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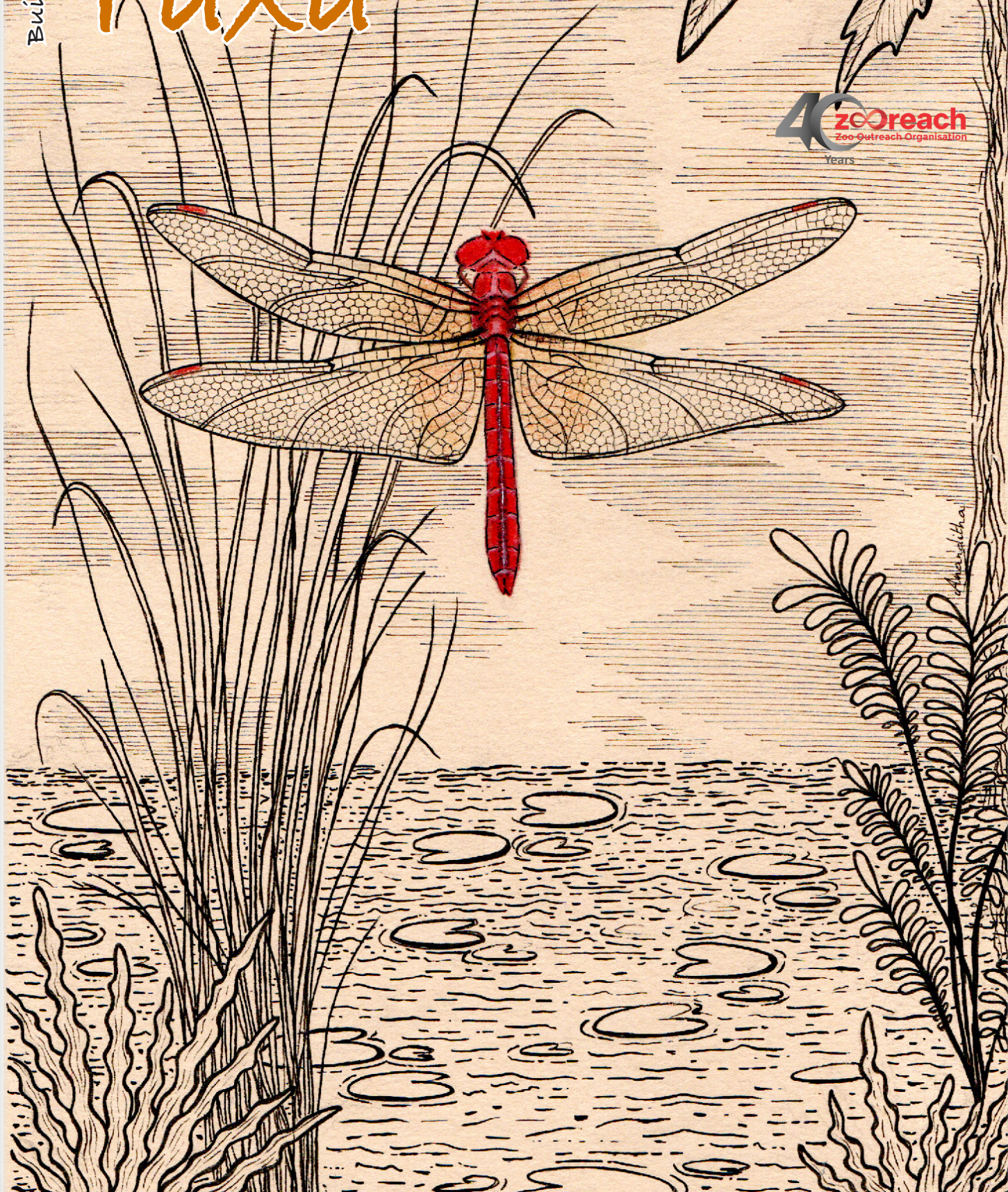
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Cover: A male Scarlet Skimmer perching on vegetation by the banks of a waterbody. Ink and watercolour illustration by Ananditha Pascal.



Phylogenetic confirmation of generic allocation and specific distinction of Mawphlang Golden-cheeked Frog *Odorrana mawphlangensis* (Pillai & Chanda, 1977) (Amphibia: Anura: Ranidae) and its updated distribution records

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Abstract: We report on the phylogenetic position (16S rRNA) of the Mawphlang Golden-cheeked Frog *Odorrana mawphlangensis* collected from Meghalaya (topotypical) and Mizoram, northeastern India. Morphologically, our new specimens agreed with the original description and subsequent redescription of *O. mawphlangensis*, thus ratifying the generic placement of *O. mawphlangensis* and its specific distinction from *O. grahami*, to which it was hypothesized to be a synonym owing to morphological similarities. The observed interspecific genetic distances within the genus *Odorrana* from our study ranged from 0.00% (*O. mawphlangensis*) to 11% (*O. fengkaiensis*). The uncorrected K2p-distance of 16S rRNA among *Odorrana* species revealed *O. mawphlangensis* is closest to its sister species *O. jingdongensis*, with a genetic distance of 3.7%. This study identifies and confirms the collected samples from Mizoram as *O. mawphlangensis* and also presents an updated distribution record from northeastern Indian state of Mizoram apart from its type locality in Meghalaya.

Keywords: Distribution records, frog, holotype, type locality, mitochondrial DNA, Mizoram, molecular phylogeny, morphology, northeastern India, taxonomy.

