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Distribution pattern of the *Microhyla heymonsi* group (Anura, Microhylidae) with descriptions of two new species from Vietnam

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[6] urn:lsid:zoobank.org:author:42911445-AE2A-485A-B2EB-EDBF1A784540
[7] urn:lsid:zoobank.org:author:76CAAC27-AB82-4CD0-AC54-4D8EA615AABF
[8] urn:lsid:zoobank.org:author:5716DB92-5FF8-4776-ACC5-BF6FA8C2E1BB
[9] urn:lsid:zoobank.org:author:FF8C086D-3028-4CC2-BD1D-0E12272444E7

Abstract. We provide the first distribution pattern of the *Microhyla heymonsi* group based on available molecular and morphological data collected from East and Southeast Asia. Our analyses show a high level of genetic diversity in the *M. heymonsi* group with nine distinct lineages from China, Myanmar, Vietnam, Laos, Malaysia, Thailand, Cambodia, as well as Singapore, and Indonesia. The study also reveals the discovery of two new species in Vietnam, *Microhyla hmongorum* sp. nov. from Lai Chau Province and *Microhyla xodangorum* sp. nov. from Kon Tum Province. When comparing the 12S–16S rRNA gene, the genetic divergence between *Microhyla xodangorum* and other congeners of the *Microhyla heymonsi* group ranges from 7.5 to 8.9% (*M.* cf. *heymonsi*) and approximately 8.4% between the new species and *M. heymonsi* s. str. from Taiwan, China. The genetic divergence between *Microhyla hmongorum* and its congeners ranges from 4.5–5.6% (*M.* cf. *heymonsi*) to 8.7% (*Microhyla xodangorum*). These new findings bring the total number of known species in the genus *Microhyla* to 48 and the recorded species of *Microhyla* from Vietnam to 14.

Keywords. *Microhyla*, morphology, molecular phylogeny, Lai Chau, Kon Tum.

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Introduction

The genus *Microhyla* Tschudi, 1838 currently contains 46 species, which are distributed from India and Sri Lanka eastwards to the Ryukyu Archipelago of Japan and southwards to Indonesia (Frost 2021). Recent studies have uncovered highly divergent lineages and a high level of undiagnosed diversity in the genus (Hasan *et al*. 2012, 2014, 2015; Howlader *et al*. 2015; Matsui *et al*. 2005, 2011, 2013; Seshadri *et al*. 2016; Wijayathilaka *et al*. 2016; Yuan *et al*. 2016; Zhang *et al*. 2018; Nguyen *et al*. 2019; Li *et al*. 2019; Hoang *et al*. 2020, 2021). Remarkably, there are complex groups of multiple species, either representing previously available names or unnamed species (Garg *et al*. 2019).

The *Microhyla heymonsi* complex is one of the most poorly studied groups in the family Microhylidae Günther, 1858. *Microhyla heymonsi* Vogt, 1911 was originally described from 'Formosa' (now Taiwan, China) based on eight male specimens (ZMB 54906–54913) (Garg *et al*. 2019). The species has subsequently been reported from southern Yunnan to Zhejiang in China (including Hainan and Taiwan) and through Indochina to the Malay Peninsula, Sumatra and Andaman and Nicobar Islands (India) (Amphibiaweb 2021; Frost 2021). However, this widespread species contains several unnamed taxa. For example, Hoang *et al*. (2021) recently described two cryptic species of this group from the Central Highlands of Vietnam, namely *Microhyla ninhthuanensis* and *Microhyla daklakensis*.

According to Garg *et al*. (2019), the *Microhyla heymonsi* group can be differentiated from all other groups by the combination of the following characters: the absence of webbing between toes; finger and toe discs with prominent dorsal terminal grooves, bifurcate distally; the presence of a small ( )-shaped dark marking in the center of its dorsum; a narrow light mid-dorsal line, extending from the tip of the snout to the vent; and a prominent blackish brown lateral band, marking or skin fold, starting from the tip of the snout to the groin.

Our phylogenetic analyses based on available sequences of the specimens from across mainland and islands of East and Southeast Asia showed that the *Microhyla heymonsi* group contains nine separate clades, including two undescribed taxa from northwestern and central Vietnam. Morphological data also support they are distinct from other named species of the *Microhyla heymonsi* group. We therefore describe the populations of *Microhyla* from the Lai Chau and Kon Tum provinces of Vietnam as new species.

Material and methods

Sampling

Field surveys were conducted in the Kon Tum and Lai Chau provinces, Vietnam in September 2018 and April 2020 by C.V. Hoang, T.Q. Phan and N.B. Sung (hereafter C.V. Hoang *et al*.). Geographic coordinates and elevations were obtained using a Garmin GPSMAP 78S (WGS 84 data). After photographing in life, specimens were euthanized in a closed vessel with a piece of cotton wool containing ethyl acetate (Simmons 2002), fixed in 80% ethanol for five hours, and then transferred to 70% ethanol for permanent storage. Tissue samples were taken from the liver and preserved separately in 70% ethanol prior to fixation. Specimens referred to in this paper are deposited in the collections of the Institute of Ecology and Biological Resources (IEBR), Vietnam National Museum of Nature (VNMN), Hanoi, Vietnam; Chengdu Institute of Biology (CIB), Chengdu, Sichuan, China; Kyoto University, Graduate School of Human and Environmental Studies (KUHE), Japan; Zoological Institute, Russian Academy of Sciences (ZISP), Saint Petersburg, Russia; Zoological Museum, Moscow Lomonosov State University, Moscow, Russia. The gender was determined by direct observation of calling males in life or by gonadal dissection.

Molecular analyses

DNA extraction and sequencing

Extraction of genomic DNA from 32 tissue samples was carried out in two stages (Table 1). For samples collected before 2020 (stage 1), we used TIANamp Genomic DNA kit (TIANGEN BIOTECH, Beijing, China), Tiangen following the manufacturers' instructions for DNA extraction. Total DNA was amplified using an Eppendorf PCR machine. PCR total volume was 25 µl, consisting of 12 µl of Mastermix, 6 µl of water, 1 µl of each primer at a concentration of 10 pmol / µl, and 5 µl of DNA. Primers used in the PCR and sequencing were as follows: 12SAL (5'-AAACTGGGATTAGATACCCCACTAT-3'; forward), 16S2000H (5'-GTGATTAYGCTACCTTTGCACGGT-3'; reverse) (Zhang *et al*. 2008) and LR-N-13398 (5'-CGCCTGTTTACCAAAAACAT-3'; forward), LR-J12887 (5'-CCGGTCTGAACTCAGATCACGT-3'; reverse) (Simon *et al*. 1994). PCR conditions: 94°C for 5 min. of initial denaturation; with 35 cycles of denaturation at 94°C for 30 s, annealing at 56°C for 30 s, and extension at 72°C for 45 s; and the final extension at 72°C for 7 min. We amplified a ~1000 base pair (bp) length fragment of the 12S rRNA–16S rRNA mitochondrial gene and the complete sequence of tRNAVal that was recently used for *Microhyla*. For samples collected in 2020 (stage 2), we used Qiagen DNA extraction kits, the protocols of Kuraishi *et al*. (2013), modified by Nguyen *et al*. (2014), for DNA extraction, amplification, and sequencing. Fragments of the mitochondrial DNA genes 16S rRNA were amplified using the primers following Kuraishi *et al*. (2013). Forward and reverse primers from 5' to 3' used for DNA amplification and sequencing with directions of sequencing indicated: H3056: CTCCGGTCTGAACTCAGATCACGTAGG and tVal-L: CGTACCTTTTGCATCATGGTC. The PCR included an initial denaturation for 5 min at 94°C and 35 cycles of 30 s at 94°C, 30 s at 55°C and 7 min at 72°C. Total DNA was amplified using PCR Eppendorf. PCR volume consisted of 25 µl, including 12 µl of Mastermix, 8 µl of water, 1 µl of each primer at concentration of 10 pmol / µl, and 3 µl of DNA. We amplified a 1979 base pair (bp) length fragment of the 12S rRNA–16S rRNA mitochondrial gene and the complete sequence of tRNAVal that was used recently for *Microhyla*. The obtained sequences were deposited in GenBank, for accession numbers see Table 1.

Phylogenetic analyses

We used 49 available sequences of 12S–16S rRNA of the *Microhyla heymonsi* group from GenBank for phylogenetic analyses, including 31 sequences (except for one sequence from Hainan, China) of the collected samples in this work. Sequences of *M. marmorata* were included in the analysis as the outgroup (Hoang *et al*. 2020). Information and accession numbers for all sequences included in the analysis can be found in Table 2. In order to elucidate the relationship between distribution patterns and

Table 1 (continued on next five pages). Specimens and sequences of the *Microhyla heymonsi* groups and outgroup representatives used in molecular analyses.

No	Voucher no	GenBank no.	Species	Collection	Locality	Reference
1	VNMN 2021.05	MT808934	*M. ninhthuanensis*	Vietnam National Museum of Nature	Phuoc Binh NP, Ninh Thuan, Vietnam	Hoang *et al.* 2021
2	CIB (HAO185)	MT808935	*M. ninhthuanensis*	Chengdu Institute of Biology	Phuoc Binh NP, Ninh Thuan, Vietnam	Hoang *et al.* 2021
3	IEBR A.5052	ON723392	*M. ninhthuanensis*	Institute of Ecology and Biological Resources	Vinh Cuu, Dong Nai, Vietnam	This study
4	IEBR A.5053	ON723393	*M. ninhthuanensis*	Institute of Ecology and Biological Resources	Vinh Cuu, Dong Nai, Vietnam	This study
5	ZMMU NAP-03780	MN534571	*M. ninhthuanensis*		Phu Quoc, Kien Giang, Vietnam	Gorin *et al.* 2020
6	KUHE:23856	AB598336	*M. ninhthuanensis*	Kyoto University, Graduate School of Human and Environmental Studies	Ranong, Thailand	Matsui 2011
7	KUHEK1845	AB201190	*M. ninhthuanensis*	Kyoto University, Graduate School of Human and Environmental Studies	Kanchanaburi, Thailand	Matsui *et al.* 2005
8	CAS:HERP:210748	KC179993	*M. ninhthuanensis*		Hlawgaw Wildlife Park, Myanmar	Sa *et al.* 2012
9	TAD_P329	KR827939	*M. ninhthuanensis*		Phang Nga, Thailand	Grosjean *et al.* 2015
10	ZISP 14249	MT808953	*M. daklakensis*	Zoological Institute of the Russian Academy of Sciences	Nam Kar NR, Dak Lak, Vietnam	Hoang *et al.* 2021
11	CIB (VNMN 06858)	MT808954	*M. daklakensis*	Chengdu Institute of Biology	Nam Kar NR, Dak Lak, Vietnam	Hoang *et al.* 2021
12	IEBR A5072 (field tag KPMĐ-2018-01)	MT808960	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Kon Plong , Kon Tum, Vietnam	Hoang *et al.* 2021
13	IEBR A5073 (field tag KP-MĐ-2018-25)	MT808961	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	Hoang *et al.* 2021
14	IEBR A5074 (field tag KP-MĐ-2018-26)	MT808962	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	Hoang *et al.* 2021
15	IEBR A5075 (field tag KP-MĐ-2018-37)	MT808956	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	Hoang *et al.* 2021
16	VNMN 04244	MT808957	*M.* cf. *heymonsi*	Vietnam National Museum of Nature	Kon Plong, Kon Tum, Vietnam	Hoang *et al.* 2021

Table 1 (continued). Specimens and sequences of the *Microhyla heymonsi* groups and outgroup representatives used in molecular analyses.

No	Voucher no	GenBank no.	Species	Collection	Locality	Reference
17	VNMN 04245	MT808958	*M.* cf. *heymonsi*	Vietnam National Museum of Nature	Kon Plong, Kon Tum, Vietnam	Hoang *et al.* 2021
18	VNMN 04450	MT808959	*M.* cf. *heymonsi*	Vietnam National Museum of Nature	Kon Plong, Kon Tum, Vietnam	Hoang *et al.* 2021
19	IEBR A.5054	ON724214	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	This study
20	IEBR A.5055	ON724213	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	This study
21	IEBR A.5056	ON724209	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	This study
22	IEBR A.5057	ON724218	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Vu Quang NP, Ha Tinh, Vietnam	This study
23	IEBR A.5058	ON724217	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Vu Quang NP, Ha Tinh, Vietnam	This study
24	IEBR A.5059	ON724216	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Vu Quang NP, Ha Tinh, Vietnam	This study
25	IEBR A.5060	ON724215	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Vu Quang NP, Ha Tinh, Vietnam	This study
26	IEBR A.5061	ON724212	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Bach Ma NP, Thua Thien Hue, Vietnam	This study
27	IEBR A.5062	ON724211	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Bach Ma NP, Thua Thien Hue, Vietnam	This study
28	IEBR A.5063	ON724210	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Bach Ma NP, Thua Thien Hue, Vietnam	This study
29	IEBR A.5064	ON745797	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Huu Lien NR, Lang Son, Vietnam	This study
30	IEBR A.5065	ON745798	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Huu Lien NR, Lang Son, Vietnam	This study
31	IEBR A.5066	ON745799	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Huu Lien NR, Lang Son, Vietnam	This study
32	IEBR A.5067	ON724208	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Trang Dinh, Lang Son, Vietnam	This study

Table 1 (continued). Specimens and sequences of the *Microhyla heymonsi* groups and outgroup representatives used in molecular analyses.

