both side, third and fourth touches eye, lower postocular touches by fourth and fifth supralabials on each side; anterior temporal bordered by two postoculars, fifth and sixth supralabial, parietal, and two posterior temporals; lower posterior temporal in contact with sixth and seventh supralabial; rostral wider than long and triangular; mental smaller than rostral, bordered by first pair of infralabials; infralabial seven on both sides, fourth largest; first pair of chin shields slightly larger than the

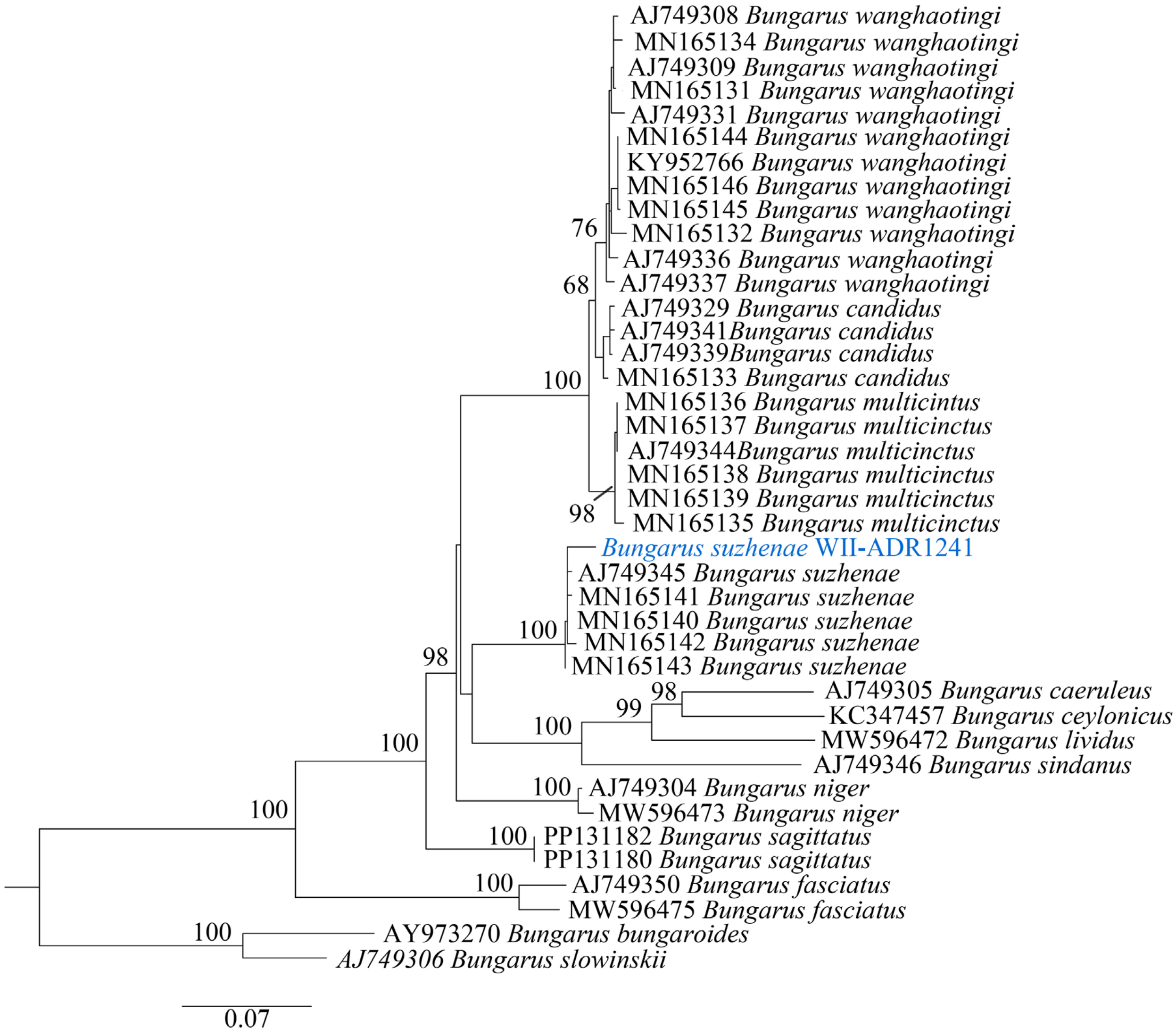

Figure 2. Maximum likelihood phylogeny of *Bungarus* based on cyt *b*. The newly generated sequences is shown in blue text. Bootstrap values <50 are not shown in the tree.

second pair chin shields; first chin shield is in contact with four infralabials on the right side and three infralabials on the left side; second chin shields contact with fourth infralabial on both sides, posteriorly bordered by three scales on the right side and fourth scales on the left side. Dorsal scales on body and tail smooth, no keel and apical pit; vertebral scale row enlarged and hexagonal; dorsal scale rows 15:15:15; ventrals 219; anal plate single; subcaudals 57, undivided; terminal scute conical; snout-vent length 664 mm and tail length 109 mm. Details of the morphometric and meristic characters of the specimen (WII-ADR1241) are given in (Table 3).

