



First Record of the Naga Hills Horned Frog, *Megophrys awuh* Mahony, Kamei, Teeling, and Biju (Anura: Megophryidae: Megophryinae), from Mizoram, India

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The Naga Hills Horned Frog (*Megophrys awuh*) has been known only from the vicinity of Kohima and Star Lakes in southern and eastern Nagaland, but was expected to have a more extensive geographical distribution due to its occurrence at a wide elevational range (1,650–2,220 m asl) (Mahony et al. 2020). Herein we provide the first record of the Naga Hills Horned Frog (Fig. 1) from Mizoram, the first record of the species outside Nagaland. The new record extends the range of this species about 300 km southwest of the closest known locality in Nagaland and also extends the elevational range of this species down to 1,478 m asl.

During a herpetofaunal survey on 16 June 2017, we collected frogs of the genus *Megophrys* in the Hmuifang Community Forest Reserve at Hmuifang Village, Aizawl District, Mizoram (23°27.213'N, 92°45.181'E; elev. 1,478 m asl; Fig. 2). Prior to fixation of specimens, we excised muscle tissue from the right thigh and stored it in absolute ethanol for DNA extraction. Specimens were deposited in the



Fig. 2. Map showing the distribution of the Naga Hills Horned Frog (*Megophrys awuh*). The orange star indicates the type locality, the orange circle a previous record, and the red circle the new record. Symbols may represent more than one proximate site.



Fig. 1. A female Naga Hills Horned Frog (*Megophrys awuh*) from Hmuifang, Mizoram, India (MZUHC 307). Photograph by Samuel Lalronunga.

herpetological collection of the Systematics and Toxicology Laboratory, Department of Zoology, Mizoram University, India (MZUHC 305–7, MZUHC 313–4).

Fragments of 16S rRNA mitochondrial gene sequences were generated following Lalronunga and Lalrinchhana (2017) for comparison with members of the *Megophrys mega-cephala* species group available in GenBank. Sequences were

Table 1. Uncorrected p-distances between species of the *Megophrys (Xenophrys) megacephala* species group (16S rRNA). GenBank accession numbers are listed in parentheses after the name of the species.

<i>M. ancrae</i> (KY022318)									
<i>M. awub</i> (KY022319)	0.105								
<i>M. awub</i> (MT793042–6)	0.094	0.022							
<i>M. dzukou</i> (KY022324)	0.079	0.121	0.119						
<i>M. megacephala</i> (KY022315)	0.200	0.220	0.220	0.237					
<i>M. oropedion</i> (KY022316)	0.091	0.111	0.106	0.119	0.197				
<i>M. numbbumaeng</i> (MN734393)	0.091	0.111	0.106	0.119	0.197	0.000			
<i>M. oropedion</i> (KY022317)	0.088	0.120	0.113	0.117	0.202	0.047	0.047		
<i>M. serchhipii</i> (KY022323)	0.095	0.094	0.099	0.123	0.209	0.105	0.105	0.108	
<i>M. zunhebotoensis</i> (KY022322)	0.093	0.090	0.087	0.115	0.218	0.099	0.099	0.112	0.098

aligned using ClustalW integrated in MEGA 7 (Molecular Evolutionary Genetics Analysis) software (Kumar et al. 2016) with the default settings. Uncorrected pairwise genetic distances (p-distance) between sequences (Table 1) were determined with MEGA 7 (Kumar et al. 2016). The genetic distance between the sequences from Hmuifang, Mizoram (n = 5, Genbank accession numbers MT793042–6), and the paratype of *M. awub* (accession number KY022319) is only 0.022. Lalengliana et al. (2016) had previously misidentified frogs of this species as *Megophrys serchhipii*, a species described by Mathew and Sen (2009) from Serchhip, Mizoram, about 18 km airline distance from the present study site.

Acknowledgements

We thank the Principal, Pachhunga University College and the Head, Department of Zoology, Mizoram University for Institutional support; Lalnunhlua, Lalkhawngaiha Sailo, Malsawmdawngliana, and Vanlalchhuanga for their assistance during fieldwork; and the Chief Wildlife Warden, Environment, Forest and Climate Change Department, Government of Mizoram, India, for issuing a research permit (A.38011/5/2011-CWLW/338). SL and EL thank the

Directorate of Science and Technology, Government of Mizoram for financial support of field collection (No. B. 13012/1/2017-DST). VRL and SL thank the Department of Biotechnology, New Delhi, for financial support to the Institutional Advanced-Level Biotech Hub (BT/22/NE/2011, 19 July 2017), which supported the molecular work in this study. We also thank the local authorities of Hmuifang Village for allowing us to conduct a survey in their area.

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