No	Voucher no	GenBank no.	Species	Collection	Locality	Reference
33	IEBR A.5068	ON724219	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Pu Mat NP, Nghe An, Vietnam	This study
34	IEBR A.5069	ON724220	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Pu Mat NP, Nghe An, Vietnam	This study
35	IEBR A.5070	ON724221	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Pu Mat NP, Nghe An, Vietnam	This study
36	IEBR A5071	ON724223	*M.* cf. *heymonsi*	Institute of Ecology and Biological Resources	Pu Mat NP, Nghe An, Vietnam	This study
37	ND.17.16	ON724225	*M.* cf. *heymonsi*	Faculty of Forest Resources and Environmental Management	Nam Dong, Thanh Hoa, Vietnam	This study
38	ND.17.17	ON724224	*M.* cf. *heymonsi*	Faculty of Forest Resources and Environmental Management	Nam Dong, Thanh Hoa, Vietnam	This study
39	ND2.17.26	ON724223	*M.* cf. *heymonsi*	Faculty of Forest Resources and Environmental Management	Nam Dong, Thanh Hoa, Vietnam	This study
40	ZPMSU 04424	MN534576	*M.* cf. *heymonsi*		Ngoc Linh, Kon Tum, Vietnam	Gorin *et al*. 2020
41	ZMMU A6044	MN534574	*M.* cf. *heymonsi*	Zoological Museum, Moscow Lomonosov State University	Cat Ba, Hai Phong, Vietnam	Gorin *et al*. 2020
42	K739	KR827935	*M.* cf. *heymonsi*		Vinh Phuc, Vietnam	Grosjean *et al*. 2015
43	AMNH A163850	DQ283382	*M.* cf. *heymonsi*		Ha Giang, Vietnam	Frost *et al*. 2006
44	Not preserved	AY458596	*M.* cf. *heymonsi*	Chengdu Institute of Biology	Sichuan, China	Zhang *et al*. 2005
45	Not preserved	ON724226	*M.* cf. *heymonsi*	Chengdu Institute of Biology	Hainan, China	This study
46	KUHE:50505	LC465686	*M. heymonsi*	Kyoto University, Graduate School of Human and Environmental Studies	Taiwan, China	Tominaga *et al*. 2019
47	ZMMU A4975	MN534575	*M. heymonsi*	Zoological Museum, Moscow Lomonosov State University	Taiwan, China	Gorin *et al*. 2020
48	ZMMU A5334-45	MN534572	*M. heymonsi*	Zoological Museum, Moscow Lomonosov State University	Taiwan, China	Gorin *et al*. 2020

Table 1 (continued). Specimens and sequences of the *Microhyla heymonsi* groups and outgroup representatives used in molecular analyses.

No	Voucher no	GenBank no.	Species	Collection	Locality	Reference
49	KU: field tag DSM 1136	HM359087	*M.* sp1		Thailand	Garg *et al*. 2019
50	KU: field tag DSM 1152	HM359088	*M.* sp1		Thailand	Garg *et al*. 2019
51	KU: field tag DSM 1153	HM359089	*M.* sp1		Thailand	Garg *et al*. 2019
52	KU: field tag DSM 1205	HM359090	*M.* sp1		Thailand	Garg *et al*. 2019
53	0974Y2	KR827937	*M.* sp1		Bangkok, Thailand	Garg *et al*. 2019
54	0974Y1	KR827938	*M.* sp1		Bangkok, Thailand	Garg *et al*. 2019
55	K3066	KR827940	*M.* sp1		Chiangmai, Thailand	Garg *et al*. 2019
56	ZMMU A6045	MN534570	*M.* sp1	Zoological Museum, Moscow Lomonosov State University	Prachuap, Thailand	Gorin *et al*. 2020
57	1999.6069	KR827934	*M.* sp1		Viangchan, Laos	Garg *et al*. 2019
58	1997.8354	KR827932	*M.* sp1		Luang Prabang, Laos	Garg *et al*. 2019
59	2006.2341	KR827943	*M.* sp1		Luang Prabang, Laos	Garg *et al*. 2019
60	2006.2337	KR827944	*M.* sp1		Luang Prabang, Laos	Garg *et al*. 2019
61	2006.2346	KR827936	*M.* sp1		Luang Prabang, Laos	Garg *et al*. 2019
62	ZISP FN-00101	MN534573	*M.* sp1	Zoological Institute of the Russian Academy of Sciences	Khammouan, Laos	Gorin *et al*. 2020
63	RM MIHEJS3	HM359092	*M.* sp2		Singapore	Garg *et al*. 2019
64	RM MIHEJS4	HM359093	*M.* sp2		Singapore	Garg *et al*. 2019

Table 1 (continued). Specimens and sequences of the *Microhyla heymonsi* groups and outgroup representatives used in molecular analyses.

No	Voucher no	GenBank no.	Species	Collection	Locality	Reference
65	Haplotype: Mhey-My1	AB530636	*M.* sp2		University Malay Campus, Malaysia	Garg *et al*. 2019
66	Haplotype: Mhey-My2	AB530637	*M.* sp2		University Malay Campus, Malaysia	Garg *et al*. 2019
67	MN534684	MN534577	*M.* sp2		Negara, Taman, Malaysia	Gorin *et al*. 2020
68	MN534685	MN534578	*M.* sp2		Negara, Taman, Malaysia	Gorin *et al*. 2020
69	ZMMU NAP-06887	MN534579	*M.* sp2	Zoological Museum, Moscow Lomonosov State University	Sumatra, Indonesia	Gorin *et al*. 2020
70	Not preserved	MH807391	*M.* sp2		Andaman Islands, India	Garg *et al*. 2019
71	VNMN07719	MT819964	*M. pineticola*	Institute of Ecology and Biological Resources	Bi Duop Nui Ba NP, Lam Dong, Vietnam	Hoang *et al.* 2020
72	VNMN07344	MT808928	*M. neglecta*	Institute of Ecology and Biological Resources	Bi Duop Nui Ba, Lam Dong, Vietnam	Hoang *et al.* 2020
73	IEBR A.4913	ON745755	*Microhyla xodangorum* sp. nov.	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	This study
74	IEBR A.4905	ON745737	*Microhyla. hmongorum* sp. nov.	Institute of Ecology and Biological Resources	Tam Duong, Lai Chau, Vietnam	This study
75	IEBR A.4906	ON745738	*Microhyla hmongorum* sp. nov.	Institute of Ecology and Biological Resources	Tam Duong, Lai Chau, Vietnam	This study
76	IEBR A.4907	ON745739	*Microhyla hmongorum* sp. nov.	Institute of Ecology and Biological Resources	Tam Duong, Lai Chau, Vietnam	This study
77	IEBR A.4910	ON745740	*Microhyla hmongorum* sp. nov.	Institute of Ecology and Biological Resources	Tam Duong, Lai Chau, Vietnam	This study
78	IEBR A.4908	ON745741	*Microhyla hmongorum* sp. nov.	Institute of Ecology and Biological Resources	Tam Duong, Lai Chau, Vietnam	This study
79	IEBR A.4909	ON745742	*Microhyla hmongorum* sp. nov.	Institute of Ecology and Biological Resources	Tam Duong, Lai Chau, Vietnam	This study
80	IEBR A.4911	ON745743	*Microhyla. hmongorum* sp. nov.	Institute of Ecology and Biological Resources	Tam Duong, Lai Chau, Vietnam	This study

Table 1 (continued). Specimens and sequences of the *Microhyla heymonsi* groups and outgroup representatives used in molecular analyses.

No	Voucher no	GenBank no.	Species	Collection	Locality	Reference
81	2004.0414	KR827933	*Microhyla hmongorum* sp. nov.		Phongsali, Laos	Garg *et al*. 2019
82	2006.2343	KR827941	*Microhyla hmongorum* sp. nov.		Luang Prabang, Laos	Garg *et al*. 2019
83	2006.2348	KR827942	*Microhyla hmongorum* sp. nov.		Luang Prabang, Laos	Garg *et al*. 2019
84	ZMMU NAP-08277	MK208932	*Microhyla hmongorum* sp. nov.	Zoological Museum, Moscow Lomonosov State University	Kachin, Myanmar	Poyarkov *et al*. 2019
85	Not preserved	KU840570	*M.* cf. *heymonsi*	Chengdu Institute of Biology	Zihuai, Sichuan, China	Goutte *et al*. 2016
86	KUHE:23856	LC465687	*M. ninhthuanensis*	Kyoto University, Graduate School of Human and Environmental Studies	Ranong, Thailand	Tominaga *et al*. 2019
	Outgroup					
87	IEBR A5076 (field tag KP-MD2018.24)	MN453610	*M. marmorata*	Institute of Ecology and Biological Resources	Kon Plong, Kon Tum, Vietnam	Hoang *et al*. 2020

Table 2. Uncorrected ('p') distance matrix showing the percentage pair wise genetic divergence 12S rRNA–16S rRNA mtDNA sequences between members of the *Microhyla heymonsi* group.

	Species	1	2	3	4	5	6	7	8
1	*M. heymonsi* s. str.								
2	*M. ninhthuanensis*	3.9–4.6	0.7–2.2						
3	*M. daklakensis*	4.9	5.1–6.2	1.1					
4	*M.* cf. *heymonsi*	2.1–4.5	3.7–6.1	4.7–6.3	0.0–3.4				
5	*Microhyla xodangorum* sp. nov.	8.4	8.3–8.7	7.8–7.9	7.5–8.9	0.0			
6	*Microhyla hmongorum* sp. nov.	5.2	4.8–5.2	6.0–6.6	4.5–5.6	8.7	0.0		
7	*M. pineticola*	9.4	10.6–11.5	9.4–9.8	9.0–10.1	10.9	11.7	0.0	
8	*M. neglecta*	9.5	10.9–11.7	10.1–10.6	9.6–10.5	12.0	11.8	5.9	0.0

phylogenetics of the *M. heymonsi* group, we add 37 available sequences of 16S rRNA of the *Microhyla heymonsi* group from Asian countries.

Phylogenetic trees were constructed by using maximum likelihood (ML) and Bayesian inference (BI) analyses. ChromasPro software (Technelysium Pty Ltd., Tewantin, Australia) was used to edit the sequences, and then aligned using the ClustalW (Thompson *et al*. 1997) option in MEGA X (Kimura 1980; Kumar *et al*. 2018) with default parameters and subsequently optimized manually in BioEdit ver. 7.0.5.2 (Hall 1999). We then checked the initial alignments by eye and adjusted slightly. Prior to ML and Bayesian tests, phylogenetic analyses were performed in MrBayes ver. 3.2 (Ronquist *et al*. 2012). We chose the optimum substitution models for entire sequences using Kakusan 4 (Tanabe 2011) based on the Akaike information criterion (AIC). The best model selected for ML was the general time reversible model (GTR: Tavaré 1986). The BI summarized two independent runs of four Markov Chains for 10 000 000 generations. A tree was sampled every 100 generations and a consensus topology was calculated for 70 000 trees after discarding the first 30 001 trees (burn-in = 3 000 000) (Nguyen *et al*. 2017). We checked parameter estimations and convergence using Tracer ver. 1.5 (Rambaut & Drummond 2009). The strength of nodal support in the ML tree was analyzed using non-parametric bootstrapping (MLBS) with 1000 replicates. We regarded tree nodes in the ML tree with bootstrap values of 75% or greater as sufficiently resolved (Hillis & Bull 1993; Huelsenbeck & Hillis 1993), and nodes with a BPP of 95% or greater as significant in the BI analysis (Leaché & Reeder 2002).

Morphological analysis

Measurements were taken in preserved specimens with a digital calliper to the nearest 0.01 mm under a dissecting microscope (Table 3). The following morphological characteristics were used (Matsui 2011; Matsui *et al*. 2013; Poyarkov *et al*. 2014):

EL = eye length, measured as the distance between the anterior and posterior corners of the eye
FL = foot length, measured from distal end of tibia to tip of toe IV
FLL = forelimb length, measured as length of straightened forelimb to tip of third finger
HAL = hand length, measured from proximal end of outer palmar [metacarpal] tubercle to tip of third finger
HL = head length, measured from tip of snout to end of jaw angle, but not measured parallel with the median line as done by Matsui (2011)
HLL = hindlimb length, measured as length of straightened hindlimb from groin to tip of fourth toe
HW = head width, measured as the maximum width of the head on the level of mouth angles in ventral view
IMTL = inner metatarsal tubercle length, taken as maximal length of inner metatarsal tubercle

IND = internarial distance, measured as the distance between central points of nostrils
IOD = interorbital distance, measured as the shortest distance between the medial edges of eyeballs in dorsal view
IPTL = inner palmar tubercle length, measured as maximal distance from proximal to distal ends of inner palmar tubercle
LAL = lower arm and hand length, measured as distance from elbow to tip of third finger
N-EL = nostril-eye length, measured as the distance between the anterior corner of the eye and the nostril
OMTL = outer metatarsal tubercle length
OPTL = outer palmar tubercle length, measured as maximal diameter of outer palmar tubercle
SL = snout length measured from the anterior corner of eye to the tip of snout
SVL = snout–vent length, measured from the tip of snout to cloaca
TL = tibia length, taken as the distance between the knee and tibiotarsal articulation)
UEW = upper eyelid width, measured as the widest distance from the medial edge of eyeball to the lateral edge of the upper eyelid
1–5TOEL = toe length (1–5), from distal end of inner metatarsal tubercle to tip of toe (1–5)
1FW = first finger width, measured at the distal phalanx
1–3FLO = finger lengths (1–3), for outer side (O) of the first
2–4FLI = finger lengths (2–4), for inner side (I) of the fourth
2–4FDW = finger disk diameters (2–4)
1–5TDW = toe disk diameters (1–5)

Terminology for describing eye coloration in life followed Glaw & Vences (1997); webbing formula followed Savage (1975).