The hemipenes of the newly reported specimen of *B. suzhenae* from India agree with the description provided by Chen et al. (2021). Hemipenis can be divided into three distal calyculate region, middle spinose region, and basal region. The top of the hemipenis is slightly bilobed. The calyculate region is covered with well-developed small calyces. The spinose zone is covered with fang-shaped large keratinized spines and the basal region is covered with tiny spines; the basal region is nearly smooth towards the proximal end.

Dorsally head, body, and tail are uniformly dark brown. The rostral upper half is dark brown, the lower half (below the level of the lower edge of external nares) white; the nasals are also white below the level of the lower edge of external nares; supralabials are partly dark brown on the upper part and lower part (more than half of the scales) white; 34 narrow white cross bands on the dorsal body; bands widening on the flank before meeting

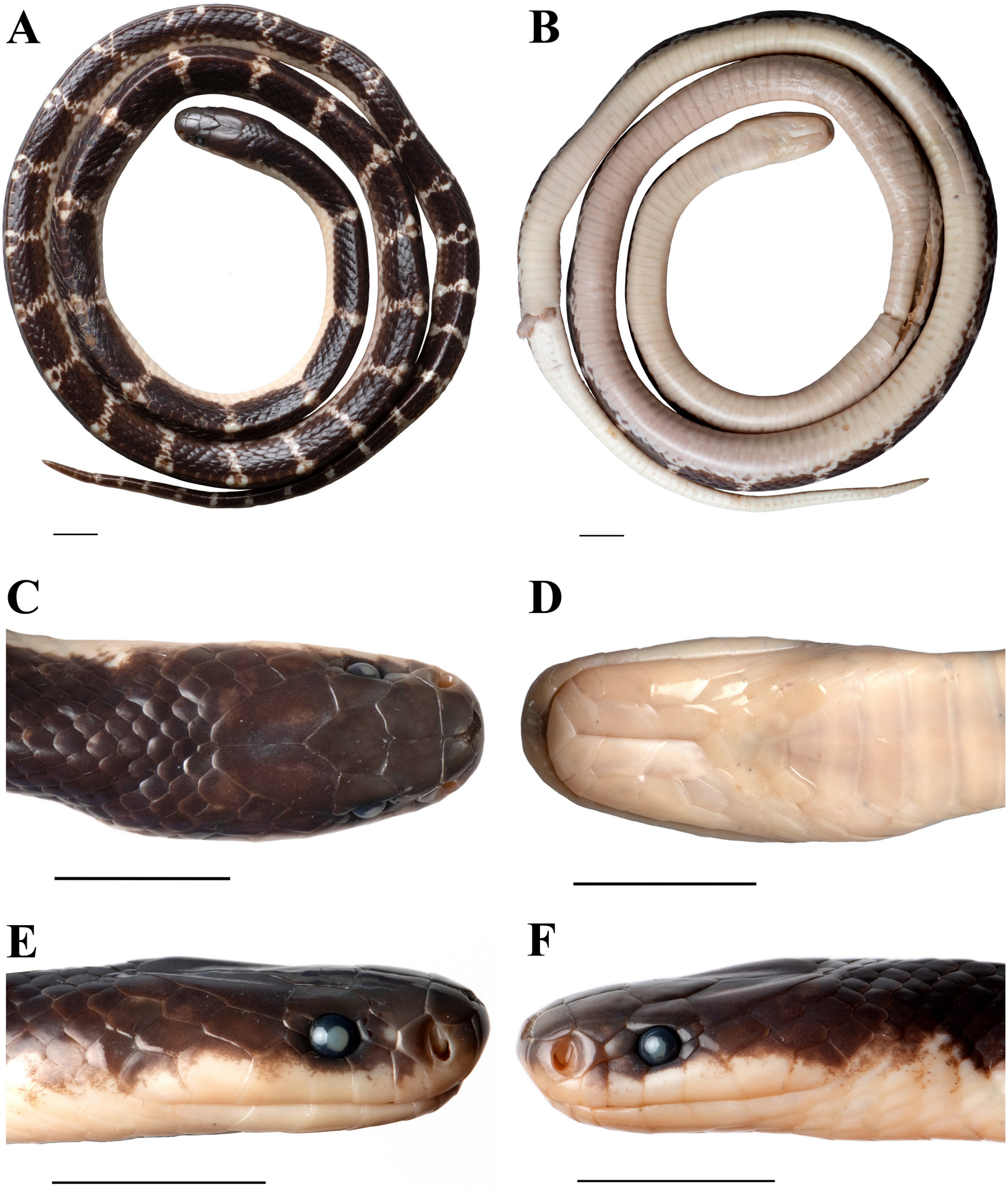

Image 1. Newly collected specimen of *Bungarus suzhenae* (WII-ADR1241) from India: Full body in A—dorsal view | B—ventral view | C—dorsal view of head | D—ventral view of head | E–F—lateral views of head, in preservation. Scale bars 10 mm. Photo: A. Das; edited by: B. Boruah