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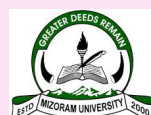
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INTRODUCTION

Odorrana mawphlangensis (Pillai & Chanda, 1977) commonly known as the Mawphlang Golden-cheeked Frog (Dinesh et al. 2023), is a large sized frog species belonging to the family Ranidae, first described by Pillai & Chanda (1977), from Mawphlang Sacred Forest in Khasi Hills, Meghalaya, India, on the basis of an adult female bearing museum number, ZSI A 6979 (ex ZSI/ERS 803). In subsequent observations, this species was reported from other northeastern Indian states of Nagaland, Arunachal Pradesh, Manipur, and Mizoram as well as from West Bengal (Frost 2025). The description of the species was based solely on the holotype which led to it being misleadingly placed as a close relative of several species, namely *Limnonectes doriae* (Boulenger, 1887) and *Limnonectes modestus* (Boulenger, 1882). This misplacement was followed in the subsequent reports by Tiwari (1981) and Dubois (1987) with Ohler & Dubois (1999) transferring this species to the genus *Limnonectes* (*Elachyglossa*) (Anderson, 1916), including the originally proposed “possible relative” of *L. modestus*. Ao et al. (2003) indicated its close resemblance to *Rana* (*Odorrana*) *andersoni*. However, there was not enough explanation to support this inference. Mahony (2008), encountered similar-looking ranid frogs at the type locality Mawphlang Sacred Forest that not only resembled *Odorrana* but also produced secretions having a distinct odour. Against the backdrop of these sightings, Mahony (2008) redescribed the holotype (ZSI/K) which re-allocated it from *Limnonectes*, to *Odorrana* based on morphological and geographical grounds.

The Ranid genus *Odorrana* comprises of 69 recognized species (Frost 2025), widely distributed in montane streams and rivers in the subtropical and tropical regions of eastern and southeastern Asia (Fei et al. 2012; AmphibiaChina 2021; Frost 2025). High-gradient streams, often located in mountain environments, are typical habitats of the *Odorrana* species, although *O. mutschmanni* (Pham et al. 2016), *O. wuchuanensis* (Xu 1983), and *O. lipuensis* (Mo et al. 2015) have been found to otherwise inhabit karstic limestone caves, with an elevation range of 447–728 m (Fei et al. 2012; Pham et al. 2016; Liu et al. 2021; Frost 2025). The distributional range of the genus comprises of the Ryukyu Archipelago (Japan), southern China, northeastern India, and the Thai-Malay Peninsula, and further extending southwards to the two large southeastern Asian islands, Sumatra and Borneo (Frost 2025). Considering the peculiar ecological niche

where this species resides, there could possibly be inter- or intra-specific divergence through geographical isolation, especially given the species complex with a wide geographical range covering varied mountain ranges and variable habitats (Wang et al. 2015). The phylogeny and diversity of *Odorrana* and the systematic status of taxa within the genus have been a matter of constant debate by taxonomists (Frost et al. 2006; Che et al. 2007; Fei et al. 2009; Kurabayashi et al. 2010; Chen et al. 2013; Li et al. 2015).

In spite of treating *Odorrana* as a subgenus of *Rana* (Dubois 1992) and expanding the genus *Huia* to include both *Odorrana* and *Rana* (*Eburana*) (Frost et al. 2006), the monophyly of *Odorrana* was finally supported by analysing mtDNA data and nuclear data separately as well as subsequent analyses of the combinations of mtDNA and nuclear data. Thus, the controversies revolving around the systematic status of *Odorrana* to be considered as a subgenus of *Rana* (*Eburana*), as well as being included with *Rana* as subgenus of *Huia* were subsequently abandoned (Matsui et al. 2005; Stuart 2008; Pyron & Wiens 2011). Recent phylogenetic studies have confirmed that *Odorrana* is monophyletic and consists of at least seven clades (Chen et al. 2013). In this study, we successfully conducted a detailed phylogenetic analysis and assessment of *O. mawphlangensis* based on 16S rRNA in addition to studying the morphological parameters of the collected samples to resolve the confusion revolving around its taxonomic position and identity.

MATERIALS AND METHODS

Survey and morphometric analysis

Visual encounter surveys (VES) were conducted in 2022 and 2023 (August to September) and a total of 12 specimens were collected during the field surveys from the Indian states of Mizoram and Meghalaya. Ten specimens were collected from Mizoram and two specimens were collected from Meghalaya (Figure 1). Out of the 10 specimens obtained from Mizoram, eight specimens were found from Murlen National Park (23.673° N, 93.293° E; 1,050 m) and two specimens were obtained from Hmuifang Community Reserve Forest (23.355° N, 92.753° E; 1,458 m). The other two specimens of Meghalaya were collected from Malki Forest in East Khasi Hills District (25.562° N, 91.893° E; 1,549.5 m). They were found in their natural habitats, i.e., on rocks near the riverbeds and in seasonal intermittent stream below hilly grass-covered