Morphological comparisons

Two unnamed taxa of *Microhyla* from Vietnam were compared with their congeners based on examined specimens (Table 3) and data from literature: Boulenger (1897, 1900, 1920); Smith (1923); Parker (1928, 1934); Andersson (1942); Bourret (1942); Parker & Osman (1948); Pillai (1977); Inger & Frogner (1979); Inger (1989); Dutta & Ray (2000); Bain & Nguyen (2004); Das *et al*. (2007); Das & Haas (2010); Matsui (2011); Fei *et al*. (2012); Matsui *et al*. (2013); Hasan *et al*. (2014); Poyarkov *et al*. (2014); Howlader *et al*. (2015); Seshadri *et al*. (2016); Wijayathilaka *et al*. (2016); Khatiwada *et al*. (2017); Zhang *et al*. (2018); Nguyen *et al*. (2019); Garg *et al*. (2019); Poyarkov *et al*. (2019); Li *et al*. (2019) and Hoang *et al*. (2020, 2021).

Principal component analysis (PCA) Fig. 1

Measurements were first size-corrected to the nearest 0.1 mm and were then used to compare the morphometric difference between the first new species from Lai Chau Province (5 ♂♂ and 3 ♀♀) and the second new species from KonTum Province (1 ♀) vs *Microhyla daklakensis* from Dak Lak Province (4 ♂♂ and 6 ♀♀), *M. ninhthuanenesis* from Ninh Thuan Province (9 ♂♂ and 2 ♀♀), and *M.* cf. *heymonsi* from Kon Tum Province (8 ♂♂ and 2 ♀♀) (Hoang *et al*. 2021). All statistical analyses were performed using PAST ver. 2.17b software (Hammer *et al*. 2001).

Results

Sequence variation

We amplified a 1155-base pair (bp) length fragment of the 12S–16S rRNA mitochondrial gene. In the final alignment of 16S rRNA, 892 sites were conserved and 254 sites exhibited variation, of which 164 were parsimony-informative. The transition-transversion bias (R) was estimated as 2.70. Nucleotide frequencies were A= 25.00%, T= 25.00%, C= 25.00%, and G= 25.00% (data for ingroup only).

Table 3 (continued on next page). Measurements (in mm) and proportions of the type series of *Microhyla hmongorum* sp. nov. and *Microhyla xodangorum* sp. nov.

Species	*Microhyla hmongorum* sp. nov.								*Microhyla xodangorum* sp. nov.
Sex	Male	Male	Male	Male	Male	Female	Female	Female	Female
Specimen	Holotype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype	Paratype	Holotype
No	IEBR A.4905	IEBR A.4906	IEBR A.4907	IEBR A.4908	IEBR A.4909	IEBR A.4910	IEBR A.4911	IEBR A.4912	IEBR A.4913
SVL	17.4	15.5	16.1	17.4	13.8	20.3	19.2	20.1	25.6
HL	5.5	4.5	4.4	5.3	4.3	5.6	4.9	5.3	5.4
HW	5.5	4.4	5.3	5.2	4.0	5.6	5.7	5.8	6.6
SL	2.2	2.1	2.0	2.1	1.9	2.1	2.3	2.4	2.9
EL	2.1	2.0	1.9	1.7	1.3	2.0	1.9	2.0	2.2
N-EL	1.3	0.9	0.9	1.0	0.9	1.1	1.1	1.0	1.4
IND	1.5	1.5	1.4	1.3	1.1	1.5	1.4	1.3	2.2
IOD	1.8	1.7	1.8	1.9	1.6	2.0	2.1	2.0	2.9
UEW	1.4	1.1	1.1	1.0	0.6	1.3	1.0	1.3	1.3
FLL	9.9	8.0	9.2	8.6	6.6	10.5	10.5	10.1	13.5
LAL	7.3	6.0	6.9	6.9	5.2	7.7	8.1	7.6	10.6
HAL	4.2	3.1	3.9	3.9	2.8	4.8	4.1	4.8	6.1
IPTL	0.6	0.5	0.5	0.7	0.5	0.7	0.7	1.0	0.6
OPTL	0.5	0.4	0.5	0.5	0.4	0.4	0.4	0.5	1.3
1FL	1.0	0.8	0.9	1.4	0.9	1.4	1.9	2.0	2.3
1FW	0.2	0.1	0.3	0.3	0.1	0.3	0.3	0.3	0.3
1FLO	0.9	0.4	0.9	0.9	0.4	0.6	1.1	1.3	1.3
2FLO	1.2	1.0	1.4	1.4	1.3	1.3	1.5	1.8	2.4
3FLO	2.6	1.8	2.2	2.5	2.0	2.9	2.7	2.9	4.1
2FLI	1.9	1.5	1.7	1.8	1.4	2.0	2.2	2.1	2.9
3FLI	2.7	2.1	2.2	2.8	2.0	3.3	3.3	3.0	4.4
4FLI	1.4	0.9	1.3	1.3	1.2	1.5	2.0	1.7	2.2
2 FDW	0.3	0.2	0.2	0.3	0.2	0.3	0.3	0.3	0.6

Table 3 (continued). Measurements (in mm) and proportions of the type series of *Microhyla hmongorum* sp. nov. and *Microhyla xodangorum* sp. nov.

Species	***Microhyla hmongorum* sp. nov.**								***Microhyla xodangorum* sp. nov.**
Sex	**Male**	**Male**	**Male**	**Male**	**Male**	**Female**	**Female**	**Female**	**Female**
Specimen	**Holotype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	**Holotype**
No	**IEBR A.4905**	**IEBR A.4906**	**IEBR A.4907**	**IEBR A.4908**	**IEBR A.4909**	**IEBR A.4910**	**IEBR A.4911**	**IEBR A.4912**	**IEBR A.4913**
3FDW	0.4	0.3	0.3	0.4	0.3	0.4	0.4	0.4	0.8
4FDW	0.3	0.3	0.2	0.3	0.2	0.3	0.4	0.3	0.5
HLL	30.5	24.4	27.4	28.8	21.9	33.9	31.6	32.3	48.3
TL	9.2	8.0	8.6	9.3	6.9	11.0	10.6	10.5	15.4
FL	14.1	10.8	12.6	13.4	9.9	15.1	14.6	15.2	21.2
1TOEL	1.1	1.1	1.6	1.2	0.8	1.2	1.5	1.3	3.8
2TOEL	2.4	2.0	2.0	1.7	1.6	1.8	2.7	2.5	5.4
3TOEL	4.2	3.3	3.1	3.4	2.6	4.2	4.4	4.7	8.4
4TOEL	5.6	4.4	5.7	5.6	3.9	6.5	6.9	6.4	10.0
5TOEL	3.0	2.3	2.6	2.6	1.8	3.4	3.1	3.0	5.4
IMTL	0.4	0.3	0.3	0.3	0.2	0.4	0.4	0.4	0.6
OMTL	0.6	0.5	0.8	0.6	0.3	0.5	0.7	0.6	0.5
1TDW	0.3	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.5
2TDW	0.4	0.3	0.3	0.4	0.2	0.6	0.6	0.4	0.8
3TDW	0.5	0.4	0.5	0.5	0.3	0.6	0.6	0.6	1.0
4TDW	0.5	0.4	0.4	0.6	0.3	0.8	0.8	0.7	1.0
5TDW	0.4	0.3	0.4	0.4	0.2	0.5	0.5	0.5	0.6

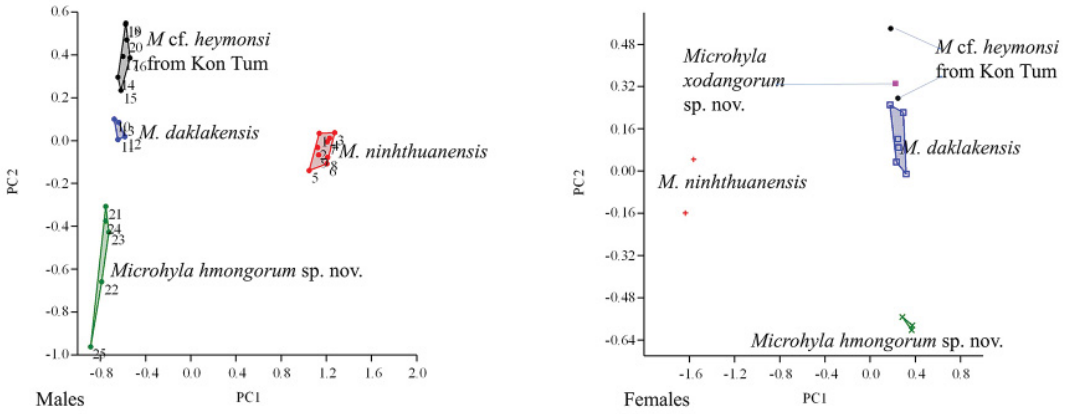

Fig. 1. Plots of the first principal component (PC1) versus the second (PC2) for the males and the females of *Microhyla hmongorum* sp. nov. (green), *Microhyla xodangorum* sp. nov. (pink), *M. ninhthuanensis* Hoang *et al*., 2021 (red), *M. daklakensis* Hoang *et al*., 2021 (blue), and *M.* cf. *heymonsi* Vogt, 1911 (black).

Interspecific uncorrected p-distance

The genetic divergence between the specimen from Kon Tum Province and other congeners of the *Microhyla heymonsi* group ranged from 7.5 to 8.9% (*M.* cf. *heymonsi*) and approximately 8.4% between the specimen from Kon Tum and *M. heymonsi* s. str. from Taiwan, China. The genetic divergence between the population from Lai Chau Province and its congeners ranged from 4.5–5.6% (*M.* cf. *heymonsi*) to 8.7% (the specimen from Kon Tum Province). These values were higher than the genetic distances between *M. ninhthuanensis* and *M. heymonsi* s. str. from Taiwan, China (3.9–4.6%) (Table 2). The genetic divergence between *M.* cf. *heymonsi* and *M. heymonsi* s. str. from Taiwan, China, ranged 2.1–4.5%, however, the genetic distance of the samples within the *M.* cf. *heymonsi* group was 0.0–3.4%.

Phylogenetic relationships of 49 available sequences of the *Microhyla heymonsi* group

The BI and ML analyses produced topologies with –ln L = 4802.164 and 4711.128, respectively with a gamma shape parameter (G: 0.176 in ML and 0.226 in BI). BI and ML analyses obtained similar topologies (Fig. 2) that differed only at several poorly supported basal nodes. Our matrilineal genealogy shows that a representative of the population from Kon Tum completely separated from other members of the *M. heymonsi* group with strong nodal support (1/95). In addition, the Lai Chau population is also clearly separated (1/100) from other members of the *M. heymonsi* group and closely related to *M. ninhthuanensis*, with strong nodal support (1/93). The *M.* cf. *heymonsi* group has complex genetic relationships, however there is still a clear dissociation from *M. heymonsi* s. str. with strong nodal support (0.98/79). The *M.* cf. *heymonsi* group has a dissociation between populations from North-Central Vietnam and those from Northeastern Vietnam and South-Central Vietnam (0.95/82). The specimen from Sichuan, China has a close genetic relationship with the population from Northeastern Vietnam (0.88/67). The specimen from Sichuan, China and the population from Northeast Vietnam dissociate from the population from South-Central Vietnam (1/97).

Distribution pattern and phylogenetic relationships of the *Microhyla heymonsi* group

The BI and ML analyses produced topologies with –ln L=4802.0201 and 4534.3416, respectively, with a gamma shape parameter (G: 0.19 in ML and 0.10 in BI). BI and ML analyses obtained similar topologies (Fig. 2) that differed only at several poorly supported basal nodes.

Our matrilineal genealogy shows that Clade 1 (including the population of *M. heymonsi* s. str. from Taiwan, China, and populations of *M.* cf. *heymonsi* from Southern China, Northeast Vietnam, North-Central Vietnam and South-Central Vietnam) is separated from Clade 2 (including the population of *Microhyla* sp1 from Northern Thailand and North-Central Laos) with a nodal support of 0.7 / 71; Clade 3 (including the populations of *M. ninhthuanensis* from Southern Vietnam, Central Thailand and Southern Myanmar) is separated from Clade 4 (including the populations of *Microhyla* sp2 from Singapore,

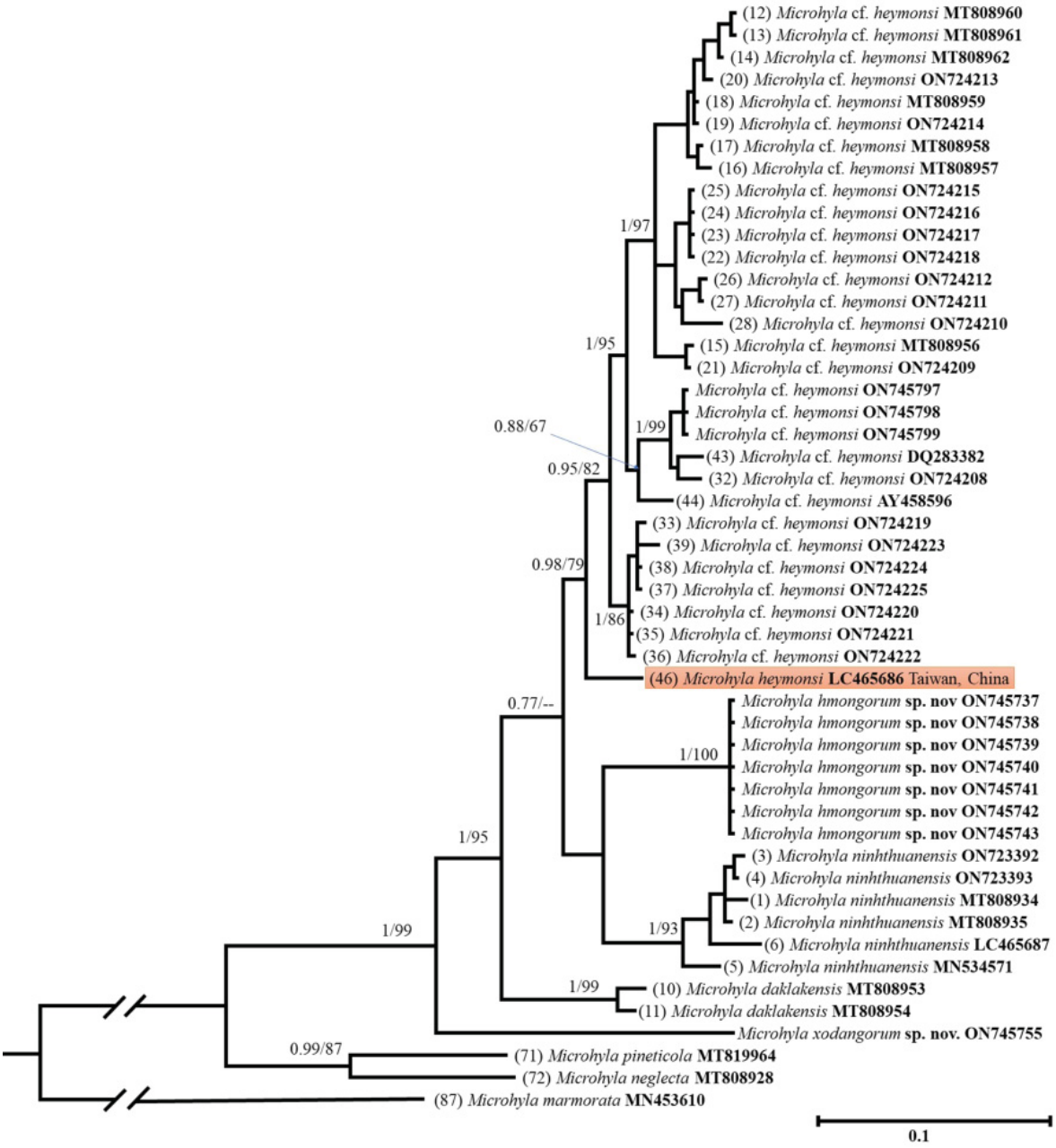

Fig. 2. Bayesian inference matrilineal genealogy of the *Microhyla heymonsi* group derived from the analysis of 12S rRNA–16S rRNA mtDNA sequences. Numbers above and under branches are Bayesian posterior probabilities and ML bootstrap values. The scale bar represents 0.1 nucleotide substitutions per site.