the ventrals; a dark spot present at the junctions where the white bands meet the ventrals; white bands 5–7, 13, 15, 18–26, 28, and 31–33 are broad at mid dorsum with a central dark spot forming a white semicircle; white band 27 is incomplete; black bands wide and not intruding to venter; 13 white cross bands on the tail; ventrally white including infralabials, mental, chin shields, gular scales, ventrals, and subcaudals; the edge of the ventrals with slightly dark brown patch; tail ventrally white with tiny brown dots in the middle. The specimen is dorsally dark

Image 2. *Bungarus suzhenae* (WII-ADR1241) in life from Nagaland-Manipur border, India. © A. Das.

brown with white transverse bands on the body and tail. Interstitial skin white. Ventrally white, subcaudals with tiny brown dots in the middle (Image 2). Difference between the newly reported specimen and original description of *B. suzhenae:* Notable difference between the type specimen (based on the original description) and our newly reported specimen (WII-ADR1241) is a lower number of ventrals in the new specimen (219 vs. 220–229), the higher number of subcaudals in the new specimen (57 vs. 51–54).

This newly reported specimen was encountered along Jessami–Meluri road (25.6393^{0}N, 94.5791^{0}E, elevation 599 m), at the Nagaland-Manipur border ca. 6 km from Meluri, Nagaland towards Jessami, Manipur. This individual was found while it was crossing the road at around 2100 h on 20 October 2012. The Tiji River flows ca. 20 m away from the collection locality. A roadkill *Bungarus niger* was also recorded 100 m away from the location of *B. suzhenae* indicating their sympatric occurrence. The surrounding landscape was mostly with secondary vegetation with extensive jhum cultivation areas. While photographing, the snake showed head-hiding behaviour and bit the snake bag in defence.

Description of *Ovophis zayuensis* (WII-ADR3316 and WII-ADR3491) (Image 3,4)

Both the specimens are adult females. Specimens are in good condition, latero-ventral incision between ventral scale 99–102 in WII-ADR3316 and between ventral scale 66–70 in WII-ADR3491. Head triangular, body stout and the dorsal scales are strongly keeled, ventrally plain pale yellow or orangish in color with no patterns. There are faint black blotches on the anterior dorsal region of the body and the blotches are dark on the posterior dorsal region. After preservation, the specimen's colour changed into smokey grey with black blotches on the dorsal side. Dorsally head is completely covered with small scales. The head length ranges 34.2–37.9 mm, the head width is 23.1–25 mm, the eye diameter is 2.5–2.6 mm, the eye-to-nostril distance is 5.5–7.3 mm, and the snout length is 10.1–11.3 mm. No supralabials touching the eye, one preocular and three postocular present. Nasal single and undivided in both specimens. There is no distinguishable temporal, parietal, and frontal scales present. The second supralabial is fused with the loreal pit. The total length of the specimens is 826–900 mm, SVL 699–746 mm, tail length 127–154 mm, ventral scales 166–167 mm, anal scale single and undivided, subcaudals 46–49 with 5–6 paired. WII-ADR3491 has nine supralabials on the left, third is the