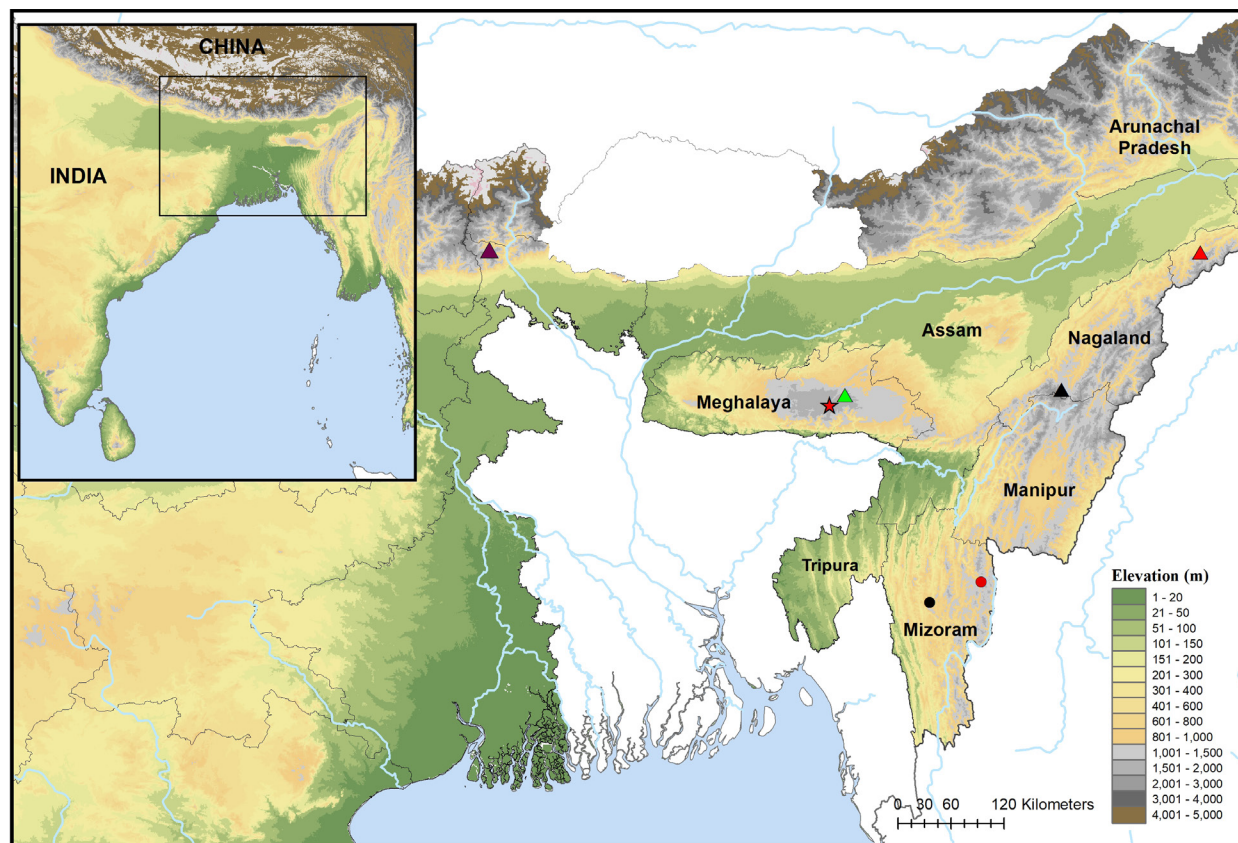


Figure 1. Map showing the known distribution with exact locality of the Mawphlang Odorous frog (*Odorrana mawphlangensis*) from Mizoram and Meghalaya. The red star mark ★ denotes the type locality of the species i.e. Mawphlang Sacred Forest in East Khasi Hills, Meghalaya. The study area for this research are designated as follows: Green triangle mark ▲ represents Malki Forest (Meghalaya), Black circle mark ● represents Hmuifang Community Reserve Forest (Mizoram), and Red circle mark ● designates Murlen National Park (Mizoram). The other highlighted marks ▲ ▲ ▲ represent the distributional records of *O. mawphlangensis* from different states of India (Frost 2025).

terrain (Frost 2025). The specimens were deposited, catalogued, and fixed in 70% ethanol solution in the Departmental Museum of Zoology, Mizoram University (MZMU). Individuals were identified using the literature of Kiyasetuo & Khare (1986) and Chanda (2002). Morphometric measurements (Table 1) follow Sengupta et al. (2010). Measurements to the nearest 0.1 mm were taken using a dial calliper (MitutoyoTM 505-507) (Table 1). Photographic vouchers were submitted to the Natural History Museum of Mizoram, Mizoram University, Aizawl, Mizoram, India (NHMM/G/2–4).

DNA extraction, PCR amplification and sequencing

We extracted genomic DNA from the liver tissues of *Odorrana* using QIAamp DNA Mini Kit (Qiagen Cat. No. 51306) following the standard protocol provided by the manufacturer. DNA integrity was analysed on 0.8% (w/v) agarose gel containing ethidium bromide. Polymerase chain reaction (PCR) was prepared for 20 µL reaction mixture containing 1X amplification buffer,

2.5 mM MgCl₂, 0.25 mM dNTPs, 0.2 pM each forward and reverse primer, 1 µL genomic DNA, and 1U Taq DNA polymerase with a pair of partial 16S rRNA primers: forward (L02510- CGC CTG TTT ATC AAA AAC AT) (Palumbi 1996) and reverse (H03063- CTC CGG TTT GAA CTC AGA TC) (Rassmann et al. 1997). The PCR thermal regime for amplification was 5 min at 95°C for initial denaturation, followed by 35 cycles of 1 min at 95°C for denaturation, 30s for annealing at 50.3°C, elongation for 1 min at 72°C, and a final elongation for 5 min at 72°C. Amplicons were observed through gel electrophoresis using a 1.5% agarose gel containing ethidium bromide. Samples were sequenced using Sanger's dideoxy method and sequencing was carried out for both forward and reverse directions (Barcode Bioscience, Bangalore, India). The newly generated partial 16S rRNA sequences were deposited in the GenBank repository to obtain the accession number.