Malaysia and Andaman Islands) with a strong nodal support (0.93 / 82); both Clade 3 and Clade 4 are separated from Clade 5 (including the populations from NW Vietnam, northern Laos and northern Myanmar) with a strong nodal support (0.91 / 76); Clades 1 and 2 are separated from Clades 3, 4 and 5 with a strong nodal support (0.9 / 79); Clade 6 (the population of *M. daklakensis* Hoang *et al*., 2021 from Nam Kar NR, Dak Lak Province, Vietnam) is separated from Clades 1–5 with a strong nodal support (0.98 / 82); Clade 7 (the population from Kon Plong, Kon Tum Province, Vietnam) is separated from Clades 1–6 with a strong nodal support (1 / 90); Clade 8 (the population of *M. neglecta* Poyarkov et al., 2020 from Bidoup-Nui Ba NP, Lam Dong Province, Vietnam) is separated from Clade 9 (population of *M. pineticola* Poyarkov et al., 2014 from Lam Dong and Province, Vietnam) with a strong nodal support (0.99 / 88) and they form a separate branch from other clades (Figs 3, 5).

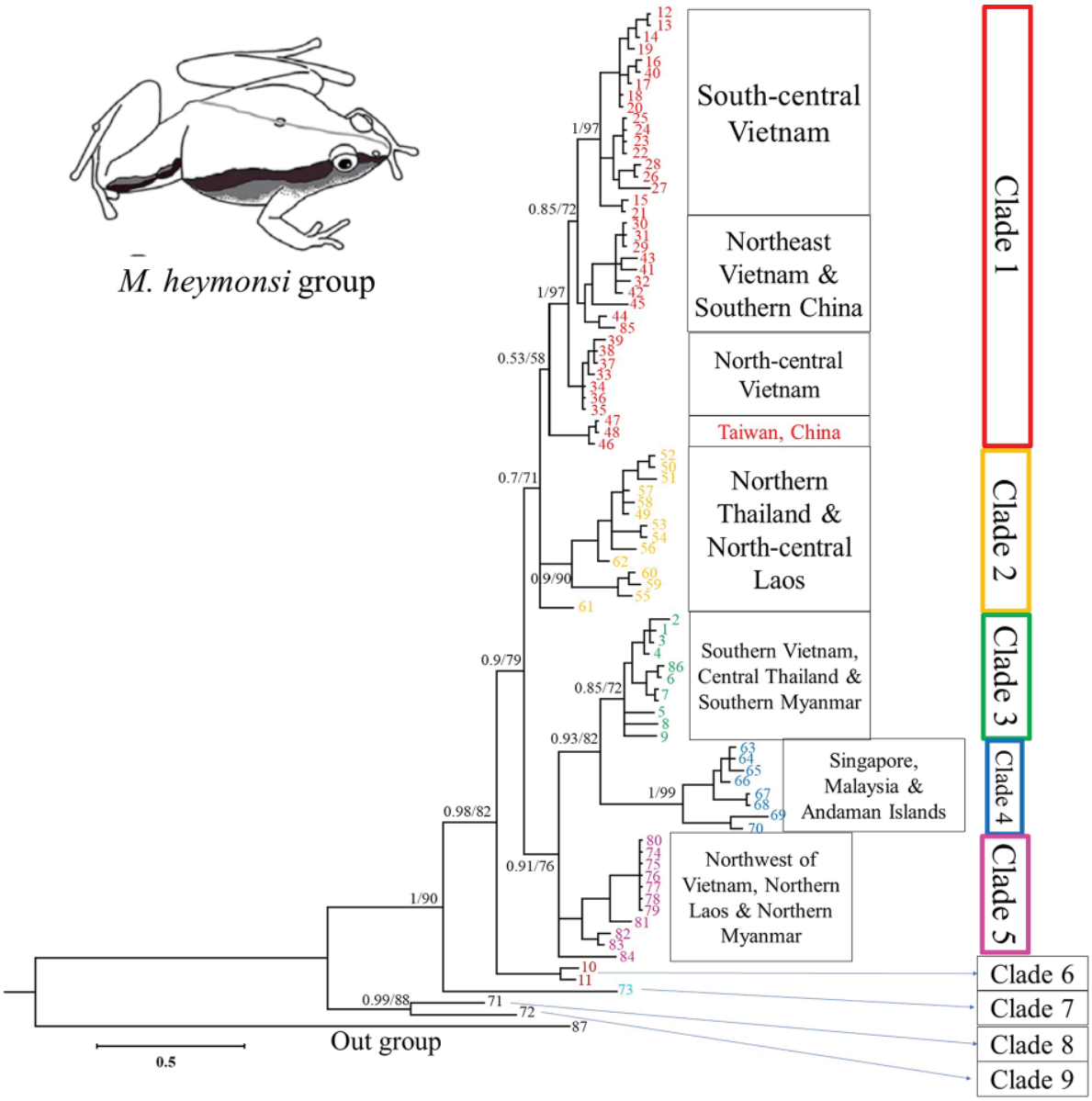

Fig. 3. Bayesian inference matrilineal genealogy of the *Microhyla heymonsi* group derived from the analysis of 16S rRNA mtDNA sequences. Numbers above and under branches are Bayesian posterior probabilities and ML bootstrap values; the scale bar represents 0.5 nucleotide substitutions per site.

Table 4. Variable loadings for principal components with Eigenvalue greater than 0.01, from morphometric characters corrected by SVL. All measurements are given in millimeter (mm) of *Microhyla hmongorum* sp. nov., *Microhyla xodangorum* sp. nov., *M. ninhthuanensis*, *M. daklakensis*, and *M*. cf. *heymonsi*.

	Male			Female		
	Axis 1	**Axis 2**	**Axis 3**	**Axis 1**	**Axis 2**	**Axis 3**
SVL	-0.010	0.157	0.012	0.007	0.136	-0.006
HL	-0.026	0.076	0.105	0.033	0.058	-0.020
HW	-0.015	0.127	0.094	0.020	0.072	-0.007
SL	0.000	0.132	-0.031	0.005	0.156	0.025
EL	-0.014	0.113	0.006	-0.005	0.105	-0.019
N-EL	0.025	0.202	-0.084	-0.016	0.223	0.082
IND	0.014	0.169	0.032	-0.027	-0.110	0.917
IOD	0.007	0.159	0.043	-0.010	0.144	0.022
UEW	0.015	0.152	0.181	0.035	0.109	0.049
FLL	0.009	0.171	-0.017	0.017	0.152	0.063
LAL	-0.003	0.177	0.003	0.003	0.165	0.031
HAL	0.002	0.203	-0.068	0.026	0.171	0.038
IPTL	-0.113	0.118	0.493	0.084	-0.047	-0.223
OPTL	0.017	0.310	0.034	-0.016	0.384	-0.009
1FL	0.024	0.298	-0.294	0.025	0.178	0.002
3FDW	0.324	0.203	-0.167	-0.265	0.272	0.101
HLL	-0.769	0.343	0.002	0.811	0.294	0.013
TL	0.004	0.191	-0.015	0.026	0.176	0.009
FL	-0.152	0.226	0.053	0.157	0.196	0.009
1TOEL	0.196	0.371	-0.259	-0.165	0.442	0.128
IMTL	0.148	0.218	0.154	-0.108	0.322	-0.031
OMTL	0.244	0.127	0.692	-0.247	0.116	-0.249
3TDW	0.381	0.240	-0.031	-0.366	0.200	-0.034
Eigenvalue	0.82	0.13	0.02	0.46	0.13	0.07
% variance	82.76	13.11	1.57	67.50	18.53	9.91

The results of this molecular analysis show that the genetic relationship between the populations of *M.* cf. *heymonsi* from southern China, northeast Vietnam, North-Central Vietnam and South-Central Vietnam and *M. heymonsi* s. str. is unclear. However, we herein consider them as a group of species (hereafter *M. heymonsi* s. str.) to facilitate the morphological comparisons.

Morphological analysis

The population from Lai Chau Province can be separated from *Microhyla daklakensis* from Dak Lak Province, *M. ninhthuanensis* from Ninh Thuan Province and *M.* cf. *heymonsi* from Kon Tum Province based on morphometric data. In males, the PCA extracted three principal component axes with eigenvalues greater than 0.01 and of these, the first two component axes accounted for 82.76% of the variation (Table 4). The first two principal component axes could separate the new form from *M.* cf. *heymonsi* from Kon Tum by 23 characters (Fig. 1), mainly based on limb and head measurements, namely: SVL, HL, HW, SL, EL, N-EL, IND, IOD, UEW, FLL, LAL, HAL, IPTL, OPTL, 1FL, 3FDW, HLL, TL, FL, 1TOEL, IMTL, OMTL, 3TDD (Table 4). Species with a larger and positive score on PC1 reflect shorter N-EL, IND, IOD, UEW, FLL, HAL, OPTL, 1FL, 3FDW, TL, 1TOEL, IMTL, OMTL and 3TDW; while a negative score signifies smaller SVL, HL, HW, EL, LAL, IPTL, HLL and FL. The PC2 with positive scores were associated with species with larger morphological traits (Table 4).

Taxonomic conclusions

Based upon the phylogenetic analyses of 16S rRNA sequences, the two populations from Lai Chau and Kon Tum provinces, Vietnam, clearly differ from each other and from other known species of the *Microhyla heymonsi* group for which comparable genetic data are available. There also exist morphological differences. Accordingly, we describe the two new species as follows:

Class Amphibia Linnaeus, 1758
Order Anura Hogg, 1839
Family Microhylidae Günther, 1858
Genus *Microhyla* Tschudi, 1838

Microhyla hmongorum sp. nov.
urn:lsid:zoobank.org:act:3158A3D2-A0D7-43C5-B7E3-C7247567E1AA
Figs 2–3, Tables 1–3

Diagnosis

Microhyla hmongorum sp. nov. is distinguished from its congeners by a combination of the following morphological characters: 1) size small (SVL 13.8–17.4 in 5 ♂♂; 19.2–20.3 in 3 ♀♀); 2) snout profile acuminate; 3) dorsal skin smooth with tiny and flat tubercles unevenly scattered, dorsolateral edges not sharp; 4) chest and belly creamy-white fades towards the groin and thighs with indistinct grayish mottling along the thighs and belly edges, chin, throat pinkish white with scattered indistinct grayish mottling; 5) first finger longer than one half of second finger.

Etymology

The specific name is a patronym for the H'Mong people, an ethnic minority people in the northwest montane regions of Vietnam. Their assistance made it possible for us to collect the type specimens of the new species in the montane forest of Lai Chau Province, northwestern Vietnam. We recommend 'Hmong Narrow-Mouth Frog' as the common English name and 'Nhái bầu hmông' as the Vietnamese name.

Material examined

Holotype

VIETNAM • adult ♂; northern Vietnam, Lai Chau Province, Tam Duong District (Fig. 4); 22°21′15.7″ N, 103°36′36.4″ E; 1362 m a.s.l.; 22 May 2020; C.V. Hoang *et al*. leg.; IEBR A.4905 (TD-LC2020.121).

Paratypes

VIETNAM • 4 adult ♂♂; same collection data as for holotype; IEBR A.4906–4907 (TD-LC2020.122, TD-LC2020.123), IEBR A.4908–4909 (TD-LC2020.129, TD-LC2020.130) • 3 adult ♀♀; same collection data as for holotype; IEBR A.4910 (TD-LC2020.124), IEBR A.4911–4912 (TD-LC2020.131, TD-LC2020.132).

Description of holotype (Fig. 4, Table 3)

Preserved specimens were in good condition.

