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A NEW CRYPTIC SPECIES OF THE GENUS *Microhyla* (AMPHIBIA: MICROHYLIDAE) FROM LANGBIAN PLATEAU, VIETNAM

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Abstract
An integrative taxonomic analysis combining molecular and morphological lines of evidence revealed a new cryptic species of the *Microhyla achatina* species group from the Langbian Plateau of southern Vietnam. The new species was previously confused with its recently described morphologically similar and sympatric sister species, *M. pineticola*. The new species can be distinguished from *M. pineticola* by the presence of a continuous dark stripe running from the posterior edge of its eye towards the groin (*vs* dark markings interrupted above the axilla), snout acuminate in lateral profile (*vs* rounded), belly colour pattern, and foot webbing. The new species is currently known only from Bidoup–Nui Ba National Park in Lam Dong Province, Langbian Plateau in southern Vietnam (at elevations of 1300–1600 m a.s.l). We suggest the new species to be considered as Near Threatened (NT) in the IUCN Red List. Our results emphasize that our understanding of the diversity of genus *Microhyla* is still far from complete, and provide further evidence for montane areas of southern Vietnam to be a centre of *Microhyla* species richness. Our study further underscores the urgent need for intensified integrative taxonomic research on *Microhyla* spp. in order to clarify the taxonomy of wide-ranging species complexes and to elaborate effective conservation measures.

***Key words*:** Bidoup–Nui Ba National Park, *Microhyla pineticola*, mtDNA, sympatry, taxonomy.

Introduction
The genus *Microhyla* Tschudi, 1838 currently contains 52 nominal species of small-sized to tiny terrestrial frogs distributed from the Ryukyus (Japan) and southern China, southward through Southeast Asia to India and Sri Lanka (Frost 2020; Gorin *et al.* 2020; Poyarkov *et al.* 2020a,b). Nearly one half (23 species) of the recognised members of this diverse genus has been described within the last 10 years (Frost 2020). Nevertheless the taxonomy of *Microhyla* remains challenging, owing to logistical problems associate with their small size. Taxonomic progress in *Microhyla* is further hampered by the independent evolution of miniaturization observed in several lineages and the resulting high degree of convergent morphological similarity (Gorin *et al.* 2020).

This, along with the common sympatric occurrences of closely-related cryptic species and widely distributed complexes comprised of highly divergent lineages (Garg *et al.* 2018; Gorin *et al.* 2020), make the genus *Microhyla* one the most taxonomically challenging groups of Asian frogs. Thus, the application of molecular phylogenetics is crucial for the construction of a proper taxonomy and understanding the diversity within *Microhyla* (Gorin *et al.* 2020).

The Pine narrow-mouth frog, *Microhyla pineticola* Poyarkov, Vassilieva, Orlov, *et al*., 2014 was described from Bidoup–Nui Ba National Park in Lam Dong Province, Langbian Plateau in southern Vietnam. In their study, Poyarkov *et al*. (2014) revised the *Microhyla* fauna of Vietnam based entirely on morphological evidence, and distinguished *M. pineticola* from the morphologically similar *M. heymonsi* Vogt, 1911, a widely distributed species found throughout Indochina. A more recent comprehensive review of *Microhyla* diversity and phylogenetic relationships (Gorin *et al.* 2020) confirmed the genetic distinctiveness of *M. pineticola* from *M. heymonsi*, and assigned both species to the *M. achatina* species group (group A in Gorin *et al.* 2020). According to the original description, *M. pineticola* is characterized by: a small dark round spot at the mid-dorsum divided by a light vertebral stripe and dorsal markings formed by dark-brown lines outlined in beige, parallel to the vertebral and dorsolateral stripes, forming a pattern resembling the grain of pinewood (Poyarkov *et al.* 2014). Poyarkov *et al.* (2014) reported significant variation in colouration within the type series of *M. pineticola*, which included specimens lacking the characteristic lines on dorsum, and specimens having a dark line extending from the posterior margin of the eye towards the flanks and groin which may or may not be continuous be interrupted above the axilla (see variation section in Poyarkov *et al.* 2014: 103–104). However, additional data on the morphological variation and the molecular differentiation of the populations assigned to *M. pineticola* were lacking.

While collecting genetic data for the phylogenetic reconstruction by Gorin *et al.* (2020), we discovered that the samples of *M. pineticola* were represented by two highly divergent haplotypes (only one of which was included in the final analysis of Gorin *et al.* 2020). In the present study we apply an integrative taxonomic approach, comparing the results of morphological analyses with those of phylogenetic analyses using mitochondrial (mtDNA) sequences (12S rRNA–16S rRNA fragment) to analyze differentiation between *M. pineticola* populations from Lam Dong Province and the newly discovered population from Dak Lak Province of southern Vietnam. We demonstrate that the type series of *M. pineticola* is comprised of two superficially similar yet genetically different cryptic lineages of individuals. Additional examination of the type series and newly collected material resulted in the discovery of stable character state differences in colouration and external morphology between the two lineages which are concordant with the results of the molecular phylogenetic analyses. Herein, we reassess the taxonomic status of the two lineages masquerading under the name '*M. pineticola*': one is redescribed as *M. pineticola* s. str., while the second we describe as a new, previously overlooked, cryptic species of *Microhyla*.

Material and methods

***Sample collection*:** We examined the type series of *Microhyla pineticola* stored in the Zoological Museum of Moscow University (Moscow, Russia; hereafter given as ZMMU), including the holotype specimen (ZMMU A-5043). Additional specimens were collected from Lam Dong and Dak Lak provinces, southern Vietnam, during several field surveys in 2009–2014 (Table 1). The locations of the surveyed localities and the distribution of *M. pineticola* complex members in Vietnam are shown in Fig. 1. Geographic coordinates and elevations were obtained using a Garmin GPSMAP 60CSx (WGS 84 datum). Specimens were fixed in 10% buffered formalin after tissue samples were preserved in 95% ethanol. Specimens were later transferred to 70% ethanol. Newly collected specimens and tissues were subsequently deposited in the herpetological collections of ZMMU (Moscow, Russia).