Phylogenetic analyses

The phylogenetic relationships among the genus *Odorrana* were assessed based on the 16S rRNA partial gene sequence. For the analysis of our dataset of 16S rRNA, we included three newly generated *O. mawphlangensis* sequences from Mizoram (MZMU 138, MZMU 139, & MZMU 2267) along with the sequence of the holotype samples collected from Meghalaya (MZMU 3020 & MZMU 3021); 21 sequences were retrieved from NCBI database, and one sequence of *Amolops indoburmanensis* (MT790757) sample was used for this study as an out-group. The sequences were aligned by using Muscle algorithm in Molecular Evolutionary Genetics Analysis 7 (MEGA 7) (Kumar et al. 2016), the mean uncorrected genetic distances (Kimura 2 parameter, K2P) (Kimura 1980) were calculated in MEGA 7 (Kumar et al. 2016). The final aligned dataset contains 535 positions of 16S rRNA gene sequences. The best-fitting models of DNA evolution was performed according to the modeltest - NG (Darriba et al. 2020), and selected GTR+G model suggested by models with the lowest Bayesian information criterion (BIC) and Akaike information criterion (AIC) scores. The phylogenetic tree was inferred using Bayesian inference (BI) and maximum likelihood (ML) approaches. ML analysis was performed in raxmlGUI-2 with one-thousand bootstrap replicates (Silvestro & Michalak 2012). The BI phylogenetic tree was reconstructed in MrBayes 3.2.5 using GTR+G model. The Markov Chain Monte Carlo (MCMC) (one cold and three hot chains) was run for 10,000,000 generations by sampling every 100 generations and set the burn-in to 25%. The analysis was terminated when the standard deviation

of split frequencies was less than 0.001. The percentage of trees in which the associated taxa clustered together is shown next to the branches (Ronquist & Huelsenbeck 2003). The generated phylogenetic tree was further illustrated using Figtree v1.4.4 software (Rambaut 2018).

Genetic distances

The resulting sequences were deposited in GenBank depository (OP979109, OP979112, MZ229896, MT814039, & MT814038). The GenBank accession numbers and other details of the species involved in the phylogenetic Bayesian inference tree have been presented in Figure 2. The uncorrected pairwise divergences in the 16S rRNA gene fragment among the members of the *Odorrana* sp. were summarised in Table 3. The observed interspecific genetic distances within the genus *Odorrana* from our study ranged from 0.00% (*O. mawphlangensis*) to 11.00% (*O. fengkaiensis*_KT31538). Moreover, an intraspecific genetic distance of *O. mawphlangensis* was detected in the range of 0.00–0.011 between the specimens from Mizoram and type locality, i.e., Meghalaya.

RESULTS

a) Morphology (also see Mahony 2008)

Odorrana mawphlangensis has some distinguishing morphological characters which are exclusive to this species, such as: the head length > head width, snout length > eye diameter, inter-orbital distance < internasal distance, forelimb length < hand length, colouration of



Image 1. A—Amplexus between a male and female *Odorrana mawphlangensis* in their natural habitat | B—An adult male *Odorrana mawphlangensis* on a rock beside a narrow stream in the forest. © H.T. Lalremsanga.