Habitus. Stocky, SVL 17.4 mm; body triangular shaped; head as long as wide (HL/HW 1.00); snout long, abruptly round in dorsal view, projecting beyond margin of lower jaw, equal to diameter of eye (SL/EL 1.02); eyes small, slightly protuberant, pupil round (Fig. 4F); dorsal surface of head flat, canthus rostralis round; loreal region steep, weakly concave; nostril round, lateral, below canthus rostralis, nostril-eyelid length (N-EL 1.3 mm) greater than one half of eye length (N-EL/EL 0.61); interorbital

distance (IOD 1.8 mm) greater than internarial distance (IND 1.5 mm) and upper eyelid width (UEW 1.4 mm); pineal spot absent, tympanum hidden, supratympanic fold weak, extending from posterior corner of eye to arm insertion; vomerine teeth absent; tongue without papillae, roundly spatulate and free at the rear half of its length; slit-like openings to a median vocal sac.

Forelimbs. Short, about two times as long as snout–vent length (FLL/SVL 0.57); hand length two times shorter than forelimb length (HAL/FLL 0.42); fingers slender, free of webbing, a little flat in cross-section, with skin fringes on fingers present, dorsoventrally flattened; first finger well developed, longer than one-half length of second finger (1FLO/2FLO 0.69), second finger slightly longer than fourth (2FLI/4FLI 1.32) and longer than one-half length of third finger (2FLI/3FLI 0.68); relative finger lengths: I<IV<II<III (Fig. 4C); dorsal surface of fingertip with median longitudinal groove, forming two scutes, grooves present in all fingers; relative finger disk widths: I<IV<II<III; nuptial pad absent; subarticular tubercles on fingers distinct, round, formula: 1:1:2:2 (given for fingers I:II:III:IV, respectively); inner metacarpal tubercle round and prominent (IPTL 0.6 mm); a paired outer metacarpal tubercle divided by a waistline into two unequally sized parts (OPTL 0.5 mm): outer part slightly oval, greater than inner part quite crescent (Fig. 4C).

Hindlimbs. Slender and slightly short (HLL 30.5 mm), tibia length longer than half of snout–vent length (TL/SVL 0.53); tibiotarsal articulation at straightened limb not reaching snout; foot longer than tibia (FL/TL 1.54); relative toe lengths: I<II<V<III<IV; tarsus smooth, inner tarsal fold absent; tips of all toes distinctly dilated into disks (Fig. 4D), wider than those of fingers (3TDW 0.5 mm, 3FDW/3TDW 0.69), dorsal surface of all toes with median longitudinal grooves at disks; relative toe disk widths: I<V<II<III<IV; webbing between toes basal and poorly developed, webbing formula: I2–2½II2–3½III3–4⅓IV4⅓–3V (Fig. 4D); subarticular tubercles on toes small, prominent, round, formula 1, 1, 2, 3, 2; inner metatarsal tubercle elongated, oval, large and prominent (IMTL 0.4); outer metatarsal tubercle round, elevated and very distinct, slightly greater (OMTL 0.6) than length of inner metatarsal tubercle.

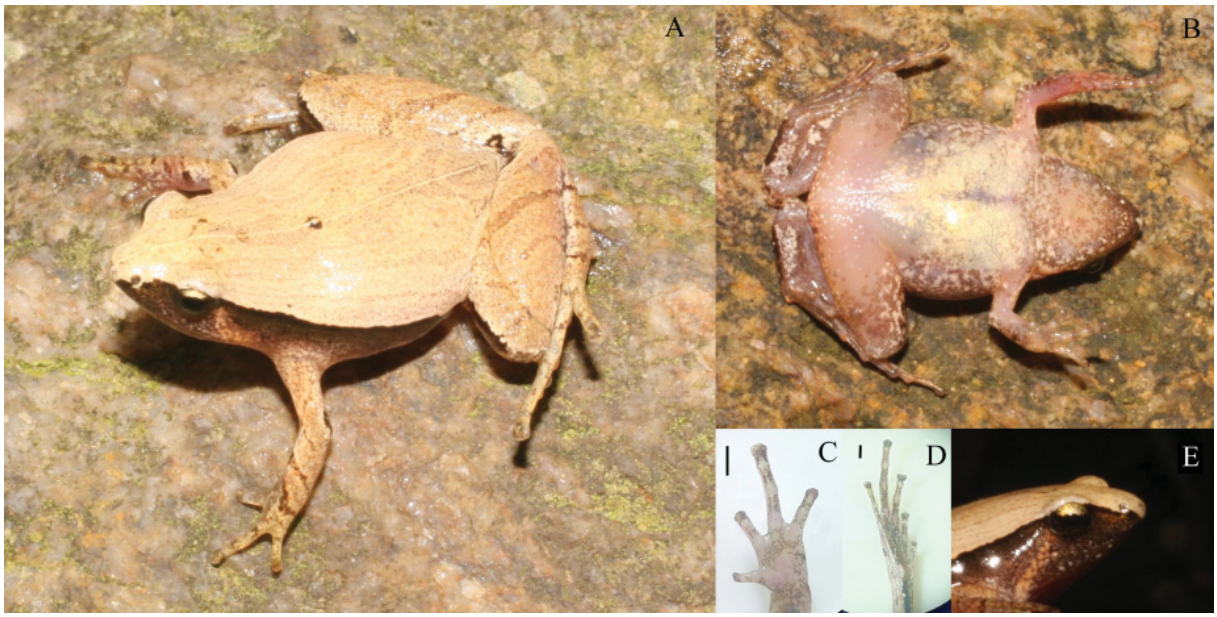

Fig. 4. *Microhyla hmongorum* sp. nov., ♂, holotype (IEBR A.4905 (TD-LC2020.121)). **A**. Dorsolateral view in life. **B**. Ventral view in life. **C**. Underside of left hand. **D**. Underside of right foot. **E**. Lateral view of the head. Scale bars = 1 mm.

Skin. Dorsal surface smooth with tiny and flat tubercles unevenly scattered; dorsolateral edges not sharp; upper eyelid without supraciliary spines; flanks of body and lateral sides of head smooth, hindlimb dorsally scattered with some low pustules; ventral side of body and limbs smooth, vent area smooth with several low tubercles in cloacal region (Fig. 4B). Cloacal opening unmodified, directed posteriorly, at lower level of thighs.

Coloration of holotype in life

Dorsal surface of head and trunk beige with dark brown dust forming blurred markings; two dark brown tiny spots between eyelids; a small dark brown marking in '( )'-shape in the center of dorsum; a mid-dorsal line extending from the tip of snout to vent; a dark brown rhombus pattern on dorsum: one side is a small dark marking in '( )'-shape, one side is a small dark brown blurred marking in '( )'-shape.

Flanks and lateral side of head dark with a dark lateral stripe running from tip of snout to nostril, fading towards upper jaw (Fig. 4A). Chest and belly creamy white fading towards the groin and thighs with indistinct grayish mottling along the thighs and belly edges. Chin, throat pinkish white with scattered indistinct grayish mottling (Fig. 4B). Limbs dorsally beige with narrow blurred dark brown crossbars; fingers and toes dorsally brown with scattered dark brown crossbars; limbs ventrally crystal-clear with scattered dark grey and white dust, getting thicker toward shank and foot. Iris bicolored, golden in upper third, dark copper in its lower two thirds; pupil oval, horizontal, black.

Coloration of holotype in preservative

After preservation in ethanol, dorsal coloration changed from beige to greyish beige; ventral surface of chest, belly, and limbs changed from crystal clear to white; dorsal pattern, dark spots on dorsum and stripes on dorsal surfaces of limbs unchanged, dark brown pattern changed to dark grey; iris completely black, pupil round, white.

Variation

The paratypes vary in body size, coloration of dorsal surface, dorsal marking and black scapular spots. Adult males are smaller than adult females. The female's belly is whiter than that of the male.

Comparisons

Microhyla hmongorum sp. nov. is distinguished from other members of the *Microhyla heymonsi* group by the following morphological characteristics: 1) body size small (SVL 13.8–17.4 in 5 ♂♂; 19.2–20.3 in 3 ♀♀) versus *M. ninhthuanensis* (SVL 17.3–18.8 in ♂♂; 21.6–23.6 in ♀♀), *M. daklakensis* (SVL 17.7–20.1 in ♂♂; 22.9–26.8 in ♀♀), *M. neglecta* (SVL 18.7–20.2 in ♂♂; 23.4–26.2 in ♀♀); 2) snout profile acuminate versus *M. ninhthuanensis*, *M. daklakensis* (snout profile rounded) and *M. heymonsi* s. str. (snout profile obtusely pointed); 3) dorsal skin smooth with tiny and flat tubercles unevenly scattered, dorsolateral edges not sharp versus *M. ninhthuanensis* (smooth, flanks shagreened; dorsolateral edges not sharp), *M. daklakensis* (smooth, flanks smoothly shagreened; dorsolateral edges not sharp), *M. heymonsi* s. str. (smooth, dorsolateral edges not sharp), *M. pineticola* (almost smooth above, with few tiny tubercles scattered in posterior part of dorsum and along the dorsolateral edges; dorsolateral edges sharp), *M. neglecta* (smooth with evenly scattered small flat tubercles; dorsolateral edges sharp); 4) chest and belly creamy white fades towards the groin and thighs with indistinct grayish mottling along the thighs and belly edges, chin, throat pinkish white with scattered indistinct grayish mottling versus *M. ninhthuanensis*, *M. daklakensis*, *M. heymonsi* s. str. (chest and belly creamy white; chin dark grey; throat white with scattered dark grey dusting), *M. pineticola* (belly purplish-grey with indistinct whitish mottling; chin dark greyish with orange speckles and a thin light coloured medial stripe continuing to chest and belly), *M. neglecta* (chest and belly yellowish with indistinct greyish marbling laterally; centre of chin grey, sides dark brown to black with a thin, light-coloured medial stripe not reaching the

chest); 5) first finger longer than one half of second finger versus *M. ninhthuanensis*, *M. pineticola*, *M. heymonsi* s. str. (first finger shorter than one half of second finger). Detailed comparisons between *Microhyla hmongorum* and other species of the *M. heymonsi* group are shown in Table 5 and of the genus *Microhyla* in total are shown in Appendix 1.

Natural history

All specimens were collected at night from 19:00 to 23:00 on the forest trails near streams in the evergreen forest at an elevation of 1300 m a.s.l. (Fig. 7A). Air temperature was 23°C and relative humidity was 89%. Other anuran species found at the type locality were *Leptobrachella ventripunctata* (Fei, Ye & Li,

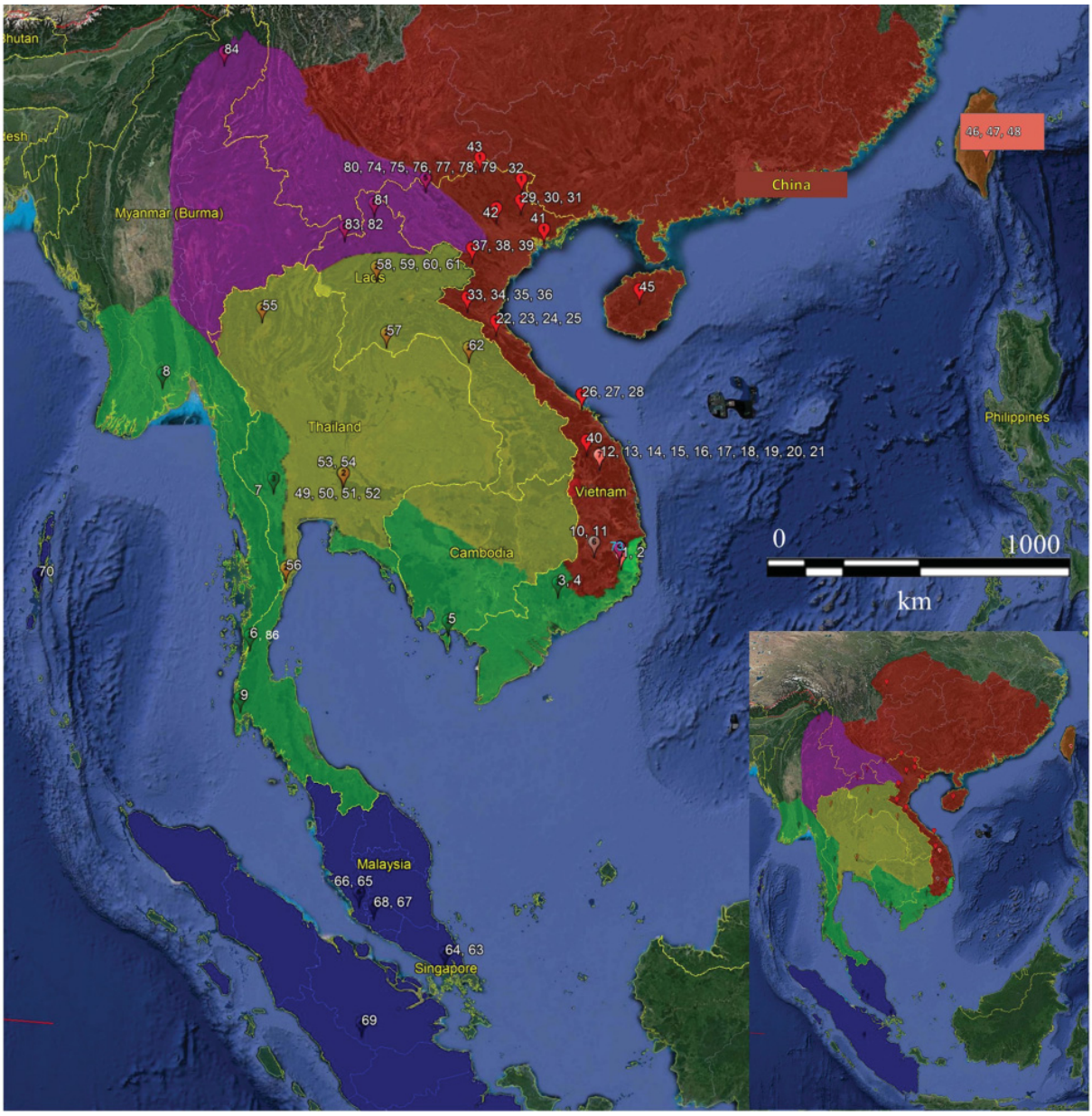

Fig. 5. Map showing the distribution pattern of the *Microhyla heymonsi* group based on available molecular and morphological data collected from East and Southeast Asia (red area: *M. heymonsi* s. str. Vogt, 1911 and *M.* cf. *heymonsi*; yellow area: *Microhyla* sp1; blue area: *Microhyla* sp2; green area: *M. ninhthuanensis* Hoang *et al*., 2021; pink area: *Microhyla hmongorum* sp. nov.).