***Morphological description*:** Specimens of the *Microhyla pineticola* complex were photographed in life and after preservation. Measurements were taken using a digital caliper to the nearest 0.01 mm and rounded to 0.1 mm. We used an Olympus stereoscopic light binocular microscope when necessary. All measurements were taken on the right side of the specimen. The morphometrics of adults and character terminology followed Poyarkov *et al.*

(2014, 2019a, 2020a,b) and included the following measurements: snout–vent length (SVL; measured from tip of snout to cloaca); head length (HL; measured from tip of snout to hind border of jaw angle); snout length (SL; measured from anterior margin of eye to tip of snout); eye length (EL; measured as the distance between anterior and posterior margins of the eye); nostril–eye length (N–EL; measured as the distance between the anterior margin of the eye and the nostril centre); head width (HW; measured as the maximum width of the head at the level of mouth angles in ventral view); internarial distance (IND; measured as the distance between central points of nostrils); interorbital distance (IOD; measured as the shortest distance between medial edges of eyeballs in dorsal view); upper eyelid width (UEW; measured as the maximum distance between medial edge of eyeball and lateral edge of upper eyelid); forelimb length (FLL; measured as the length of straightened forelimb to tip of third finger); lower arm and hand length (LAL; measured as the distance between elbow and tip of third finger); hand length (HAL; measured as the distance between proximal end of outer palmar (metacarpal) tubercle and tip of third finger); first finger length (1FL, measured as the distance between tip and distal end of inner palmar tubercle); inner palmar tubercle length (IPTL; measured as the maximum distance between proximal and distal ends of inner palmar tubercle); outer palmar tubercle length (OPTL; measured as the maximum diameter of outer palmar tubercle); third finger disc diameter (3FDD); hindlimb length (HLL; measured as the length of straightened hindlimb from groin to tip of fourth toe); tibia length (TL; measured as the distance between knee and tibiotarsal articulation); foot length (FL; measured as the distance between distal end of tibia and tip of fourth toe); inner metatarsal tubercle length (IMTL; measured as the maximum length of inner metatarsal tubercle); first toe length (1TOEL), measured as the distance between distal end of inner metatarsal tubercle and tip of first toe; third toe disc diameter (3TDD); outer metatarsal tubercle length (OMTL; measured as the maximum length of outer metatarsal tubercle). Additionally, we took the following measurements for the holotype description: second to fourth finger lengths (2–3FLO, 4FL-I; for outer side (O) of the second and third, and inner side (I) of the fourth, measured as the distance between the tip and junction of the neighboring finger); second to fifth toe lengths (measured as the outer lengths for toes II–IV, as the inner length for toe V; 2–5TOEL); finger disc diameter for fingers I–II and IV (1–2FDD, 4FDD); toe disc diameter for toes I–II and IV–V (1–2TDD, 4–5TDD). Toe webbing and subarticular tubercle formulas were given following Savage (1975). The sex and maturity of the specimens was checked by minor dissections and by direct observations of calling behaviour in living males prior to collection.

The diagnosis of the genus *Microhyla* and morphological characters for comparison were taken from original descriptions and taxonomic reviews from: Atmaja *et al.* (2019); Bain & Nguyen (2004); Biju *et al.* (2019); Das & Haas (2010); Das *et al.* (2007); Garg *et al.* (2018); Hasan *et al.* (2014); Hoang *et al.* (2020); Howlader *et al.* (2015); Khatiwada *et al.* (2017); Matsui (2011); Matsui *et al.* (2013); Matsui & Tomiaga (2020); Nguyen *et al.* (2019); Li *et al.* (2019); Parker (1928); Pillai (1977); Poyarkov *et al.* (2014, 2019a, 2020a,b); Vineeth *et al.* (2018); Wijayathilaka *et al.* (2016); Zhang *et al.* (2018).

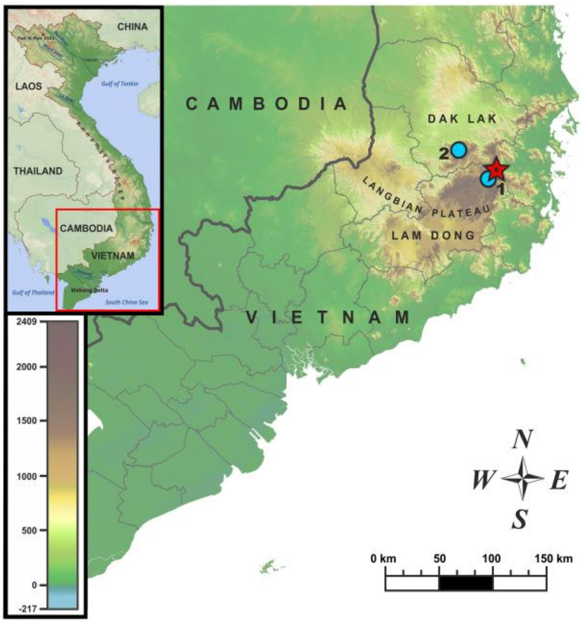

Figure 1. Distribution of *Microhyla pineticola* sensu stricto (circles) and the new species (star) in southern Vietnam; 1, Bidoup–Nui Ba National Park, Lam Dong Province; 2, Chu Yang Sin National Park, Dak Lak Province.

***Laboratory methods*:** Total genomic DNA was extracted from ethanol-preserved femoral muscle tissue or liver tissue using a standard phenol–chloroform–proteinase K extraction protocol with consequent isopropanol precipitation (Hillis *et al.* 1996). Isolated genomic DNA was visualized in agarose electrophoresis in the presence of ethidium bromide; total DNA concentration was measured in 1 μL using NanoDrop 2000 (Thermo Scientific), and consequently adjusted to 175 ca. 100 ng DNA/μL. We amplified an mtDNA fragment partially covering the 12S rRNA–16S rRNA genes and the complete sequence of tRNA-Val resulting in a continuous fragment 2399 bp in length. These markers have proven to be particularly useful in phylogenetic and taxonomic studies of the genus *Microhyla* (e.g. Matsui 2011; Hasan *et al.* 2012, 2014; Matsui *et al.* 2013; Wijayathilaka *et al.* 2016; Poyarkov *et al.* 2019a, 2020b; Gorin *et al.* 2020). DNA amplification was performed in 20-μL reactions using ca. 50 ng genomic DNA, 10 nmol of each primer, 15 nmol of each dNTP, 50 nmol additional MgCl2, Taq PCR buffer (10 mM Tris-HCl, pH 8.3, 50 mM KCl, 1.1 mM MgCl2 and 0.01% gelatine) and 1 U of 185 Taq DNA polymerase. Primers used in PCR and sequencing, along with the PCR conditions followed Gorin *et al.* (2020). The PCR products were loaded onto 1.5% agarose gels in the presence of ethidium bromide and visualised in electrophoresis. The successful targeted PCR products were outsourced to Evrogen® (Moscow, Russia) for PCR purification and sequencing. Sequence data collection and visualisation were carried out on an ABI 3730xl Automated Sequencer (Applied Biosystems). The newly obtained sequences were deposited in GenBank under accession numbers MW147155–MW147166 and MW147168–MW147172 (Table 1).