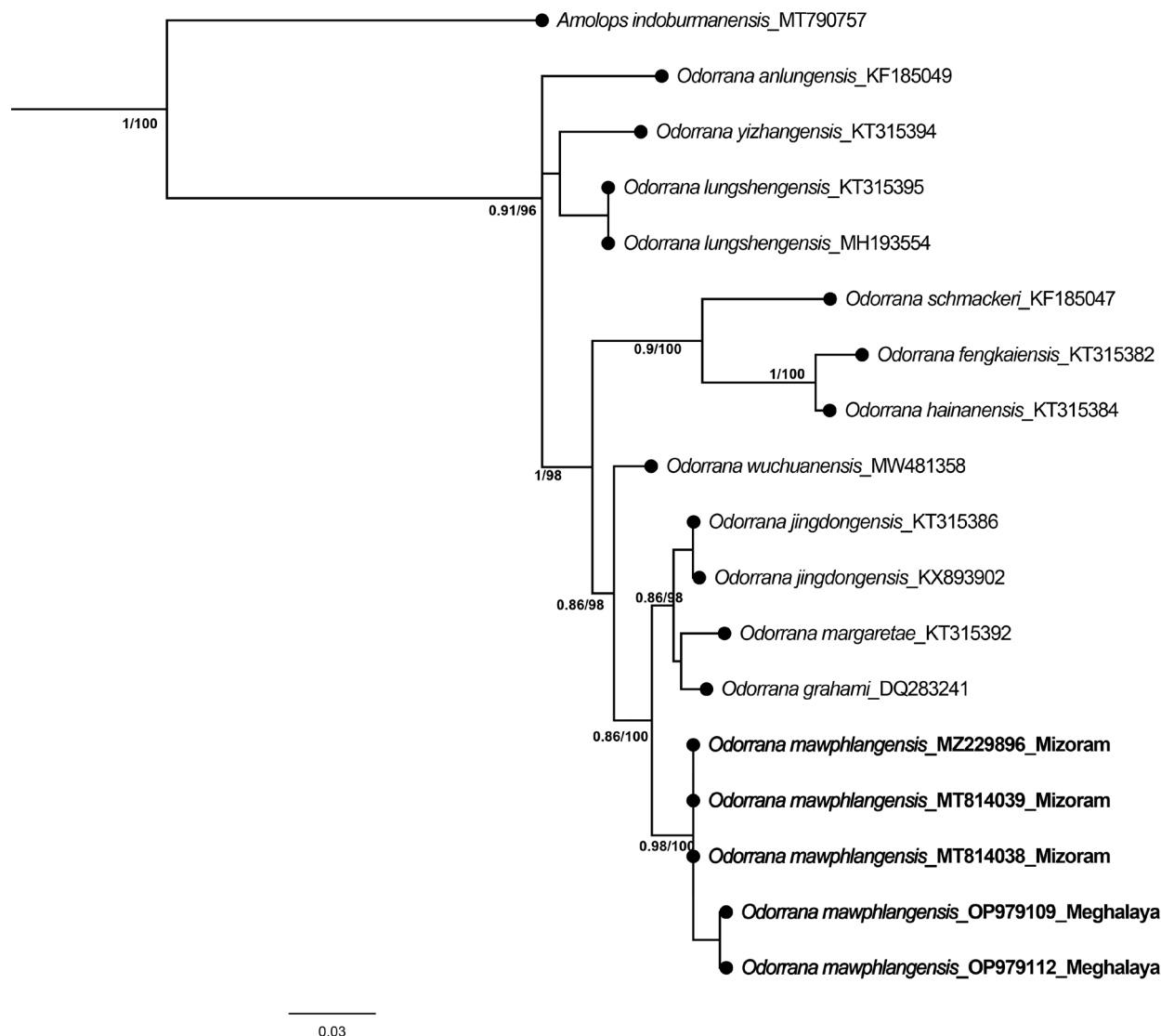


Figure 2. Phylogenetic Bayesian inference tree of *Odorrana* based on the 16S rRNA partial gene fragment sequence. Numbers at tree nodes indicated to BI/BS support values, respectively; values above 90 considered well-supported and below 90 considered moderately supported. The species in bold text denote the samples collected and examined from Mizoram and Meghalaya. The GenBank accession numbers have been mentioned alongside the various species.

the body, which is dorsally primarily green anteriorly, with large randomly spaced brown spots, lip-stripe yellow to bronze/brown in adult. The body colouration of the collected samples was green at the anterior part of the dorsum with large brownish spots randomly spaced and the posterior part of the dorsum was brownish in colour. In all the collected specimens, it was observed that the head is longer than its width (i.e. HL > HW) with the HL/HW ratio of 22.12 : 17.51 and the snout length is longer than the eye diameter (i.e., SL > ED) with the SL/ED ratio of 6.57 : 5.58. Moreover, it was observed that the inter-orbital distance is less than the internasal distance and the length of the forelimb is shorter than

the hindlimb length. All these observed morphological parameters indicated that the collected samples were *O. mawphlangensis*. The tympanum diameter (TYD) constituted 60.24% of the eye length (EL). Image 2 depicts a preserved sample of *O. mawphlangensis* (MZMU 138) collected from Mizoram.

From our collected specimens of *O. mawphlangensis*, morphometric analyses resulted in the following comparisons (vs. Chanda 1994; Ao et al. 2003; Mahony 2008):

(i) Snout-vent length (SVL) was in the range of 31.8–94.4 mm. The largest male among the collected specimens had SVL of 80.0 mm. Chanda (1994) provided