Table 5 (continued on next page). Selected diagnostic characters for the comparisons between the species of the *Microhyla heymonsi* group.

	SVL male	SVL female	Snout profile	Dorsum skin	Ventral color
Microhyla hmongorum sp. nov.	13.8–17.4 (n=5)	19.2–20.3 (n=3)	Acuminate	Smooth with tiny and flat tubercles unevenly scattered; dorsolateral edges not sharp	Chest and belly creamy-white fades towards the groin and thighs with indistinct grayish mottling along the thighs and belly edges; chin, throat pinkish white with scattered indistinct greyish mottling
Microhyla xodangorum sp. nov.	?	25.6	Rounded	Almost smooth with flat tubercles evenly scattered in dorsum; dorsolateral edges sharp	Chest and belly yellowish with indistinct greyish mottling laterally; chin grey with thickly greyish mottling and a thin, light-coloured medial stripe not reaching the chest
M. daklakensis	17.7–20.1	22.9–26.8	Rounded	Smooth, flanks smoothly shagreened; dorsolateral edges not sharp	Chest and belly creamy white; chin dark grey; throat white with scattered dark grey dusting
M. ninhthuanensis	17.3–18.8	21.6–23.6	Rounded	Smooth, flanks shagreened; dorsolateral edges not sharp	Chest and belly creamy white; chin dark grey; throat white with scattered dark grey dusting
M. pineticola	17.2–19.5	18.0–23.0	Acuminate	Almost smooth above with few tiny tubercles scattered in posterior part of dorsum and along the dorsolateral edges; dorsolateral edges sharp	Belly purplish-grey with indistinct whitish mottling; chin dark greyish with orange speckles and a thin light-coloured medial stripe continuing to chest and belly
M. neglecta	18.7–20.2	23.4–26.2	Acuminate	Smooth with evenly scattered small flat tubercles; dorsolateral edges sharp	Chest and belly yellowish with indistinct greyish marbling laterally; centre of chin grey, sides dark-brown to black with a thin, light-coloured medial stripe not reaching the chest
M. heymonsi s. str.	16.5–22.0	18.0–26.5	Rounded Obtusely-pointed	Smooth, dorsolateral edges not sharp	Chest and belly creamy white; chin dark grey; throat white with scattered dark grey dusting

Table 5 (continued). Selected diagnostic characters for the comparisons between the species of the *Microhyla heymonsi* group.

	F1 versus F2	Disks on distal end of fingers	Dorsal peripheral grooves on toe disks	Tibiotarsal	Foot webbing	Distribution
Microhyla hmongorum sp. nov.	F1 > ½ F2	present	present	Shorter than snout	I2–2½II2–3½III3–4⅓IV4⅓–3V	NW Vietnam, S China, N Laos and northeastern Myanmar
Microhyla xodangorum sp. nov.	F1 > ½ F2	present, F2–F4 weak	present, weak	well beyond snout	I1½–2½II1¾–3III2¾–3¾IV4–2½V	Kon Tum pl., S Vietnam
M. daklakensis	F1 > ½ F2	present	present	Shorter than snout	I2–2½II2–3III3–4IV4⅓–3V	Dak Lak
M. ninhthuanensis	F1 ≤ ½ F2	present	present	Shorter than snout	I2–2½II2–3III3–4IV4⅓–3V	Southern Vietnam, Central Thailand and Southern Myanmar
M. pineticola	F1 ≤ ½ F2	present, F2–F4 weak	present, weak	Shorter than snout, but beyond the eye level	I1½–2½II1¾–3III2¾–3¾IV4–2½V	Chu Yang Sin NP, Langbian pl., S Vietnam
M. neglecta	F1 > ½ F2	present	present, weak	Well beyond snout	I1½–2½II1¾–3III2¾–3¾IV3¾–2½V	Langbian pl., S Vietnam
M. heymonsi s. str.	F1 ≤ ½ F2	present	Usually present	Shorter than snout	I2–2½II2–3III3–4IV4⅓–3V	S China, NE India, SE Asia to Sumatra

1990) and *Limnonectes bannaensis* Ye, Fei, Xie & Jiang, 2007. Larval stages, eggs and advertisement call of the new species are unknown.

Distribution

Microhyla hmongorum sp. nov. is known from Hoang Lien Range, NW Vietnam. Garg *et al*. (2019) reported this species from Phongsali and Luang Prabang provinces of Laos and Poyarkov *et al*. (2019) recorded the species from Kachin of Myanmar. It is expected to be found in southwestern Yunnan Province, China as well (Fig. 5).

Microhyla xodangorum sp. nov.
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Figs 1–3, 5–6, 7B, Tables 1–3, 5

Diagnosis

Microhyla xodangorum sp. nov. is distinguished from its congeners by a combination of the following morphological characteristics: 1) size large (SVL 25.6 in a single ♀); 2) snout profile round; 3) dorsal skin almost smooth with flat tubercles evenly scattered in dorsum; dorsolateral edges sharp; 4) chest and belly yellowish with indistinct greyish mottling laterally; chin grey with thickly greyish mottling and a thin, light-coloured medial stripe not reaching the chest; 5) first finger longer than one half of second finger; 6) disks on distal end of fingers II–IV weak; 7) tibiotarsal articulation at straightened limb well beyond snout.

Etymology

The specific name is a patronym for the Xo Dang people, an ethnic minority people in Kon Tum Province, Vietnam. Their assistance made it possible for us to collect the holotype of the new species in the montane forest of the Kon Tum Plateau, Central Highlands of Vietnam. We recommend 'Xodang Narrow-mouth Frog' as the common English name and 'Nhái bầu xơ đăng' as the Vietnamese name.

Material examined

Holotype

VIETNAM • adult ♀; Central Vietnam, Kon Tum Province, Kon Plong District, Mang Canh Commune (Fig. 6); 14°38'49.2″ N, 108°15′39.9″ E; ca 1253m a.s.l.; 15 Sep. 2018; C.V. Hoang leg.; IEBR A.4913 (KP-MĐ-2018-21).

Description of holotype (Fig. 6)

Preserved specimens were in good condition.

Habitus. Stocky, size medium (SVL 25.6 mm); head wider than long (HL / HW 0.83); snout long, abruptly round in dorsal view, projecting beyond margin of lower jaw, longer than diameter of eye (SL / EL 1.29); eyes small, slightly protuberant, pupil round (Fig. 6A); nostril oval, lateral, nostril-eyelid length (N-EL 1.4 mm) shorter than eye length (EL 2.2 mm); dorsal surface of head flat, loreal region acute, canthus rostralis round; interorbital distance greater than internarial distance (IOD / IND 1.31) and upper eyelid width (IND / UEW 1.68); tympanum hidden, supratympanic fold weak, from posterior corner of eye to arm insertion; vomerine teeth absent, tongue without papillae, oval and free at rear half of its length.

Forelimbs. Short, about one-half of snout-vent length (FLL / SVL 0.52); hand two times shorter than forelimb length (HAL / FLL 0.45); fingers slender, free of webbing, round in cross-section, dermal fringes weak; first finger longer than one-half length of second finger (1FLO / 2FLO 0.53); second finger slightly longer than fourth (2FLI / 4FLI 1.35) and shorter than third (2FLI / 3FLI 0.67); relative finger lengths:

I<IV< II<III (Fig. 6C). All disks bearing narrow peripheral grooves, dorsal surface of each fingertip with median longitudinal groove, forming two scutes; relative finger disk widths: I<IV<II<III; nuptial pad absent; subarticular tubercles on fingers distinct, round, formula: 1:1:2:2; inner metacarpal tubercle (IPTL 0.6) oval, prominent; an outer metacarpal tubercle quite round (OPTL 1.3).

Hindlimbs. Slender and long (HLL 48.3 mm), tibia length longer than half of snout–vent length (TL/SVL 0.60); tibiotarsal articulation at straightened limb well beyond snout; foot longer than tibia (FL/TL 1.38); relative toe lengths: I<II=V<III<IV; tarsus smooth, inner tarsal fold absent; tips of all toes distinctly dilated into disks, slightly wider than those of fingers (3TDW 1.0 mm, 3FDW/3TDW 0.78), dorsal surface of all toes with median longitudinal grooves at disks; relative toe disk widths: I<V<II<III=IV; webbing between toes basal and poorly developed, webbing formula: I1½–2½II1¾–3III2¾–3¾IV4–2½V (Fig. 6D); dermal fringe distinct on toes; subarticular tubercles prominent, all present, circular, formula 1, 1, 2, 3, 2; outer metatarsal tubercle oval and distinct (OMTL 0.5) than length of inner metatarsal tubercle elongated, oval and prominent (IMTL 0.6).

Skin. Dorsal surface of head and body almost smooth with flat tubercles evenly scattered on dorsum; dorsolateral edges sharp; dorsal surface of hind limbs and cloacal region with few low tubercles scattered; ventral surfaces smooth, present few tubercles in belly face of thighs near cloacal region.

Coloration of holotype in life (Fig. 6A–B)

Dorsal surface of head and trunk beige with dark brown dust, forming the markings; a dark brown marking triangle shape between eyelids, continuing and then extending to the groin as a faint dark brown hourglass shape; the biggest black circle ‘o’ shape between middle of hourglass shape; few tiny black scapular spots and black dots scattered around the hourglass shape. Flanks and lateral head dark brown, supratympanic fold and armpit region beige; upper jaw dark brown with few tiny beige spots below the eye level; dorsal surfaces of limbs beige with dark brown crossbars and few small black spots (Fig. 6A). Chest and belly yellowish with indistinct greyish mottling laterally. Chin grey with thickly

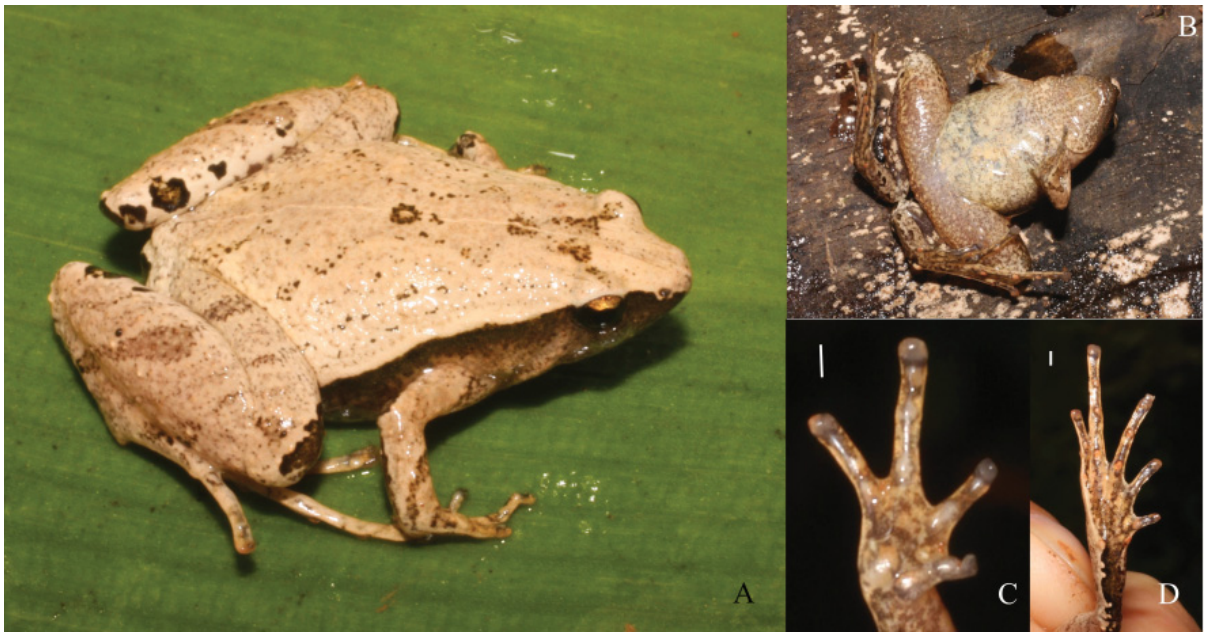

Fig. 6. *Microhyla xodangorum* sp. nov., ♀, holotype (IEBR A.4913 (KP-MĐ-2018-21)). **A**. Dorsolateral view in life. **B**. Ventral view in life. **C**. Underside of right hand. **D**. Underside of right foot. Scale bars = 1 mm.

greyish mottling and a thin, light-coloured medial stripe not reaching the chest (Fig. 6B). Iris golden in upper one-third with black reticulation, dark copper in its lower two-third, darkly pigmented at anterior and posterior corners; pupil round, black (Fig. 6A).

Coloration of holotype in preservative

After preservation in ethanol, dorsal coloration changed from beige to whitish grey; ventral surface of chest, belly, and limbs changed from dark-beige to dark grey; dorsal pattern, dark spots on dorsum and stripes on dorsal surfaces of limbs unchanged, dark brown pattern changed to dark grey; iris completely black, pupil round, white.