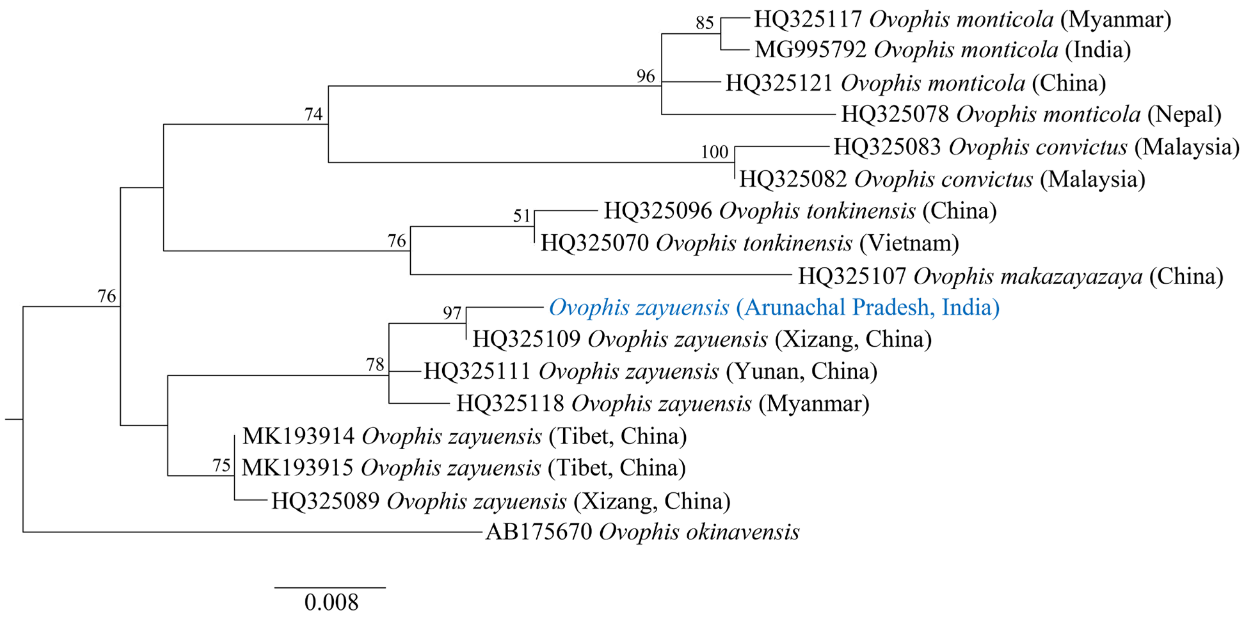

Figure 3. Maximum likelihood phylogeny of *Ovophis* based on 16s gene. The newly generated sequence is shown in blue text. Bootstrap values <50 are not shown in the tree.

Table 4. Morphometric and meristic data of newly collected specimens of *Ovophis zayuensis*. All the measurements are given in millimetre.

Voucher ID	WII-ADR3491	WII-ADR3316
Sex	female	female
Snout- vent length (SVL)	746	699
Tail length (TL)	154	127
Head length (HL)	37.9	34.2
Head width (HW)	25	23.1
Head height (HH)	14.3	14.2
Eye diameter	2.6	2.5
Ventrals	167	166
Subcaudals	49	46 (missing tip)
Anal plate	single	single
Dorsal scale row	25:23:19	23:23:19
Supralabial	9,8	9,9
Infralabial	10,11	9,9
Preocular	1,1	1,1
Postocular	3,3	3,3
Nasal	undivided	undivided

largest measuring 4.3 mm; eight supralabials on the right, third is the largest measuring 3.6 mm. Infralabials 10 on the left, the fourth is the largest measuring 3.2 mm; 11 infralabials on the right and the sixth is the largest measuring 2.8 mm, dorsal scale rows 25:23:19. WII-ADR3316 has nine supralabials on both sides, third is the largest measuring 3.7 mm. Infralabials nine on both sides, on the right sixth is the largest measuring 3.5 mm, and on the left, fifth is the largest measuring 3.3 mm, dorsal scales rows 23:23:19.

The individual WII-ADR3491 was recorded at Dri River bank (28.8056^{0}N, 95.9321^{0}E, elevation 1,288 m), near Etabe village (~2.5 km north-east from Anini), Dibang Valley district, Arunachal Pradesh. This individual was found while it was moving on the ground along the edge of a first-order stream on 16 August 2022 at 2000 h. The stream edge was covered with small to moderate-sized boulders covered with moss and leaf litter, fern, and other vegetation. The recorded locality was ~100 m from the Dri river near Etabe village. Along the stream, we observed a few anuran species such as *Xenophrys* sp. and *Amolops beibengensis* on the vegetation and also an unidentified rodent species. The second individual WII-ADR3316 was collected from the newly constructed Chigu Pani road, Anini, Dibang Valley (29.0182^{0}N, 95.9755^{0}E, elevation 1,800 m). The habitat in this region was disturbed due to the recent construction of roads, small streams were blocked by retaining walls. It was found perched in a bush 50 cm above the ground around 1900 h between the walls, blocking the stream. There was a mild yet constant drizzle throughout the night. Many *Amolops* froglets were found near the blocked stream and on the road. This individual was a bit aggressive while trying to bag, it puffed up, flattened