***Phylogenetic analyses*:** The 12S rRNA–16S rRNA Microhylidae data set of Gorin *et al.* (2020) with the addition of a sequence of the recently described *M. hongiaoensis* Hoang, Luong, Nguyen *et al*. 2020 and our newly obtained sequences were used to reconstruct a matrilineal genealogy of *Microhyla*. The initial data set was pruned to one sequence per species, with the exception of *M. pineticola* and the morphologically similar *Microhyla* sp. from southern Vietnam. In total, 12S rRNA–16S rRNA data for 93 specimens were included in the final analysis, including 64 samples of ca. 53 *Microhyla* species (representing all recognized species within the genus), 28 outgroup sequences of other microhylid representatives, and a sequence of *Rhacophorus schlegelii* (Günther, 1858), which was used to root the tree (Table 1). We initially aligned the nucleotide sequences in MAFFT v. 6 (Katoh *et al.* 2002) with default parameters, and subsequently slightly adjusted it in BioEdit v. 7.0.5.2 (Hall 1999). The mean uncorrected genetic distances (p-distances) between individuals were estimated in MEGA 6.0 (Tamura *et al.* 2013). We used IQ-TREE webserver (Nguyen *et al.* 2015; Trifinopoulos *et al.* 2016) to estimate the optimal evolutionary models for the subsequent analyses. The best-fitting models of DNA evolution were GTR+I +G, JC+G and GTR+G, for 12S rRNA, tRNA-Val and 16S rRNA genes, respectively, as suggested by the Akaike information criterion (AICc).

We inferred the matrilineal genealogy using Maximum Likelihood (ML) and Bayesian Inference (BI) approaches. We conducted ML analysis in the IQ-TREE webserver. One-thousand bootstrap pseudoreplicates via the ultrafast bootstrap (UFBS; Hoang *et al.* 2018) approximation algorithm were employed and nodes having ML UFBS values of 95 and above were considered highly supported, while the nodes with values of 90–94 were considered well-supported (Bui *et al.* 2013). We implemented the BI analysis in MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003). We ran Metropolis-coupled Markov chain Monte Carlo (MCMCMC) analyses with one cold and three heated chains for 20 million generations and sampled every 2,000 generations. The two independent MCMCMC runs were performed; we checked that the effective sample sizes (ESSs) were all above 200 by exploring the likelihood plots using TRACER v. 1.6 (Rambaut *et al.* 2014). The initial 1000 trees were discarded as burn-in. The confidence in tree topology was assessed by the frequency of nodal resolution (posterior probability; BI PP) (Huelsenbeck & Ronquist 2001). We regarded tree nodes with BIPP values over 0.95 to be strongly supported; values between 0.95 and 0.90 were regarded as moderately supported; while the lower values were considered to have no nodal support (Huelsenbeck & Hillis 1993).

Results

***Sequence variation*:** Among the 2399 bp of the final 12S rRNA–16S rRNA alignment, 1295 sites were conserved, while 1101 sites exhibited variation, of which 847 were parsimony informative. The transition–transversion bias (R) was estimated as 2.11. Nucleotide frequencies were A = 33.60%, T = 24.30%, C = 23.63%, and G = 18.47% (data given for ingroup only).

***MtDNA genealogy*:** The ML and BI analyses resulted in identical topologies, which differed only in a non-supported node of the basal radiation of *Microhyla* (Fig. 2). Both analyses achieved high resolution of phylogenetic relationships among *Microhyla* species and all major nodes in the tree were sufficiently resolved (UFBS≥95%; PP≥0.95). Overall, our updated mtDNA genealogy was largely consistent with the phylogeny of Gorin *et al.* (2020), suggesting strong support for monophyly of the *Microhyla–Glyphoglossus* assemblage (100/1.0; hereafter nodal support values given for UFBS/PP, respectively), and no support for *Microhyla* monophyly (53/-). Within the *Microhyla–Glyphoglossus* assemblage, ten major clades / lineages were recovered, generally agreeing with the results of Gorin *et al*. (2020) (Fig. 2, hereafter species group names follow Gorin *et al.* 2020). Clade A consisted of 15 morphospecies of the *M. achatina* species group, including *M. achatina* Tschudi, 1838; *M. heymonsi*; *M. borneensis* Parker, 1928; *M. gadjahmadai* Atmaja, Hamidy, Arisuryanti *et al*., 2018; *M. irrawaddy* Poyarkov, Gorin, Zaw *et al*. 2019; *M. kodial* Vineeth, Radhakrishna, Godwin *et al*., 2018; *M. malang* Matsui, 2011; *M. mantheyi* Das, Yaakob & Sukumaran, 2007; *M. minuta* Poyarkov, Vassilieva, Orlov *et al*., 2014; *M. nepenthicola* Das & Haas, 2010; *M. orientalis* Matsui, Hamidy & Eto, 2013; the two undescribed species-level lineages *Microhyla* sp. 1 from Sarawak, Malaysia, and *Microhyla* sp. 2 from Sagaing, Myanmar, and the two lineages of '*M. pineticola*' from southern Vietnam (Fig. 2, Clade A). The phylogenetic relationships and taxonomic content of other species groups (Clades B–J) fully agreed with the results of Gorin *et al*. (2020), including the *M. fissipes* group (Clade B), the *M. berdmorei* group (Clade D), the *M. superciliaris* group (Clade E), the *M. ornata* group (Clade F), the *M. butleri* group (Clade G), *M. palmipes* Boulenger (Clade H), the *M. annectens* group (Clade I), and *Glyphoglossus* Günther (Clade J) (see Fig. 2 for details). The only important difference from the taxonomic arrangement by Gorin *et al.* (2020) is the phylogenetic position of *M. fodiens* Poyarkov, Gorin, Zaw *et al*., 2019 from Myanmar, which was earlier provisionally assigned to the *M. achatina* species group (Poyarkov *et al*. 2019a; Gorin *et al*. 2020). In our mtDNA-genealogy *M. fodiens* is an orphaned species, suggested as a sister lineage (100/1.0) to the moderately supported clade joining the members of *M. achatina* species group + *M. fissipes* groups (93/0.62) (Fig. 2, Clade C). Genealogical relationships within the *M. achatina* species group were generally sufficiently resolved, suggesting that all members of this group with the exception of *M. heymonsi* and '*M. pineticola*' form a strongly supported clade (100/1.0), joining species from Sundaland, Myanmar, and southern India. The only Vietnamese taxon in this clade is *M. minuta* and it is distantly related to the other species. The wide-ranging *M. heymonsi* formed a strongly supported ML clade with '*M. pineticola*' from southern Vietnam, but and unsupported clade in in the BI analysis (97/0.89).