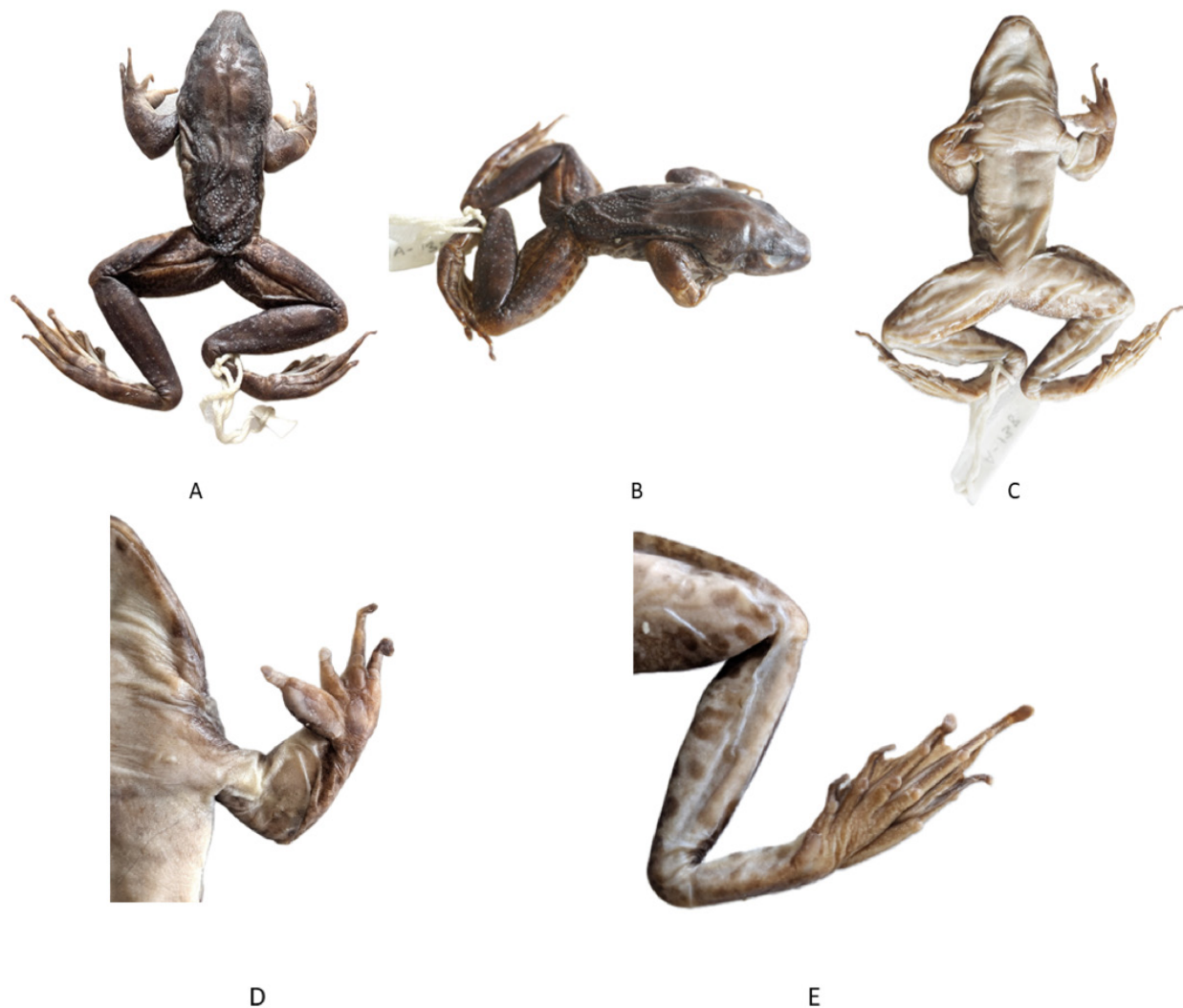


Image 2. Preserved *Odorrana mawphlangensis* sample (MZMU 138) collected from Hmuifang Community Reserve Forest (Mizoram) showing: A—Dorsal view | B—Lateral view | C—Ventral view | D—Forelimb | E—Hindlimb. © Angshuman Das Tariang.

SVL in the range of 60.0–90.0 mm. Ao et al. (2003) reported SVL of 80.0 mm in males and a range of 96–106 mm for females while Mahony (2008) redescribed the holotype from Mawphlang Sacred Forest by reporting an adult female with SVL of 84.3 mm.

(ii) Head width (HW) ranged from 11.2–31.7 mm and Head length (HL) ranged from 14.2–41.9 mm. As per Mahony (2008), HW was reported as 31.0 mm and HL as 34.4 mm.

(iii) The range of eye diameter (ED) or eye length (EL) was 3.7–11.2 mm and Mahony (2008) reported ED of 10.1 mm.

Internasal distance (IN) was in the range of 1.7–9.9 mm whereas Mahony (2008) reported it at 10.8 mm.

(iv) Eye-nostril distance (EN) was in the range of

1.9–6.2 mm against 7.1 mm as per Mahony (2008).

(v) The greatest tympanum diameter (TYD) was in the range of 1.9–5.4 mm against 5.3 mm by Mahony (2008).

(vi) The mean inter-orbital distance (IUE) was found to be 3.7 mm which is shorter than the mean internasal space (IN), i.e., 4.4 mm (i.e., IUE < IN).

(vii) The forelimb length (FLL) ranged 5.2–19.7 mm and was shorter in length than the hand length (HAL) which was in the range of 8.0–26.0 mm (i.e., FLL < HAL).

(viii) Tibia length (TL) was observed to be longer than the femur length (FL) (i.e., TL > FL), ranging 16.0–49.7 mm and 14.8–40.1 mm, respectively. Mahony (2008) had reported TL of 51.6 mm and FL of 47.5 mm.

Table 1. Morphometric measurements (in mm) of the specimens of *Odorrana mawphlangensis* collected from Mizoram (Murlen National Park and Hmuifang Community Reserve Forest) and Meghalaya (Malki Reserve Forest).