Comparisons

Microhyla xodangorum sp. nov. differs from other species of the *M. heymonsi* group by the following characteristics: 1) size large (SVL 25.6 in a ♀) versus *Microhyla hmongorum* sp. nov. (SVL 13.8–17.4 in 5 ♂♂; 19.2–20.3 in 3 ♀♀), *M. ninhthuanensis* (SVL 17.3–18.8 in ♂♂; 21.6–23.6 in ♀♀), versus *M. pineticola* (SVL 17.2–19.5 in ♂♂; 18.0–23.0 in ♀♀); 2) snout profile round versus *Microhyla hmongorum*, *M. pineticola*, *M. neglecta*, (snout profile acuminate) and *M. heymonsi* s. str. (snout profile obtusely-pointed); 3) dorsum skin almost smooth with flat tubercles evenly scattered in dorsum; dorsolateral edges sharp versus *Microhyla hmongorum* (smooth with tiny and flat tubercles unevenly scattered, dorsolateral edges not sharp), *M. ninhthuanensis* (smooth, flanks shagreened; dorsolateral edges not sharp), *M. daklakensis* (smooth, flanks smoothly shagreened; dorsolateral edges not sharp), *M. heymonsi* s. str. (smooth, dorsolateral edges not sharp), *M. pineticola* (almost smooth above with few tiny tubercles scattered in posterior part of dorsum and along the dorsolateral edges), *M. neglecta* (smooth with evenly scattered small flat tubercles); 4) chest and belly yellowish with indistinct greyish mottling laterally; chin grey with thickly greyish mottling and a thin, light-coloured medial stripe not reaching the chest versus *Microhyla hmongorum* (chest and belly creamy white fading towards the groin and thighs with indistinct grayish mottling along the thighs and belly edges, chin, throat pinkish white with scattered indistinct grayish mottling), *M. ninhthuanensis*, *M. daklakensis*, *M. heymonsi* s. str. (chest and belly creamy white; chin dark grey; throat white with scattered dark grey dusting), *M. pineticola* (belly purplish-grey with indistinct whitish mottling; chin dark greyish with orange speckles and a thin light-coloured medial stripe continuing to chest and belly), *M. neglecta* (chest and belly yellowish with indistinct greyish marbling laterally; centre of chin grey, sides dark brown to black with a thin, light-coloured medial stripe not reaching the chest); 5) first finger longer than one half of second finger versus *M. ninhthuanensis*, *M. pineticola*, *M. heymonsi* s. str. group (first finger shorter than one half of second

Fig. 7. A. Habitat of *Microhyla hmongorum* sp. nov. in Tam Duong District, Lai Chau Province, Vietnam. **B**. Habitat of *Microhyla xodangorum* sp. nov. in Kon Plong District, Kon Tum Province, Vietnam. Photos by C.V. Hoang.

finger); 6) disks on distal end of fingers II–IV weak versus *Microhyla hmongorum*, *M. daklakensis*, *M. ninhthuanensis*, *M. heymonsi* s. str. (disks on distal end of all fingers); 7) tibiotarsal articulation at straightened limb well beyond snout versus *Microhyla hmongorum*, *M. daklakensis*, *M. ninhthuanensis*, *M. heymonsi* s. str. (shorter than snout). Detailed comparisons between *Microhyla xodangorum* and other species of the *M. heymonsi* group are shown in Table 5 and of the genus *Microhyla* in total are shown in Appendix 1.

Natural history

All specimens were collected at night from 19:00 to 23:00 on the ground near the banks of a small stream in dipterocarp forest (Fig. 7B). Air temperatue was 21°C and relative humidity was 97%. Larval stages, eggs and the advertisement call of the new species are unknown.

Distribution

Microhyla xodangorum sp. nov. is currently only known from the type locality in Kon Tum Plateau, Kon Tum Province, Vietnam (Fig. 7B). The species was found at an elevation of ca 1250 m a.s.l. Based on its habitat and altitudinal range, the new species is likely endemic to the Central Highlands of Vietnam. However, the extent of its actual distribution range requires further studies.

Discussion

In this study, we provide the first distribution pattern of species in the *Microhyla heymonsi* group, based on available molecular and morphological data collected from across East and Southeast Asia. This study also shows that the genetic diversity in the *Microhyla heymonsi* group is still relatively complex with a number of putatively undescribed species. The *Microhyla heymonsi* group consists of nine genetically distinct lineages. Notably, there are populations with overlapping distribution patterns in Central Vietnam: *M. pineticola* and *M. neglecta* were recorded in the same evergreen forest mixed with pine forest in Lam Dong Province and *Microhyla xodangorum* and *M.* cf. *heymonsi* were found in the same habitat in Kon Tum Province. The Central Highlands of Vietnam are likely an emissive center for species in the *M. heymonsi* group. Recent studies dealing with the diversity of *Microhyla* and *Nanohyla* Poyarkov, Gorin & Scherz, 2021 revealed the same results (Poyarkov *et al*. 2014, 2019; Gorin *et al*. 2020, 2021; Hoang *et al*. 2020, 2021). Therefore, we hypothesize that during the formation of species of *Microhyla* and *Nanohyla* in the Central Highlands, there has been a strong topographic dissection for a long time; then, the weathering over time has worn away the previous barriers, along with the wide distribution of the previously fragmented species populations. Moreover, most recently Krzikowski *et al*. (2022) highlighted the extraordinary endemism rate of amphibians in the Central Highlands of Vietnam and thus the special role in amphibian diversification and evolution. The discovery of *Microhyla hmongorum* sp. nov. and *Microhyla xodangorum* sp. nov. brings the total number of known species in the genus *Microhyla* to 48 and of representatives of *Microhyla* in Vietnam to 15.

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Appendix 1 (continued on next seven pages)

Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838.

Abbreviations used in the Appendix

DML	=	presence of absence of light dorsomedial (vertebral) line
F	=	relative length of finger I (I < one-half length of II, I > one-half length of II, present as a nub or pronounced bulge)
FD	=	disks on distal end of fingers
FMG	=	dorsal median longitudinal grooves on finger disks
MTT	=	number of metatarsal tubercles
SCT	=	presence or absence of superciliary tubercles
TD	=	disks on distal end of toes
Tibiotarsal	=	where on body tibiotarsal projection stretches at adpressed limb
TMG	=	dorsal median longitudinal grooves on toe disks
Webbing	=	webbing formula according to Savage (1975), if it was not possible, extent of webbing on feet is described in words.

** It is unknown whether the only know specimen of *M. fusca* is male or female.
*** Measurements of F1 in Bain & Nguyen (2004) are different from those of Matsui (2011) used in the present paper.

Appendix 1 (continued)
Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838.

No	Species	SVL (mm)		Habit	Snout profile	Dorsum skin	F1***	FD	FMG	TD	TMG	MTT	SCT	DML
		M	F											
1	*M. achatina*	16	23	Slender	Obtusely pointed	Smooth or feebly tubercular	F1 <½ F2	present	present	present	present	2	absent	present
2	*M. annamensis*	15.2–19.8	18.2–22.6	Moderately stocky	Bluntly round	Warty, strongly tubercular	F1 <½ F2	present	present	present	present	2	absent	absent
3	*M. annectens*	14.4–15.6	18.2–18.4	Slender	Round	Smooth	F1 <½ F2	present	present	present	present	1	absent	absent
4	*M. arboricola*	13.2–15.0	15.9–17.0	Moderately slender	Pointed	Feebly granular	F1 <½ F2	present, F2–F4	present, weak	present	present	1	absent	absent
5	*M. aurantiventris*	25.2–27.0	30	Moderately stocky	Round	Slightly shagreened with numerous tiny tubercles	F1 >½ F2	present, F2–F4	present, weak	present	present	2	absent	absent
6	*M. beilunensis*	19.08–23.73	26.39–28.25	Moderately slender	Bluntly Round	Smooth, small tubercles	F1 <½ F2	present, weak	absent	present	present	2	absent	absent
7	*M. berdmorei*	23.8–28.9	26.2–45.6	Slender	Obtusely pointed	Smooth, small tubercles	F1 <½ F2	present, weak	present	present	present	2	absent	absent
8	*M. borneensis*	10.6–12.8	17.9–18.8	Stocky	Obtusely pointed	Smooth, small tubercles	nub or bulge	weak or absent	present	present	present	2	absent	absent
9	*M. butleri*	20.0–25.0	21.0–26.0	Slender	Round	Smooth or tubercular	F1 >½ F2	present, weak	present	present	present	2	absent	absent
10	*M. chakrapanii*	22	?	Moderately stout	Obtusely round	Smooth	F1 >½ F2	absent	absent	present	absent	2	absent	absent
11	*M. darevskii*	27.0–32.6	?	Stocky, flattened	Round	Slightly tubercular or pustulate	F1 >½ F2	absent	absent	weak	present	2	absent	absent
12	*M. darreli*	15.0–15.7	?	Rather slender	Subovoid	Shagreened to sparsely granular	F1 >½ F2	present, weak	absent	present, weak	present	2	absent	absent
13	*M. fanjingshanensis*	19.0–22.7	22.5–23.0	Slender	Round	Roughish with tiny tubercles	F1 >½ F2	absent	absent	present	present	2	absent	present
14	*M. fissipes*	18.0–27.5	20.0–28.0	Moderately slender	Round	Smooth or slightly tubercular	F1 >½ F2	absent	absent	absent	absent	2	absent	absent
15	*M. fodiens*	12.6–20.8	?	Stout	Round	Feebly tubercular	F1 <½ F2	absent	absent	absent	absent	2	absent	absent
16	*M. fowleri*	29.5–32.5	32.2–41.5	Stocky	Obtusely pointed	Rugose, pustular	F1 >½ F2	weak or absent	absent	present	present	2	absent	absent
17	*M. fusca*	23.0**		Slender	Acuminate	Shagreened, faint middorsal ridge	F1 >½ F2	present, F3	?	weak, T2–T5	present, T4	2	absent	absent

Appendix 1 (continued)
Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838.

No	Species	SVL (mm)		Habit	Snout profile	Dorsum skin	F1***	FD	FMG	TD	TMG	MTT	SCT	DML
		M	F											
18	*M. gadjahmadai*	18.20–21.32	20.37–25.51	Stout body	Dorsally round	Low tubercles	F1 > ½ F2	present, weakly dilated	present	present	present	2	absent	present
19	*M. daklakensis*	17.7–20.1	22.9–26.8	Stocky	Round	Smooth	F1 > ½ F2	present	present	present	present	2	absent	present
20	*M.* '*heymonsi*'	16.5–22.0	18.0–26.5	Stocky	Round Obtusely-pointed	Smooth	F1 ≤ ½ F2	present	Usually present	present	Usually present	2	absent	present
21	*Microhyla hmongorum* sp. nov.	13.8–17.4 (n=5)	19.2–20.3 (n=3)	Stocky	Acuminate	Smooth	F1 > ½ F2	present	present	present	present	2	absent	present
22	*M. hongiaoensis*	13.6–14.7	18.3–18.6	Slender	Bluntly round	Slightly bumpy with low tubercles	F1 < ½ F2	present, weak F2–F4	absent	present	present, weak T2–T5	2	absent	absent
23	*M. irrawaddy*	12.3–17.1	16.7–20.9	Very slender	Acuminate	Granular	F1 > ½ F2	present, F2–F4	absent	absent	present, weak T2–T5	?	absent	absent
24	*M. karunaratnei*	15.8–19.1	19.6–21.0	Moderately stocky	Round	Smooth	F1 > ½ F2	present	present	present	present	2	absent	absent
25	*M. kodial*	16.9–17.4	18.0–20.4	Slender	Round	tuberculated	F1 > ½ F2	present, weak (F2–F4)	absent	present	absent	2	absent	absent
26	*M. laterite*	15.3–16.6	18.4	Very small sized	Obtuse	Smooth	F1 > ½ F2	present	present	present	present	2	present	absent
27	*M. maculifera*	12.0–13.3	11.8	Moderately stout	Bluntly round	Dorsolateral rows of tubercles	F1 > ½ F2	absent	absent	present, weak	absent	1	absent	absent
28	*M. malang*	18.7–22.2	19.0–23.4	Stocky	Round	Smooth	F1 < ½ F2	present	present	present	present	2	absent	absent
29	*M. mantheyi*	15.0–29.2	14.8–24.1	Stocky	Pointed	Granular, feebly pustular	F1 < ½ F2	present	present	present	present	2	absent	absent
30	*M. marmorata*	18.8–21.5	21.1–23.2	Moderately stocky	Bluntly ound	Smooth, or feebly pustular	F1 < ½ F2	present	present	present	present	2	absent	absent
31	*M. mihintalei*	21.7–27.3	24.4	Slender	Sub-ovoid	Smooth	F1 ≤ ½ F2	absent	absent	absent	absent	2	present	absent
32	*M. minuta*	14.7–15.9	15.7–17.2	Slender	Bluntly round	Granular, feebly pustular	F1 ≤ ½ F2	present, F2–F4	present, weak	present	present	2	absent	absent

Appendix 1 (continued)
Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838.