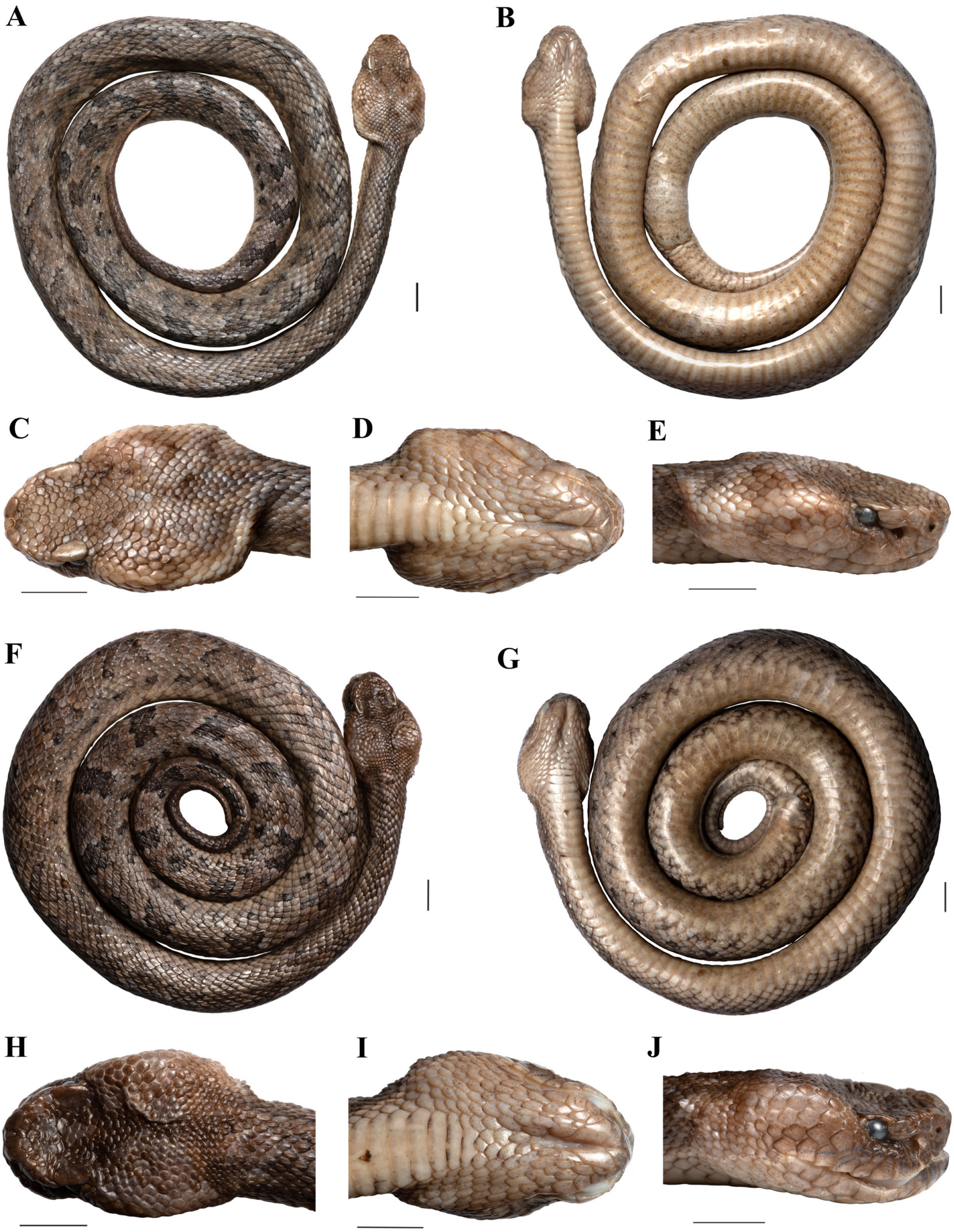

Image 3. Newly collected specimen of *Ovophis zayuensis* from India: A–E—WII-ADR3491 | F–J—WII-ADR3316. Full body in A & F—dorsal view | (B & G)—ventral view | C & H—dorsal view of head | D & I—ventral view of head | E & J—lateral views of head, in preservation. Scale bars 10 mm. © A. Das; edited by: B. Boruah

