Confirmation of the Occurrence of Jerdon’s White-lipped Horned Frog, *Megophrys major* (Boulenger 1908) (Anura: Megophryidae: Megophryinae), in Mizoram, India

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Jerdon’s White-lipped Horned Frog (*Megophrys major*) was thought to be widely distributed from northeastern India to southeastern Vietnam (Mahony et al. 2018). However, recent studies have shown that *M. major* is a species complex and that previous records of this species are in need of confirmation (Vassilieva et al. 2016; Chen et al. 2017; Mahony et al. 2017, 2018). Mathew and Sen (2010) had listed Mizoram within this species’ range, but did not mention a specific location or cite any vouchered specimens. Lalropeki (2018) recorded the species from the Tamdil wetland in Mizoram, but the brief description and morphometric measurements do not differentiate it from other members of the *Megophrys* major complex of southern Asia. Jerdon’s White-lipped Horned Frog is known definitively only from the states of Meghalaya, Manipur, and Nagaland in northeastern India (Mahony et al. 2018). Herein, we use molecular data to confirm the occurrence of the species in Mizoram.

During a herpetofaunal survey on 16 June 2017, we collected a gravid female *Megophrys major* (Fig. 1) from the

Fig. 1. A female Jerdon’s White-lipped Horned Frog (*Megophrys major*) from Saitual, Mizoram, India (MZUHC 444). Photograph by Samuel Lalronunga.

Fig. 2. Map showing the distribution of Jerdon’s White-lipped Horned Frog (*Megophrys major*). The orange star indicates the type locality, orange circles mark previous records, and the red circle indicates the new record. Symbols may represent more than one proximate site.
outskirts of Saitual Village, Saitual District, Mizoram, India (23°49.237’N, 92°43.886’E; elev. 1,004 m asl; Fig. 2). Prior to fixation, we excised muscle tissue from the right thigh and stored it in absolute ethanol for DNA extraction. The specimen was deposited in the herpetological collections of the Systematics and Toxicology Laboratory, Department of Zoology, Mizoram University, India (MZUHC 444).

A fragment of 16S rRNA mitochondrial gene sequences was generated following Lalronunga and Lalrinchhana (2017) for comparison with other members of the *Megophrys major* species group available in GenBank. Sequences were 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 sequence of *M. major* from Saitual, Mizoram (MT797633) and the sequence of *M. major* (MH647514) from Manipur used in the review of the *Megophrys major* complex of southern Asia (Mahony et al. 2017) is only 0.002.

### Acknowledgements

We thank the Principal, Pachhunga University College; Head, Department of Zoology, Mizoram University for Institutional support; 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). VRL and SL thank the Department of Biotechnology, New Delhi for financial support of the Institutional Advanced-Level Biotech Hub (BT/22/NE/2011, 19 July 2017), which supported the molecular work for this study.

### Literature Cited


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

<table>
<thead>
<tr>
<th>Species</th>
<th>M. flavipunctata (KY022307)</th>
<th>M. glandulosa (KX811761)</th>
<th>M. himalayana (MH647526)</th>
<th>M. major (MH647514)</th>
<th>M. major (MT797633)</th>
<th>M. medogensis (KX811767)</th>
<th>M. monticola (KY022312)</th>
<th>M. oreocrypta (KY022306)</th>
<th>M. periosa (MH647522)</th>
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