Our analysis strongly suggested that '*M. pineticola*' from southern Vietnam is represented by two, highly divergent, reciprocally monophyletic, sympatric lineages (100/1.0). One lineage corresponds to *M. pineticola* sensu stricto and includes the holotype of *M. pineticola* (ZMMU A-5043), two paratypes (ZMMU A-5080, A-4331) (all three specimens from Bidoup–Nui Ba National Park, Lam Dong Province; Fig. 1, locality 1), and two newly collected specimens from Chu Yang Sin National Park, Dak Lak Province (ZMMU A-6029, A-7269; Fig. 1, locality 2) (Fig. 2). The other lineage includes eight specimens from the same area of Bidoup–Nui Ba National Park as the *M. pineticola* holotype—all of which were indentified by Poyarkov *et al.* (2014) as paratypes of '*M. pineticola*' (originally listed under numbers ZMMU A-4331 and A-5080; new numbers ZMMU A-7302–7306, A-7308, A-7310–7311) (Fig. 2).

***Genetic distances*:** The uncorrected p-distances for the 16S rRNA mtDNA fragment among the members of the *M. achatina* species group are shown in Table 2. The interspecific distances among the members of the *M. achatina* species group varied from p=2.2% (between *M. irrawaddy* and *Microhyla* sp. 2) to p=14.5% (between *M. fodiens* and *M. borneensis*). The two lineages of '*M. pineticola*' showed a significant level of genetic distinctiveness (p=5.2%) between them and both were found to be most closely related to their putative sister species *M. heymonsi* (p=7.0–8.7%). Genetic differentiation among the examined samples of *M. pineticola* s. str. and the second lineage of '*M.* cf. *pineticola*' from Bidoup–Nui Ba National Park was minimal (uncorrected within-group p-distance 0.1% and 0.4%, respectively) (Table 2).

Table 1. Sequences and voucher specimens of *Microhyla* and outgroup taxa used in this study; NP, National Park; FR, Forest Reserve; Is., Island; Mt. Mountain; H, holotype; — not available.

Species	Locality	Museum / Sample ID	12S rRNA	16S rRNA	Reference
Ingroup					
Microhyla achatina	Indonesia, Java, Ujung Kulong	ZMMU A-5070	MN534670	MN534462, MN534563	Gorin *et al*. 2020
Microhyla annamensis	Vietnam, Lam Dong, Bidoup-Nui Ba NP	ZMMU A-5075-06	MN534748	MN534533, MN534639	Gorin *et al*. 2020
Microhyla annectens	Malaysia, Selangor, Genting	ZMMU A-6042-1	MN534746	MN534531, MN534637	Gorin *et al*. 2020
Microhyla arboricola	Vietnam, Dak Lak, Chu Yang Sin NP	ZMMU A-4845-60	MN534759	MN534543, MN534650	Gorin *et al*. 2020
Microhyla aurantiventris	Vietnam, Gia Lai, Kon Ka Kinh NP	ITBCZ-4360	MN534727	MH286427	Nguyen *et al*. 2019; Gorin *et al*. 2020
Microhyla beilunensis	China, Sichuan	CIB 20070248	AB634611	AB634669	Matsui *et al*. 2011
Microhyla berdmorei	Thailand, Suratthani, Khao Sok NP	ZMMU NAP-04133	MN534711	MN534503, MN534604	Gorin *et al*. 2020
Microhyla borneensis	Malaysia, Sarawak, Kidi (Bidi)	UNIMAS FN1874ZAC600	—	MN534550, MN534657	Gorin *et al*. 2020
Microhyla butleri	Malaysia, Tasik Pedu Lake, Kedah	ZMMU NAP-06827	MN534734	MN534521, MN534625	Gorin *et al*. 2020
Microhyla chakrapanii	India, Andaman Island, Havelock	ZISP 13874	MN534698	MN534490, MN534591	Gorin *et al*. 2020
Microhyla darreli	India, Kerala, Thiruvananthapuram	ZSI/WGRC/V/A/962	—	MH807390	Garg *et al*. 2018
Microhyla eos	India, Arunachal Pradesh, Namdapha NP	ZSIC 14312	—	MN160599	Biju *et al*. 2019
M. fanjingshanensis	China, Guizhou	—	MF538787		Zhao *et al*. 2018
Microhyla fissipes	Taiwan, Kaohsiung, Mt. Zhongliao Shan	ZMMU A-5333	MN534695	MN534487, MN534588	Gorin *et al*. 2020
Microhyla fodiens	Myanmar, Magway, Kan Pauk	ZMMU A-5960	MK208926		Gorin *et al*. 2020
Microhyla gadjahmadai	Indonesia, Sumatra, Lampung	MZB Amp 15291	AB634622	AB634680	Matsui *et al*. 2011
Microhyla heymonsi	Taiwan, Pingtong, Yongchin, Qi Kong	ZMMU A-4975	MN534679	MN534471, MN534572	Gorin *et al*. 2020
Microhyla hongiaoensis	Vietnam, Lam Dong, Bidoup-Nui Ba NP	CIB-VNMN 07617	—	MN475176	Hoang *et al*. 2020
Microhyla irrawaddy	Myanmar, Magway, Pakkoku	ZMMU A-5966	MK208928		Gorin *et al*. 2020
Microhyla karunaratnei	Sri Lanka, Sinharaja FR	released	MN534738	MN534524, MN534629	Gorin *et al*. 2020
Microhyla kodial	India, Karnataka, Mangaluru	—	—	MF919454	Vineeth *et al*. 2018
Microhyla kuramotoi	Japan, Okinawa, Ishigaki Is.	released	MN534700	MN534492, MN534593	Gorin *et al*. 2020
Microhyla laterite	India, Karnataka, Udupi, Manipal	BNHS 5965	KT600670	KT600663	Seshadri *et al*. 2016
Microhyla malang	Malaysia, Sarawak, Kubah NP	ZMMU A-6043	MN534662	MN534454, MN534555	Gorin *et al*. 2020
Microhyla mantheyi	Malaysia, Taman Negara NP	ZMMU NAP-6745	MN534665	MN534457, MN534558	Gorin *et al*. 2020
Microhyla marmorata	Vietnam, Kon Tum, Kon Plong	ZPMSU 04854	MN534750	MN534535, MN534641	Gorin *et al*. 2020
Microhyla mihintalei	Sri Lanka, Rathambaldama	released	MN534726	MN534515, MN534619	Gorin *et al*. 2020
Microhyla minuta	Vietnam, Dong Nai, Cat Tien NP	ZMMU A-5048-91	MN534667	MN534459, MN534560	Gorin *et al*. 2020
Microhyla mixtura	China, Sichuan, Wanyuan, Mt. Hua'eshan	CIB 20170526001	MH234529	MH234540	Zhang *et al*. 2018
Microhyla mukhlesuri	Bangladesh, Chittagong	IABHU-3959	MN534692	MN534484, MN534585	Gorin *et al*. 2020
Microhyla mymensinghensis	Bangladesh, Mymensingh	IABHU-4129	MN534699	MN534491, MN534592	Gorin *et al*. 2020
Microhyla nanapollexa	Vietnam, Kon Tum, Kon Plong	ZMMU A-5635	MN534757	MN534541, MN534648	Gorin *et al*. 2020
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7303 [H]	MW147168	MW147155	this work
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7302	—	MW147160	this work
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7308	—	MW147159	this work
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7311	—	MW147158	this work
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7305	—	MW147156	this work
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7306	—	MW147157	this work
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7310	—	MW147161	this work