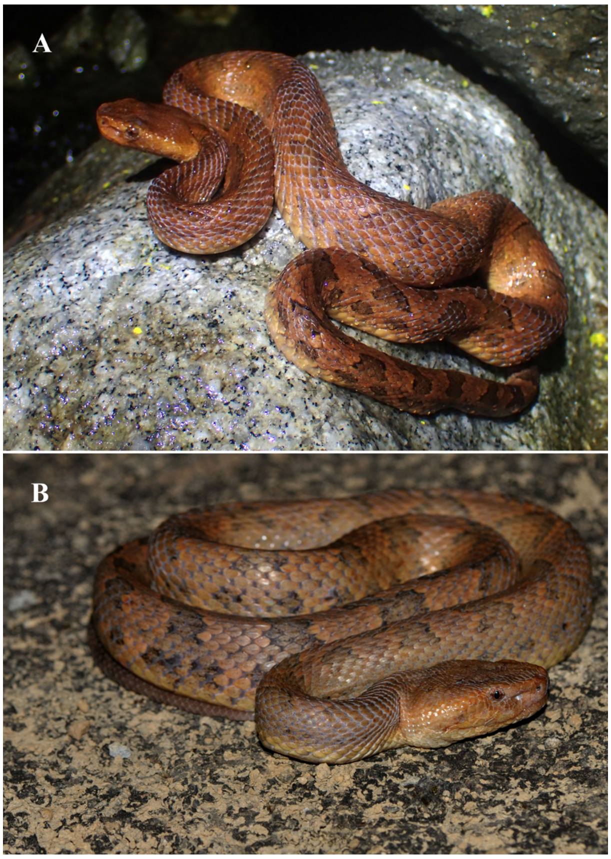

Image 4. *Ovophis zayuensis* in life from Arunachal Pradesh, northeastern India. A. WII-ADR3316, B. WII-ADR3491. © A. Das (A) | B. Boruah (B).

its body, and struck the snake hook. The next day around 2000 h on the same road, close to a small stream two other individuals of *O. zayuensis* male and female were spotted crossing the road from both sides. The blocked streams were seen to be harbouring tadpoles of multiple species of frogs including *Amolops* sp. and *Megophrys* sp. These two snakes were removed from the roadside and released by the stream.

DISCUSSION

There are over 400 known species of snakes in India (Uetz et al. 2024), where 1.2 million snakebite deaths were recorded during the years 2000–2019 (Suraweera et al. 2020). The Mountain Pit Viper *Ovophis monticola* Günther, 1864 has recently shown to cause medically significant envenoming (Ralph et al. 2023) while the *Bungarus* species have always been among the big four snakes of medical importance from India (Simpson & Norris 2007; Suraweera et al. 2020; Sunagar et al. 2021). *Bungarus suzhenae* and *Ovophis zayuensis* are two venomous snakes being reported for the first time from India, from the border of Nagaland-Manipur and Arunachal Pradesh, respectively.

Among the 18 known species of *Bungarus*, the maximum diversity is congregated in southeastern Asia. Until now eight species of *Bungarus* have been reported from India and are known for frequently causing fatal envenoming in the region (Suraweera et al. 2020; Sunagar et al. 2021). Despite several fatalities by other *Bungarus* species, the commercial antivenom is manufactured only against the most widespread congener *B. caeruleus* (Sunagar et al. 2021). This new finding reported here also indicates the lack of systematic studies on this group of snakes especially in northeastern India. Identification of *Bungarus* species is still a challenge which is evident by the recent discovery of *B. suzhenae* from China and Myanmar. *Bungarus* species with white cross bands—*B. andamanensis* Biswas & Sanyal, 1978; *B. bungaroides* Cantor, 1839; *B. caeruleus* Scheider, 1801; *B. multicinctus* Blyth, 1861; *B. sindanus* Boulenger, 1897; *B. slowinskii* Kuch, Kizirian, Nguyen, Lawson, Donnelly & Mebs, 2005; *B. suzhenae* Chen, Shi, Vogel, Ding & Shi, 2021; *B. walli* Wall, 1907; *B. canidus* Linnaeus, 1758; *B. magnimaculatus* Wall & Evans, 1901; and *B. persicus* Abtin, Nilson, Mobaraki, Hosseni & Dehgannejhad, 2014—are most complex and difficult to identify only based on external appearance (Leviton et al. 2003; Chen et al. 2021).

The genus *Ovophis* has eight known species globally (Malhotra et al. 2011), and now two species from India, namely: *O. monticola* and *O. zayuensis*. Though not commonly found in conflict with humans some species of *Ovophis* are capable of delivering a severely painful or life-threatening bite (Ralph et al. 2023). The venom composition of these less medically significant snakes and their clinical effects on humans still need to be studied (Tan et al. 2021). The current distribution range of *O. zayuensis* extends into the upper region of Dibang Valley, Arunachal Pradesh, Northeast India. However, it is important to carefully look into the distribution of *O. zayuensis* from the rest of Arunachal Pradesh. Being in the transition zone, the geographical range of these and other such species is likely to overlap in northeastern India. Therefore, proper identification of such venomous species and understanding of geographic distribution is crucial for general awareness, venom research as well as development of lifesaving antivenin.