Locality	Murlen NP								Hmuifang RF		Malki RF	
Museum number	MZMU 1836	MZMU 1995A	MZMU 2129	MZMU 2856	MZMU 2858	MZMU 2859	MZMU 2861	MZMU 2866	MZMU 138	MZMU 139	MZMU 3020	MZMU 3021
SVL	57.3	54.6	43.2	38.8	36.3	31.8	31.9	32.8	80.0	94.4	44.3	46.1
HW	21.3	21.0	18.7	14.4	12.1	11.8	11.2	11.2	27.8	31.7	16.9	11.9
HL	25.3	21.8	22.2	17.1	14.4	15.0	14.2	15.7	37.0	41.9	20.8	20.3
MN	21.4	19.1	19.6	14.1	13.6	14.0	11.7	13.2	33.7	34.4	18.6	17.8
MFE	18.6	15.8	15.8	10.3	9.2	11.3	10.7	9.8	26.8	29.4	15.3	14.1
MBE	11.9	11.1	10.5	7.1	7.5	7.0	6.6	6.7	19.2	20.2	9.8	8.3
IFE	7.4	6.2	6.4	6.3	5.6	5.5	5.2	6.1	13.7	14.8	8.0	8.4
IBE	10.3	10.1	10.2	9.4	9.9	9.7	8.5	9.1	19.6	22.3	11.7	13.0
IN	1.7	2.2	1.8	3.5	3.4	3.5	3.6	3.6	7.8	9.9	6.0	5.5
EN	3.2	3.1	2.8	2.2	2.0	1.9	2.4	2.4	6.2	6.2	3.2	3.2
ED	5.1	5.4	5.0	3.7	3.9	4.2	3.7	4.4	8.0	11.2	6.4	5.9
SN	2.3	2.7	3.2	1.9	1.9	2.2	2.0	2.4	2.9	4.5	3.0	2.7
SL	6.8	6.6	7.0	4.6	5.3	4.9	4.6	5.1	8.6	11.7	7.0	6.5
TYD	4.8	4.9	3.8	2.4	2.1	2.4	1.9	2.3	4.8	5.4	3.1	2.4
TYE	1.7	1.8	1.3	2.0	1.6	0.9	0.7	1.1	2.6	2.2	1.9	1.6
IUE	2.2	2.1	1.8	3.7	3.1	2.8	2.6	4.6	4.1	7.9	4.4	4.3
UEW	3.2	3.7	3.4	3.4	2.7	2.3	2.1	2.1	6.2	6.1	3.4	3.6
FLL	8.9	8.6	9.4	9.4	7.9	5.3	5.2	6.1	16.0	19.7	9.2	10.1
HAL	14.3	11.9	11.7	11.8	9.4	8.0	8.0	9.3	18.1	26.0	13.0	12.0
TFL	10.4	7.2	7.9	7.2	6.6	4.5	4.3	6.3	10.5	17.9	7.7	8.0
FL	30.6	27.4	24.7	16.3	17.0	15.2	14.8	16.9	37.1	40.1	20.8	21.0
TL	26.7	24.6	20.4	17.8	16.0	18.4	16.4	19.0	42.9	49.7	24.4	25.6
TFOL	40.0	33.9	32.6	27.3	24.0	23.8	21.9	26.1	57.6	59.1	34.3	34.4
FOL	30.6	26.2	22.9	17.3	16.4	15.9	14.3	16.8	38.1	39.5	24.1	23.7
FTL	24.4	22.2	21.3	13.2	14.5	12.5	10.1	13.4	33.0	32.1	20.5	19.8

SVL—Snout-vent length | HW—Head width | HL—Head length | MN—Distance from the back of the mandible to the nostril | MFE—Distance from the back of the mandible to the front of the eye | MBE—Distance from the back of the mandible to the back of the eye | IFE—Distance between the front of the eyes | IBE—Distance between the back of the eyes | IN—Internasal space | EN—Distance from the front of the eye to the nostril | ED—Eye diameter | SN—Distance from the nostril to the tip of the snout | SL—Distance from the front of the eye to the tip of the snout | TYD—Greatest tympanum diameter | TYE—Distance from tympanum to the back of the eye | IUE—Minimum distance between upper eyelids | UEW—Maximum width of inter upper eyelid | FLL—Forelimb length | HAL—Hand length | TFL—Third finger length | FL—Femur length | TL—Tibia length | TFOL—Length of tarsus and foot | FOL—Foot length | FTL—Fourth toe length.

b) Field observations and comparisons

The largest specimen was a female, catalogued as MZMU 138. From our collected specimens of *O. mawphlangensis*, morphometric analyses have revealed that the largest specimen was obtained from Hmuifang Community Reserve Forest with SVL of 94.4 mm (an adult female) and the smallest specimen belonged to Murlen National Park with SVL of 31.8 mm (a juvenile). A number of adult specimens of *O. mawphlangensis* that were encountered at Malki Reserve Forest and Hmuifang Community Reserve Forest (Image 1A,B). Amplexing behaviour between two adults was also

observed (Image 1A).

c) Phylogenetic Relationships

In phylogenetic reconstructions (Figure 2) using both BI and ML analyses, the trees revealed identical topologies that support the relationships of the genus *Odorrana*. All 17 sequences of *Odorrana* sp. were clustered and formed distinct monophyletic clade from an out-group, *Amolops indoburmanensis* (Figure 2). The samples used for phylogenetic analysis have been mentioned in Table 2. From our analysis, *Odorrana mawphlangensis* nested different from other species

Table 2. Samples used for phylogenetic analysis with their GenBank accession numbers and other details.

Taxa	Voucher number	Locality	Accession number	Reference
<i>A. indoburmanensis</i>	MZMU 1650	Mizoram, India	MT790757	-
<i>O. anlungensis</i>	HNNU 1008-109	China	KF185049	Chen et al. 2013
<i>O. yizhangensis</i>	SYSa001870	China	KT315394	Wang et al. 2015
<i>O. lungshengensis</i>	SYSa002229	China	KT315395	Wang et al. 2015
<i>O. lungshengensis</i>	806	China	MH193554	Li et al. 2018
<i>O. schmackeri</i>	HNNU 0908-349	China	KF185047	Chen et al. 2013
<i>O. fengkaiensis</i>	SYSa001025	China	KT315382	Wang et al. 2015
<i>O. hainanensis</i>	SYSa000636	China	KT315384	Wang et al. 2015
<i>O. wuchuanensis</i>	GZNU20180608019	China	MW481358	Luo et al. 2021
<i>O. jingdongensis</i>	SYSa002995	China	KT315386	Wang et al. 2015
<i>O. jingdongensis</i>	IEBR 3948	Vietnam	KX893902	Ngo et al. 2016
<i>O. margaretae</i>	SYSa002317	China	KT315392	Wang et al. 2015
<i>O. grahami</i>	CAS 207504	China	DQ283241	Frost et al. 2006
<i>O. mawphlangensis</i>	MZMU 2267	Mizoram, India	MZ229896	-
<i>O. mawphlangensis</i>	MZMU 139	Mizoram, India	MT814039	-
<i>O. mawphlangensis</i>	MZMU 138	Mizoram, India	MT814038	-
<i>O. mawphlangensis</i>	MZMU 3021	Meghalaya, India	OP979109	-
<i>O. mawphlangensis</i>	MZMU 3020	Meghalaya, India	OP979112	-

with well supported bootstrap values (Figure 2; Table 3).