Table 1 continued. Sequences and voucher specimens of *Microhyla* and outgroup taxa used in this study; NP, National Park; Mt. Mountain; H, holotype; — not available.

Species	Locality	Museum / Sample ID	12S rRNA	16S rRNA	Reference
Microhyla neglecta sp. nov.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-7304	—	MW147162	this work
Microhyla nepenthicola	Malaysia, Borneo, Sarawak, Kubah NP	ZMMU A-6028-1	MN534658	MN534450, MN534551	Gorin *et al*. 2020
Microhyla nilphamariensis	Bangladesh, Nilphamari	IABHU-4212	MN534721	MN534614	Gorin *et al*. 2020
Microhyla okinavensis	Japan, Okinawa island, Yomitan son, Kina	ZMMU A-6027-1	MN534704	MN534496, MN534597	Gorin *et al*. 2020
Microhyla orientalis	Indonesia, Java, Yogyakarta	ZMMU A-5067-1	MN534663	MN534455, MN534556	Gorin *et al*. 2020
Microhyla ornata	Sri Lanka, Rathambaldama	released	MN534723	MN534512, MN534616	Gorin *et al*. 2020
Microhyla palmipes	Indonesia, Bali, Bedegul	MZB Amp 16255	AB634612	AB634670	Matsui *et al*. 2011
Microhyla perparva	Indonesia, Kalimantan, Balikpapan	KUHE UN	AB634614	AB634672	Matsui *et al*. 2011
Microhyla petrigena	Malaysia, Sabah, Maliau Basin	BORN 22412	AB634616	AB634674	Matsui *et al*. 2011
Microhyla picta	Vietnam, Ba Ria-Vung Tau, Phuok Buu NP	ZMMU A-4918-45	MN534719	MN534510, MN534612	Gorin *et al*. 2020
Microhyla pineticola s. str.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-5043[H]	MW147172	MW147166	this work
Microhyla pineticola s. str.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-5080	MN534673	MN534465, MN534566	Gorin *et al*. 2020
Microhyla pineticola s. str.	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-4331	MW147169	MW147163	this work
Microhyla pineticola s. str.	Vietnam, Dak Lak, Chu Yang Sin NP	ZMMU A-6029	MW147170	MW147164	this work
Microhyla pineticola s. str.	Vietnam, Dak Lak, Chu Yang Sin NP	ZMMU A-7269	MW147171	MW147165	this work
Microhyla pulchella	Vietnam, Lam Dong, Bidoup–Nui Ba NP	ZMMU A-5045	MN534765	MN534549, MN534656	Gorin *et al*. 2020
Microhyla pulchra	Laos, Khammouan, Nakai-Nam Theun	ZISP FN-00154	MN534716	MN534507, MN534609	Gorin *et al*. 2020
Microhyla rubra	India, Andhra Pradesh, Bapatla	ZMMU A-5006-19	MK208936		Poyarkov *et al*. 2019; Gorin *et al*. 2020
Microhyla sholigari	India, Karnataka, Udupi District, Manipal	ATREE MISH 3	KT600669	KT600676	Seshadri *et al*. 2016
Microhyla superciliaris	Malaysia, Pahang, Temerloh	KUHE 52558	AB634624	AB634682	Matsui *et al*. 2011
Microhyla taraiensis	Nepal, Mechi, Jamun Khadi, Jhapa	—	MF496241		Khatiwada *et al*. 2018
Microhyla tetrix	Thailand, Suratthani, Khao Sok NP	ZMMU A-6032	MN534740	MN534526, MN534631	Gorin *et al*. 2020
Microhyla zeylanica	Sri Lanka, Central Province, Nuwara Eliya	released	MN534737	MN534523, MN534628	Gorin *et al*. 2020
Microhyla sp. 1	Malaysia, Borneo, Sabah, Danum Valley	RMBR 2171	MN534660	MN534452, MN534553	Gorin *et al*. 2020
Microhyla sp. 2	Myanmar, Sagaing	USNM 523975	—	MG935884	Mulcahy *et al*. 2018
Glyphoglossus capsus	Malaysia, Sarawak, Padawan, Mt. Penrissen	UNIMAS MYS:9389	—	KJ488544	Das *et al*. 2014
Glyphoglossus guttulatus	Thailand, Kanchanaburi, Pilok	KUHE 35163	AB634627	AB634685	Matsui *et al*. 2011
Glyphoglossus minutus	Malaysia, Pahang, Temerloh	KUHE 52463	AB598316	AB598340	Matsui 2011
Glyphoglossus molossus	Thailand, Tak, Barrntak	KUHE 35182	AB201182	AB201193	Matsui *et al*. 2005
G. yunnanensis	China, pet trade	KUHE 44148	AB634626	AB634684	Matsui *et al*. 2011
Outgroups					
Chaperina fusca	Malaysia, Sabah, Crocker Range	BORN 8478	AB598318	AB598342	Matsui 2011
Ctenophryne geayi	Brasil, Pará, Rio Xingu, Fazenda Caracol	MPEG 25397	KM509124		Peloso *et al*. 2016
Dyscophus guineti	Pet trade	KUHE 33150	AB634648	AB634706	Matsui *et al*. 2011
Dyscophus insularis	Pet trade	KUHE 35001	AB634649	AB634707	Matsui *et al*. 2011
Gastrophryne carolinensis	USA, Florida, Camel Lake	CAS 214349	KM509133		Peloso *et al*. 2016
Gastrophryne olivacea	USA, Texas, Dimmit	KUHE 33224	AB634650	AB634708	Matsui *et al*. 2011
Gastrophrynoides immaculatus	Malaysia, Negeri Sembilan	UKM HC 279	AB634647	AB634705	Matsui *et al*. 2011
Kalophrynus pleurostigma	Indonesia, Sumatra, Lampung	MZB Amp 15295	AB634642	AB634700	Matsui *et al*. 2011
Kalophrynus yongi	Malaysia, Pahang, Cameron	KUHE 15531	AB634646	AB634704	Matsui *et al*. 2011