Northeastern India is known to have Tibeto-Yunanese, Indo-Malayan, and its own unique faunal elements (Das 1996; Giri et al. 2019; Lalronunga et al. 2020; Vogel et al. 2020; Deepak et al. 2021; Das et al. 2021). The

Identification key to the *Bungarus* species of northeastern India

Crossbands on body and tail absent 1
1A. Mid-dorsal scale distinctly enlarged .... *Bungarus niger*
1B. Mid-dorsal scale not enlarged .... *Bungarus lividus*
Crossbands present 2
2A. Crossbands yellow and black .... *Bungarus fasciatus*
2B. Crossbands white 3
3A. White crossbands not paired, 26–38 in number .... *Bungarus suzhenae*
3B. White crossbands not paired, 46–60 in number .... *Bungarus bungaroides*

Identification key to the *Ovophis* species from India

Ventral scales
A. 135–154 .... *O. monticola*
B. 158–176 .... *O. zayuensis*

new record of *B. suzhenae* from India indicates the possibility of the occurrence of other *Bungarus* species reported from Myanmar such as *B. magnimaculatus*, *B. wanghaotingi,* and *B. flaviceps*. Therefore, a systematic study is necessary across northeastern India to document the diversity of medically important snakes. With the present report of *B. suzhenae,* the number of *Bungarus* species in India increases to nine, and the distribution range of *B. suzhenae* is extended by ca. 321 km north-west from the nearest known locality, Yingjiang County, Yunnan Province, China. The geographical area of occurrence of *B. suzhenae* is currently ca. 38,000 km^2 within China, Myanmar, and northeastern India. In earlier documentation, other *Bungarus* species such as *B. bungaroides*, *B. fasciatus,* and *B. niger* were reported from Nagaland (Ao et al. 2004; Dasgupta & Raha 2006; Das 2018). Singh (1995) and Sinate et al. 2021 also reported *B. fasciatus* and *B. niger* from Manipur respectively. Since the present specimen of *B. suzhenae* was encountered at the Nagaland-Manipur border, there is a possibility of the occurrence of the species in other parts of Manipur. In a herpetofaunal biodiversity report of Nagaland, Grewal et al. (2011) provided a photograph of a road-killed unknown *Bungarus* sp. from Pungro-Shatuza road (nearest distance ca. 13 km from the present locality) which is similar to *B. suzhenae* (based on the lower number (<40) of unpaired white cross bands on body). Therefore, the distribution range of this medically important snake is likely to be wider than hitherto known in the region. Despite several reports of fatal snake bites by other species, commercial Indian antivenoms are only manufactured against *Daboia russelii, Naja naja, Echis carinatus,* and *Bungarus caeruleus.* Hence, it is important to recognise other medically important Indian snake species as it also has great significance in the field of snake antivenom design and manufacture (Simpson & Norris 2007).

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Appendix 1. Details of the GenBank sequences used in this study. The sequence of *Bungarus suzhenae* and *Ovophis zayuensis* generated in this study is given in bold.