d) Conservation Status

With the recent amendment of the Wildlife Protection Act in 2022, 37 species of amphibians have been protected under Schedule-I and Schedule-II categories. *Odorrana mawphlangensis* has been included in Schedule-II category. This species is currently listed as 'Data Deficient' and needs further research and assessment (IUCN 2023).

DISCUSSIONS

There were numerous brief accounts and reports on the occurrence of this species in the past (Chanda 1990; Sarkar et al. 1992; Dutta 1997; Chanda 2002; Ao et al. 2003; Devi & Shamungou 2006; Sarkar & Ray 2006; Das & Dutta 2007; Ahmed et al. 2009; Matthew & Sen 2010; Lalremsanga 2017; Siammawii et al. 2021). However, these studies were reports solely based on the external morphological characters and a detailed phylogenetic analysis was not performed in any of the studies. Thus, there was confusion on its identity and a detailed confirmation was awaited.

Mahony (2008) redescribed the species based on re-examination of its holotype, illustrated the same and transferred it to the genus *Odorrana*. Mahony (2008) also suggested that it might be conspecific with *O. grahami*, based on some morphological similarities. He stated that further studies on the phylogenetic position and distinction are required so as to confirm the monophyly as well as establishing the taxonomic identity of the species involved.

In the present study, based on 16s rRNA data, we ratify the generic allocation of *Odorrana mawphlangensis* (see Mahony 2008) and establish that its closest sister taxon is the Yunnanese species *O. jingdongensis* (Fei et al. 2001) with a genetic distance of 3.7%. The hypothesis that *O. mawphlangensis* might be a junior synonym of *O. grahami* (Mahony 2008) is not supported from this study. It is noteworthy that *O. mawphlangensis* forms a distinct clade separate from sister taxa *O. grahami* and *O. jingdongensis* (Boulenger 1917; Fei et al. 2001).

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Table 3. The uncorrected K2p -distance of 16S rRNA partial gene sequence among members of the *Odorrana* sequences.

	Taxon	K2p distance																
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	<i>O. mawphlangensis</i> _OP979109_Meghalaya																	
2	<i>O. mawphlangensis</i> _OP979112_Meghalaya	0.004																
3	<i>O. mawphlangensis</i> _MZ229896_Mizoram	0.011	0.011															
4	<i>O. mawphlangensis</i> _MT814039_Mizoram	0.011	0.011	0.000														
5	<i>O. mawphlangensis</i> _MT814038_Mizoram	0.011	0.011	0.000	0.000													
6	<i>O. fengkaiensis</i> _KT315382	0.110	0.110	0.096	0.096	0.096												
7	<i>O. hainanensis</i> _KT315384	0.108	0.108	0.093	0.093	0.093	0.020											
8	<i>O. jingdongensis</i> _KT315386	0.037	0.037	0.025	0.025	0.025	0.099	0.092										
9	<i>O. wuchuanensis</i> _MW481358	0.049	0.049	0.036	0.036	0.036	0.091	0.083	0.034									
10	<i>O. margaritae</i> _KT315392	0.051	0.051	0.039	0.039	0.039	0.120	0.112	0.022	0.043								
11	<i>O. yizhangensis</i> _KT315394	0.083	0.083	0.070	0.070	0.070	0.112	0.099	0.068	0.060	0.073							
12	<i>O. lungshengensis</i> _KT315395	0.078	0.078	0.065	0.065	0.065	0.088	0.076	0.063	0.055	0.073	0.041						
13	<i>O. grahami</i> _DQ283241	0.042	0.042	0.029	0.029	0.029	0.110	0.102	0.018	0.034	0.022	0.078	0.073					
14	<i>O. schmackeri</i> _KF185047	0.093	0.093	0.079	0.079	0.079	0.076	0.073	0.092	0.084	0.102	0.104	0.086	0.087				
15	<i>O. jingdongensis</i> _KX893902	0.039	0.039	0.027	0.027	0.027	0.102	0.094	0.002	0.036	0.020	0.070	0.065	0.020	0.095			
16	<i>O. lungshengensis</i> _MH193554	0.078	0.078	0.065	0.065	0.065	0.088	0.076	0.063	0.055	0.073	0.041	0.000	0.073	0.086	0.065		
17	<i>O. anlungensis</i> _KF185049	0.082	0.082	0.068	0.068	0.068	0.105	0.100	0.071	0.068	0.079	0.061	0.056	0.076	0.100	0.069	0.056	
18	<i>Amolops indoburmanensis</i> _MT790757	0.186	0.186	0.168	0.168	0.168	0.180	0.177	0.171	0.165	0.177	0.160	0.161	0.172	0.186	0.168	0.161	0.171

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