Table 1 continued. Sequences and voucher specimens of *Microhyla* and outgroup taxa used in this study; NP, National Park; — not available.

Species	Locality	Museum / Sample ID	12S rRNA	16S rRNA	Reference
Kaloula baleata	Indonesia, Sumba	KUHE 32313	AB634629	AB634687	Matsui *et al*. 2011
Kaloula rugifera	China	—	KP682314		Deng *et al*. 2016
Metaphrynella pollicaris	Malaysia, Pahang, Fraser's Hill	KUZ 21655	AB634634	AB634692	Matsui *et al*. 2011
Metaphrynella sundana	Malaysia, Borneo, Sabah, Crocker	BORN 8191	AB634635	AB634693	Matsui *et al*. 2011
Micryletta inornata	Thailand, Phrae, Mae Yom	KUHE 20497	AB598317	AB598341	Matsui, 2011
Micryletta nigromaculata	Vietnam, Hai Phong, Cat Ba NP	ZMMU A-5934	MH756150		Poyarkov *et al*. 2018; Gorin *et al*. 2020
Micryletta steinegeri	Taiwan, Yunlin	KUHE 35937	AB634638	AB634696	Matsui *et al*. 2011
Oreophryne monticola	Indonesia, Bali, Batu Karu	MZB Amp 16265	AB634651	AB634709	Matsui *et al*. 2011
Otophryne robusta	Guyana, District 8, Mt. Wokomung	ROM 42963	KM509171		Peloso *et al*. 2016
Phrynella pulchra	Malaysia, Trengganu, Hulu Trengganu	UKMHC 820	AB634636	AB634694	Matsui *et al*. 2011
Phrynomantis bifasciatus	Pet trade	KUHE 33277	AB634652	AB634710	Matsui *et al*. 2011
Rhacophorus schlegelii	Japan, Hiroshima	—	AB202078	AB202078	Sano *et al*. 2005
Scaphiophryne gottlebei	Pet trade	KUHE 34977	AB634653	AB634711	Matsui *et al*. 2011
Synapturanus salseri	Brazil, Amazonas, Manaus	MZUSP	KM509207		Peloso *et al*. 2016
Uperodon taprobanicus	Sri Lanka	KUHE 37252	AB634633	AB634691	Matsui *et al*. 2011

Table 2. Uncorrected p-distance (percentage) between the sequences of 16S rRNA mtDNA fragment (below the diagonal), error estimates (above the diagonal), and intraspecific genetic p-distance (on the diagonal) of the *Microhyla achatina* species group members included in phylogenetic analyses.

Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
M. neglecta sp. nov.	**0.4**	0.9	1.1	1.6	1.1	1.3	1.1	1.2	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.4
M. pineticola s. str.	5.2	**0.1**	1.1	1.5	1.0	1.1	1.0	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.2	1.3
M. heymonsi	8.7	7.0	—	1.6	1.1	1.2	1.0	1.1	1.1	1.0	1.0	1.1	1.1	1.2	1.2	1.2
M. borneensis	13.1	12.5	11.9	—	0.9	1.1	1.2	1.5	1.3	1.5	1.7	1.6	1.3	1.3	1.4	1.9
M. nepenthicola	10.3	8.3	7.8	3.0	—	0.6	0.7	1.0	1.0	1.1	1.2	1.1	1.0	0.9	1.0	1.6
Microhyla sp. 1	10.9	9.1	7.7	4.8	2.6	—	0.8	1.1	1.0	1.1	1.2	1.1	1.2	1.0	1.2	1.4
M. malang	10.1	8.3	7.3	5.6	2.2	3.5	—	1.0	1.1	1.1	1.2	1.1	1.1	1.0	1.1	1.5
M. orientalis	9.5	7.9	7.1	9.5	5.7	6.9	5.7	—	1.0	1.1	1.1	1.2	1.0	0.9	1.0	1.5
M. mantheyi	11.1	8.9	7.8	7.4	5.3	4.9	5.7	5.7	—	1.0	1.1	1.0	1.0	0.9	1.1	1.4
Microhyla sp. 2	11.3	9.7	7.7	11.3	8.4	8.6	8.2	8.0	7.7	—	0.6	0.9	1.1	1.1	1.2	1.4
M. irrawaddy	10.5	8.9	6.9	11.6	8.0	7.8	7.8	7.7	7.7	2.2	—	0.9	1.2	1.1	1.2	1.4
M. kodial	11.7	9.3	6.8	10.9	7.6	8.0	8.0	8.0	7.2	6.4	6.0	—	1.1	1.1	1.2	1.4
M. achatina	9.3	9.4	7.3	8.6	6.5	6.9	6.9	5.9	6.5	6.9	6.9	8.3	—	0.8	1.1	1.5
M. gadjahmadai	10.5	9.5	8.4	8.9	6.5	7.1	7.7	6.3	5.7	7.3	6.9	7.8	5.3	—	0.9	1.5
M. minuta	10.1	8.3	8.2	8.0	5.3	6.7	5.7	6.1	6.3	8.0	8.0	8.7	6.9	6.1	—	1.5
M. fodiens	10.3	10.0	9.6	14.5	12.2	12.0	12.2	12.0	11.0	11.8	11.6	12.4	10.6	11.6	11.0	—