Taxa	Voucher numbers	Locality	AccessionNo. (cyt– *b*)	Reference
B. bungaroides	KIZ 98R0186	Medog, Medog County, Tibet, China	AY973270	Kuch et al. 2005
B. caeruleus	UK H7	Pakistan	AJ749305	Kuch 2007
B. candidus	UK B39	Vicinity of Jambah, Losarang District, Indramayu Regency, West Java, Indonesia	AJ749329	Kuch 2007
B. candidus	UK BcBa	Bali Island, Indonesia	AJ749339	Kuch 2007
B. candidus	UK B21	Vicinity of Jambah, Losarang District, Indramayu Regency, West Java, Indonesia	AJ749341	Kuch 2007
B. candidus	SYNU R180411	Endau Rompin National Park, Taman Negara, Johor, Malaysia	MN165133	Chen et al. 2021
B. ceylonicus	RS-135	Sri Lanka	KC347457	Pyron et al. 2013
B. fasciatus	UK B24	Vicinity of Jolo, Central Java, Indonesia	AJ749350	Kuch 2007
B. fasciatus	MZMU978	Mizoram, India	MW596475	Biakzuala et al. 2021
B. lividus	YSR187	Baridua, Meghalaya, India	MW596472	Biakzuala et al. 2021
B. multicinctus	CIB104228	Nanning Zoo, Guangxi, China (locality uncertain)	MN165137	Chen et al. 2021
B. multicinctus	UK Bm1	Zhejiang, China	AJ749344	Kuch 2007
B. multicinctus	CIB DL18090209	Wuyi Moutain, Fujian, China	MN165138	Chen et al. 2021
B. multicinctus	CIB DL18090210	Wuyi Moutain, Fujian, China	MN165139	Chen et al. 2021
B. multicinctus	CIB93923	Guangxi, China	MN165136	Chen et al. 2021
B. multicinctus	SYNU R180305	Haikou, Hainan, China	MN165135	Chen et al. 2021
B. niger	Bnig	Nepal	AJ749304	Kuch 2007
B. niger	MZMU975	Mizoram, India	MW596473	Biakzuala et al. 2021
B. sindanus	Bsin1	Pakistan	AJ749346	Kuch 2007
B. slowinskii	IEBR 1172	Na Hau Commune, Van Yen District, Yen Bai,Vietnam	AJ749306	Kuch 2007
B. suzhenae	CAS 221526	Naung Mon Township, Rabaw Kachin State, Burma (Myanmar)	AJ749345	Kuch 2007
B. suzhenae	CIB116088	Yingjiang, Yunnan, China	MN165140	Chen et al. 2021
B. suzhenae	CIB116089	Yingjiang, Yunnan, China	MN165141	Chen et al. 2021
B. suzhenae	CIB116090	Yingjiang, Yunnan, China	MN165142	Chen et al. 2021
B. suzhenae	CIB116091	Yingjiang, Yunnan, China	MN165143	Chen et al. 2021
B. suzhenae	**WIIADR1241**	**Nagaland-Manipur border, India**	**PP808595**	**This study**
B. wanghaotingi	ROM 35250	Quang Thanh, Cao Bang, Vietnam	AJ749308	Kuch 2007
B. wanghaotingi	ROM 35256	Chi Linh, Hia Duong, Vietnam	AJ749309	Kuch 2007
B. wanghaotingi	UK BT6	Nakhon Si Thammarat, Thailand	AJ749331	Kuch 2007
B. wanghaotingi	UK BT8	Nakhon Si Thammarat, Thailand	AJ749336	Kuch 2007
B. wanghaotingi	FMNH 255259	Hin Nam No National Biodiversity Conservation Area, Boualapha District, Khammouan, Laos	AJ749337	Kuch 2007
B. wanghaotingi	FMNH 255260	Nam Et Phou Louey Mountain, Phou Louey National Biodiversity, Conservation Area, Vieng Tong, Huaphahn, Laos	AJ749338	Kuch 2007
B. wanghaotingi	CIB FCDZ20170806	Dongzhong, Fangchenggang, Guangxi, China	MN165131	Chen et al. 2021
B. wanghaotingi	CIB104227	Beiliu, Guangxi, China	MN165134	Chen et al. 2021
B. wanghaotingi	SYNU R170408	Bang Lang National Park, Yala, Thailand	MN165132	Chen et al. 2021
B. wanghaotingi	CIB ML20170801	Menglun, Yunnan, China	MN165145	Chen et al. 2021
B. wanghaotingi	CIB MLMY20170801	Mengla, Yunnan, China	MN165144	Chen et al. 2021
B. wanghaotingi	JK20181101	Jinghong, Yunnan, China	MN165146	Chen et al. 2021
B. wanghaotingi	GP 3375	Xishuangbanna, Yunnan Province, China	KY952766	Xie et al. 2018
Naja atra	-	China	DQ343648	Yan et al. 2008

O. zayuensis	**WII-ADR3491**	**Dibang Valley district, Arunachal Pradesh, India**	**PP794643**	**This study**
O. zayuensis	GP90	Xizang Autonomous Region, China	HQ325109	Malhotra et al. 2011
O. zayuensis	GP92	Yunnan Province, China	HQ325111	Malhotra et al. 2011
O. zayuensis	CAS 233203	Chin State, Myanmar	HQ325118	Malhotra et al. 2011
O. zayuensis	CHS099	Tibet, China	MK193914	Li, J. N et al. 2020
O. zayuensis	CHS101	Tibet, China	MK193915	Li, J. N et al. 2020
O. zayuensis	GP89	Xizang Autonomous Region, China	HQ325089	Malhotra et al. 2011
O. tonkinensis	MVZ 226627	Vinh Phu Province, N Viet Nam	HQ325096	Malhotra et al. 2011
O. tonkinensis	B581	China	HQ325070	Malhotra et al. 2011
O.monticola makazayazaya	GP24	Yunnan Province, China	HQ325107	Malhotra et al. 2011
O. monticola	CAS 224424	Kachin State, Myanmar	HQ325117	Malhotra et al. 2011
O. monticola	V16	North East India	MG995792	
O. monticola	CAS 234866	Chin State, Myanmar	HQ325121	Malhotra et al. 2011
O. monticola	ZMB 70216	Gandaki Zone, W Nepal	HQ325078	Malhotra et al. 2011
O. okinavensis	-	-	AB175670	Dong & Kumazawa 2005
O. convictus	B629	Pulau Langkawi, West Malaysia	HQ325083	Malhotra et al. 2011
O. convictus	B628	Pulau Langkawi, West Malaysia	HQ325082	Malhotra et al. 2011
Protobothrops mucrosquamatus	B106	Vin Phuc Province, N Viet Nam	AY294271	Herrmann et al. 2004

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