No	Species	SVL (mm)		Habit	Snout profile	Dorsum skin	F1***	FD	FMG	TD	TMG	MTT	SCT	DML
		M	F											
33	*M. mixtura*	20.5–23.7	23.8–26.6	Stout	Round	Smooth, with tubercles	F1 <½ F2	present, weak	absent	present	present	2	absent	absent
34	*M. mukhlesuri*	16.5–21.0	17.3–18.4	Moderately slender	Round	Smooth	F1 >½ F2	absent	absent	absent	absent	2	absent	absent
35	*M. mymensinghensis*	14.2–17.6	15.2–21.3	Stocky	Truncated	Smooth	F1 >½ F2	absent	absent	absent	absent	2	absent	absent
36	*M. nanapollexa*	?	16.6	Slender	Round	Smooth	nub or bulge	present	present	present	present	1	absent	absent
37	*M. nilphamariensis*	14.8–20.0	18.7–21.0	Stout	Round	Smooth	F1 >½ F2	absent	absent	absent	absent	2	absent	absent
38	*M. ninhthuanensis*	17.3–18.8	21.6–23.6	Stocky	Round	Smooth	F1 ≤ ½ F2	present	present	present	present	2	absent	present
39	*M. okinavensis*	22.5–28.2	26.5–30.8	Moderately slender	Round	Smooth or slightly tubercular	F1 ≤ ½ F2	absent	absent	absent	absent	2	absent	absent
40	*M. orientalis*	15.8–17.4	15.8–17.4	Moderately slender	Round	Smooth or slightly tubercular	F1 <½ F2	weak, F2–F4	present	present	present	2	absent	present
41	*M. ornata*	13.4–24.9	24.9–26.2	Moderately slender	Round	Smooth or slightly tubercular	F1 ≤ ½ F2	absent	absent	absent	absent	2	absent	absent
42	*M. palmipes*	16	21.8	Slender	Round	Smooth or slightly tubercular	nub or bulge	present	absent	present	absent	2	absent	absent
43	*M. perparva*	10.5–11.9	12.4–14.5	Moderate	Obtusely pointed	Smooth	nub or bulge	present	absent	present	present	1	present	absent
44	*M. petrigena*	13.9–16.2	15.1–17.8	Moderately stout	Obtusely pointed	Smooth, flank and posterior tubercles	nub or bulge	present	present, weak	present	present	1	absent	absent
45	*M. picta*	25.2–30.1	27.2–33.4	Stout	Round	Smooth or slightly warty	F1 <½ F2	absent	absent	absent	absent	2	absent	absent
46	*M. neglecta*	18.7–20.2	23.4–26.2	Stocky	Acuminate	Smooth	F1 >½ F2	present	present	present	present, weak	2	absent	present
47	*M. pineticola*	17.2–19.5	18.0–23.0	Stocky	Acuminate	Smooth	F1 ≤ ½ F2	present, F2–F4	present	present	present, weak	2	absent	present
48	*M. pulchella*	14.7–21.6	18.1–25.8	Moderately stocky	Bluntly round	Smooth	F1 <½ F2	present, F2–F4	present, weak	present	present, weak	1(2)	absent	absent
49	*M. pulchra*	23.0–32.0	28.0–36.5	Stocky	Obtusely pointed	Smooth, feebly granular	F1 <½ F2	absent	absent	absent	absent	2	absent	absent

Appendix 1 (continued)
Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838.

No	Species	SVL (mm)		Habit	Snout profile	Dorsum skin	F1***	FD	FMG	TD	TMG	MTT	SCT	DML
		M	F											
50	*M. pulverata*	17.5–19.5	18.8–20.2	Moderately stocky	Bluntly round	Smooth, or feebly pustular	F1 < ½ F2	present	present	present	present	2	absent	absent
51	*M. rubra*	20.0–27.5	20.5–29.5	Stout	Round	Smooth, feebly tuberculated	F1 ≤ ½ F2	absent	absent	absent	absent	2	absent	absent
52	*M. sholigari*	?	11.0–15.0	Moderately slender	Truncated	Smooth	F1 > ½ F2	present	absent	present	present	2	absent	present
53	*M. superciliaris*	?	12	Slender	Round	Smooth	F1 < ½ F2	present	absent	present	present, weak	2	present	absent
54	*M. taraiensis*	19.9–20.9	22.1–24.9	Stout	Round	Granular	F1 > ½ F2	absent	absent	absent	absent	2	absent	absent
55	*Microhyla xodangorum* sp. nov.	?	25.6	Stocky	Round	Smooth	F1 > ½ F2	present, F2–F4 weak	present	present	present, weak	2	absent	present
56	*M. zeylanica*	14.4–18.3	15.8–20.0	Moderately slender	Round	Smooth or slightly tubercular	F1 > ½ F2	absent	absent	present	absent	2	absent	absent

Appendix 1 (continued)
Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838. n/a = not applicable.

No	Tibiotarsal	Foot webbing	Distribution	Source
1	To snout or just beyond	I2 – 2½II2 – 3¼III3 – 4IV 4– 3V	Java, Bali	Parker 1928; Bain & Nguyen 2004; Poyarkov *et al*. 2014
2	Well beyond snout	I1 – 2¼II1 – 2½III1½ – 2¾IV3 – 1V	Langbian pl. S Vietnam	Bain & Nguyen 2004; Poyarkov *et al*. 2014
3	Well beyond orbit	I1 – 1II1 – 1III1 – 3IV3 – 1V	Malaya, Borneo, Philippines	Parker 1928; Inger 1966; Bain & Nguyen 2004
4	Well beyond snout	I1⅔ – 2¼II2 – 3III2½ – 3½IV3 – 1½V	Langbian pl., S Vietnam	Poyarkov *et al*. 2014
5	Reaching slightly beyond snout	I1¾ – 2II1½ – 2¾III2 – 3⅓IV3¼ – 1½V	Kon Tum pl., S Vietnam	Nguyen *et al*. 2019
6	To the eye	Basal	Zhejiang Province, C China	Zhang *et al*. 2018; Hoang *et al*. 2021
7	Well beyond snout	I1 – 1II1 – 2III1 – 2IV2 – 1V	S China, SE Asia to G. Sundas	Bain & Nguyen 2004; Poyarkov *et al*. 2014
8	Shorter than snout	I1 – 2II1 – 3III2½ – 3⅓IV3½ – 2V	Sarawak	Das & Haas 2010; Matsui 2011
9	Shorter than snout	I2 – 2½II1¾ – 3III2⅓ – 3½IV3½ – 2¼V	S China, SE Asia to Malaya	Bain & Nguyen 2004; Poyarkov *et al*. 2014
10	Beyond snout (?)	Basal; between T3 – T4 to proximal tubercle	Andamans	Pillai 1977
11	Well beyond snout	I1 – 1II1 – 1III1 – 1IV1 – 1V	Ngoc Linh mt., C Vietnam	Poyarkov *et al*. 2014
12	Shorter than eye	I2 – 2¼II1¾ – 3III2 – 3IV3 – 2¼V	S India	Garg *et al*. 2019
13	Between eye to nostril	Basal	Guizhou Province, China	Li *et al*. 2019
14	Shorter than snout	I2 – 2½II2 – 3½III3 – 4IV4 – 3V	S Thailand, Indochina to Malaya	Kuramoto & Joshy 2006 ; Poyarkov *et al*. 2014
15	Not reaching orbit level	I1 – 2II1¾ – 3III2¾ – 3¾IV 4 – 2¾V	Myanmar	Poyarkov *et al*. 2019
16	Well beyond snout	I1 – 1II1 – 1III1 – 2IV2 – 1V	N Thailand, S China	Bain & Nguyen 2004; Fei *et al*. 2009
17	To the eye	Basal, continue as folds up toes	Langbian pl., S Vietnam	Andersson 1942; Bain & Nguyen 2004
18	Well beyond snout	I2 – 2¼II1¾ – 3III3 – 4IV4 – 2¾V	Sumatra, Indonesia	Atmaja *et al*. 2018
19	Shorter than snout	I2 – 2½II2 – 3III3 – 4IV4⅓ – 3V	Dak Lak	Hoang *et al*. 2021
20	Shorter than snout	I2 – 2½II2 – 3III3 – 4IV4⅓ – 3V	S China, NE India, SE Asia to Sumatra	Bain & Nguyen 2004; Matsui *et al*. 2013; Poyarkov *et al*. 2014
21	Shorter than snout	I2 – 2½II2 – 3½III3 – 4⅓IV4⅓ – 3V	NW Vietnam, S China, N Laos and NE Myanmar	This study
22	Well beyond snout	I1 – 2II1 – 2½III1 – 2½IV2½ – 1V	Langbian pl. S Vietnam	Hoang *et al*. 2021
23	Reaching eye level	I2 – 3II2 – 3III3 – 4½IV4½ – 2¾V	Myanmar	Poyarkov *et al*. 2019

Appendix 1 (continued)
Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838. n/a = not applicable.

No	Tibiotarsal	Foot webbing	Distribution	Source
24	Beyond snout (?)	I 2 – 2½ II 2 – 3½ III 2½ – 3¾ IV 4 – 2 V	S Sri Lanka	Fernando & Siriwardhane 1996; Dutta & Manamendra-Arachchi 1997; Dutta & Ray 2000
25	Well beyond snout	weak, Basal	W S India	Vineeth *et al.* 2018
26	Well beyond snout	I1 – 2II1 – 2III1⅔ – 2IV3 – 1V	W S India	Seshadri *et al.* 2016
27	To snout or just beyond	Basal	Sabah, Borneo	Bain & Nguyen 2004
28	To snout or just beyond	I1 – 2II1 – 2⅔III1⅔ – 3IV3 – 1V	Borneo	Das & Haas 2010; Matsui 2011
29	Well beyond snout	I1 – 2II1 – 2III2 – 3IV3 – 1½V	S Thailand, Malaya	Das *et al.* 2007; Poyarkov *et al.* 2014
30	Well beyond snout	I1 – 2II1 – 1¾III1½ – 2¾IV2¾ – 1V	C Vietnam, Laos	Bain & Nguyen 2004; Poyarkov *et al.* 2014
31	To snout	basal	Sri Lanka	Wijayathilaka *et al.* 2016
32	Shorter than snout, but beyond the eye level	In.a. – n.a.II2 – 3½III3 – 4IV4 – 3V	Dong Nai, S Vietnam	Poyarkov *et al.* 2014
33	Shorter than snout	I2 – 2½II1¾ – 3¼III3 – 4IV4¼ – 2¾V	C & E China	Bain & Nguyen 2004; Fei *et al.* 2009; Poyarkov *et al.* 2014
34	To snout	I2 – 2½II2 – 3½III3 – 4IV4 – 2¾V	Bangladesh	Hasan *et al.* 2014
35	To snout	I2 – 2½II2 – 3½III3 – 4IV4¼ – 2¾V	Bangladesh	Hasan *et al.* 2014
36	Well beyond snout	I1 – 2II1 – 2½III2½ – 2½IV2½ – 1V	Ngoc Linh mt., C Vietnam	Bain & Nguyen 2004
37	To snout	Basal	Bangladesh, central and eastern Nepal, N India	Hoang *et al.* 2021; Howlader *et al.* 2015; Khatiwada *et al.* 2017
38	Shorter than snout	I2 – 2½II2 – 3III3 – 4IV4⅓ – 3V	Ninh Thuan	Hoang *et al.* 2021
39	To snout	I1½ – 2II1½ – 3¼III2¾ – 4IV4 – 2½V	Okinawa	Poyarkov *et al.* 2014; Kuramoto & Joshy 2006
40	To the eye	In.a. – n.a.II2 – 3¼III3 – 4¼IV4¼ – 3V	Bali	Matsui *et al.* 2013
41	Shorter than snout	I2 – 2½II1¾ – 3½III3 – 4IV4 – 2¾V	Sri Lanka, India to Andamans	Kuramoto & Joshy 2006; Dutta & Manamendra-Arachchi 1997; Poyarkov *et al.* 2014
42	To snout or just beyond	In.a. – n.a.II2⅓ – 3¾III3¼ – 4IV4 – 3V	Malaya & Sundas	Parker 1928; Bain & Nguyen 2004; Poyarkov *et al.* 2014
43	Well beyond snout	I1 – 1II1 – 1III1 – 2IV2 – 1V	Borneo	Bain & Nguyen 2004

Appendix 1 (continued)
Selected diagnostic characters for the comparisons between the species of the genus *Microhyla* Tschudi, 1838. n/a = not applicable.

No	Tibiotarsal	Foot webbing	Distribution	Source
44	Well beyond snout	I1 – 1II1 – 1III1 – 2IV2 – 1V	Borneo	Bain & Nguyen 2004
45	Shorter than eye	I2 – 2¾II1¾ – 2¾III2¾ – 3¾IV 4 – 2½V	SE Vietnam	Bain & Nguyen 2004; Schenkel 1901; Poyarkov *et al*. 2014
46	Well beyond snout	I1½ – 2½II1¾ – 3III2¾ – 3¾IV3¾ – 2½V	Langbian pl., S Vietnam	Hoang *et al*. 2021
47	Shorter than snout, but beyond the eye level	I1½ – 2½II1¾ – 3III2¾ – 3¾IV4 – 2½V	Chu Yang Sin NP, Langbian pl., S Vietnam	Poyarkov *et al*. 2014; Hoang *et al*. 2021
48	Well beyond snout	I1½ – 2II1 – 2III1 – 2½IV2¼ – 1V	Langbian pl., S Vietnam	Poyarkov *et al*. 2014
49	To snout or just beyond	I1½ – 2II1 – 3III2 – 3¼IV3½ – 2V	S China, Thailand, Indochina	Bain & Nguyen 2004; Fei *et al*. 2009; Poyarkov *et al*. 2014
50	Well beyond snout	I1 – 2II1 – 2½III1¾ – 3IV3 – 1V	C Vietnam	Bain & Nguyen 2004; Poyarkov *et al*. 2014
51	Shorter than snout	I1½ – 2II1½ – 3III2½ – 3IV4 – 2½V	S & E India, Sri Lanka	Dutta & Manamendra-Arachchi 1997
52	Shorter than snout	I1½ – 2II2½ – 3½III2½ – 3½IV3¾ – 2V	SW India	Dutta & Ray 2000
53	To snout or just beyond	I1 – 1II1 – 1III1 – 2IV2 – 1V	Malaya, Sumatra	Dutta & Ray 2000; Bain & Nguyen 2004; Parker 1928
54	To snout	I2 – 3II2¾ – 3¾III3 – 4¼IV4 – 2¾V	E Nepal	Khatiwada *et al*. 2017; Hoang *et al*. 2021
55	well beyond snout	I1½ – 2½II1¾ – 3III2¾ – 3¾IV4 – 2½V	Kon Tum pl., S Vietnam	This study
56	To the eye	I2 – 2¼II1¾ – 3½III2¼ – 3¾IV 4 – 2V	C Sri Lanka	Dutta & Manamendra-Arachchi 1997; Dutta & Ray 2000