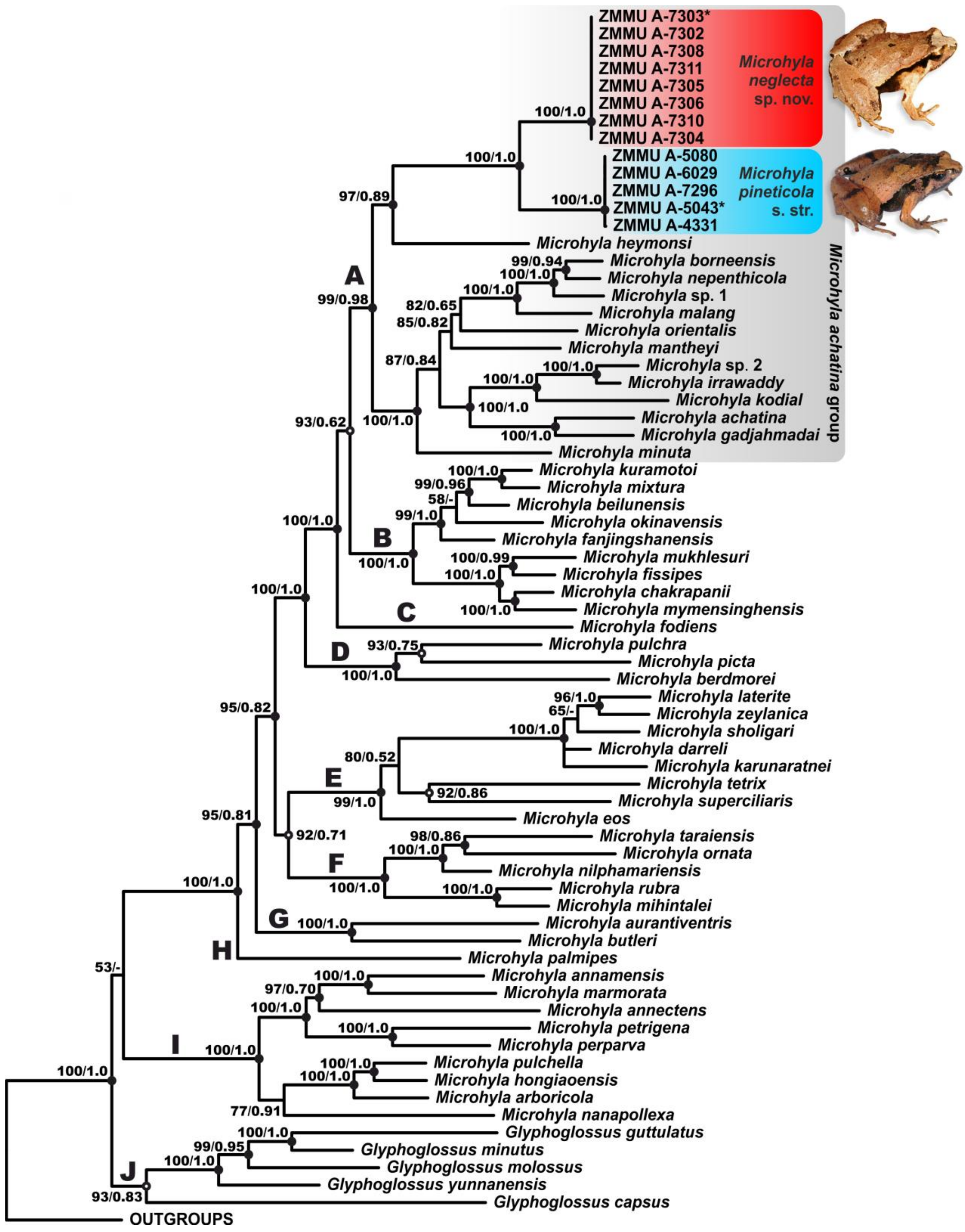

Figure 2. Maximum Likelihood tree of *Microhyla* derived from the analysis of 2399 bp of alignment including 12S rRNA, tRNA-Val and 16S rRNA gene fragments. For voucher specimen information and GenBank accession numbers see Table 1. Red and blue colours denote the new species and *M. pineticola* sensu stricto respectively, holotypes denoted with asterisks (*); grey denotes *M. achatina* species group members. Numbers at tree nodes correspond to UFBS/PP support values, respectively; well-supported nodes are marked with solid circle, moderate-support is indicated with empty circle, no circle means no-support; outgroup taxa are not shown; © Photos: Nikolay A. Poyarkov.

Systematics
Our molecular analyses of the type series of *Microhyla pineticola* and additional specimens, have demonstrated that specimens used in the original description actually belong to two sympatric mtDNA lineages. The specimens used in the *M. pineticola* description were collected in 2009, 2010 and 2011 in three locations within the Da Nhim River Valley, in the vicinity of Giang Ly Ranger Station of the Bidoup–Nui Ba National Park (ca. 2–4 km between the localities). The members of both lineages were sympatric.

Our mtDNA-based genealogy suggests that the two mtDNA lineages of '*M. pineticola*' are sister lineages (Fig. 2). The level of divergence in 16S rRNA gene between these lineages is larger than would be expected within a single species (p=5.2%). This value is much greater than the formal threshold of p=3.0%, widely used as an indicator of species-level status in the surveys of anuran biodiversity (Vences *et al.* 2005a, 2005b; Vieites *et al.* 2009), and also exceeds minimal interspecific distances in the *M. achatina* species group (Table 2), and among *Microhyla* species in general (see Gorin *et al.* 2020).

Though the members of the two sympatric mtDNA-lineages of '*M. pineticola*' are superficially similar in overall body habitus and have a variable dorsal pattern, a thorough reexamination of the material has revealed a number of stable differences in colouration, pattern, and body morphology (see Comparisons). These results were concordant with the observed genetic divergence and allowed us to readily distinguish the specimens belonging to the two different mtDNA lineages. Overall, the integrative taxonomic analyses strongly support our hypothesis that the original description of *M. pineticola* was based on the type series which included the members of two sister species of *Microhyla*, different both morphologically and genetically, and which were unnoticed by Poyarkov *et al.* (2014).

In the present paper the type series of *M. pineticola* is formally split in accordance with the International Code of Zoological Nomenclature (ICZN 1999); the former paratypes of *M. pineticola* (eleven specimens from ZMMU A-4331, three specimens from ZMMU A-5080) are below designated as holotype (new collection ID ZMMU A-7303) and paratypes (new collection IDs ZMMU A-7297–7302, ZMMU A-7304–7310) of the new species we describe herein. Below, we provide a detailed description and a revised diagnosis for *M. pineticola* sensu stricto, and describe the second lineage of '*M.* cf. *pineticola*' from Bidoup–Nui Ba National Park as a new species.

Microhylide Günther, 1858
Microhyla Tschudi, 1838

Microhyla pineticola
Poyarkov, Vassilieva, Orlov *et al*., 2014
Pine narrow-mouth frog
(Figs. 3, 4F; Tables 3, 4)

Holotype. Adult female, ZMMU A-5043 (field number NAP-01032), collected from Mt. Bidoup (12°957.24 N, 108°3944.28 E; alt. 1,800 m a.s.l.), Bidoup–Nui Ba National Park, Da Nhim River Valley, Da Chais Commune, Lac Duong District, Lam Dong Province, Vietnam, by N.A. Poyarkov on 01 May 2009 (see Poyarkov *et al.* 2014: 100).

Paratypes (*n*=3): adult males, ZMMU A-4331 (field number NAP-00414) and ZMMU A-4331 (field number NAP-00451); adult female, ZMMU A-5080 (field number NAP-01750); data same as that for the holotype (only those paratypes which proved to be conspecific to ZMMU A-5043 are listed here).

Other materials examined (*n*=2): adult male, ZMMU A-6029 (field number ABV-00579), collected from Chu Yang Sin National Park (12.413029° N, 108.367939° E; alt. 1,100 m a.s.l.), Dak Lak Province, Vietnam, by N.A. Poyarkov and A.B. Vassilieva on 23 May 2014; adult female, ZMMU A-7296 (field number ABV-00571), collected from Chu Yang Sin National Park (12.418742° N, 108.364608° E; alt. 970 m a.s.l.), Dak Lak Province, Vietnam, by N.A. Poyarkov on 22 May 2014.

Revised diagnosis: *Microhyla pineticola* is diagnosed by a combination of the following morphological attributes: body stocky, triangular, body size small (SVL 17.4–18.6 mm in males and 20.0–22.3 mm in females); dorsum feebly granular with small tubercles; head triangular, snout rounded in lateral profile (Fig. 4F); finger I short, less than one-half the length of finger II; tips of three outer fingers weakly dilated, forming weak discs, with a dorsal, median, longitudinal groove; tips of all toes distinctly dilated into discs, dorsally with a weak median longitudinal groove producing the appearance of two scutes; expanded toe discs less than twice

Plate 46

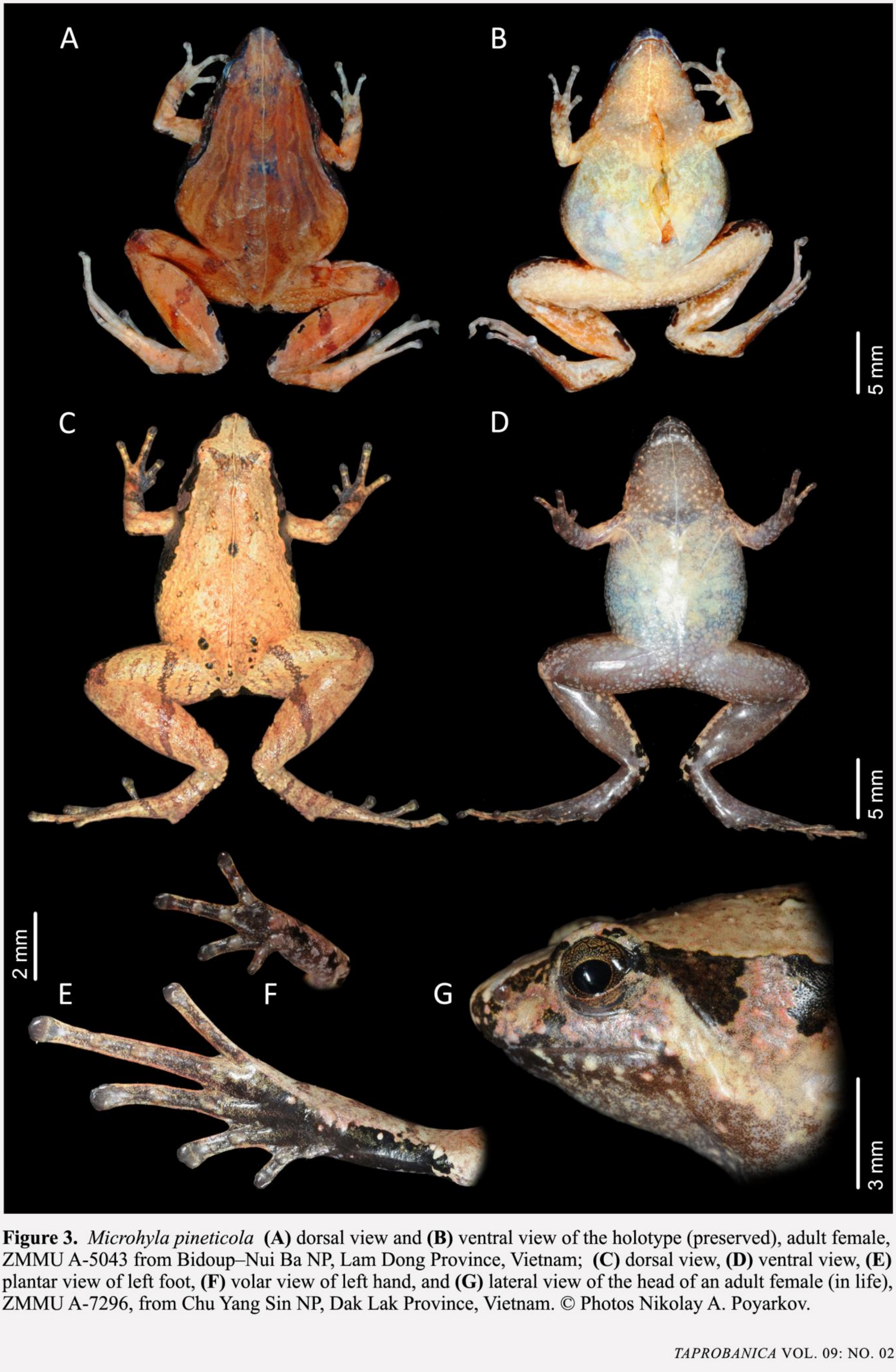

Figure 3. *Microhyla pineticola* **(A)** dorsal view and **(B)** ventral view of the holotype (preserved), adult female, ZMMU A-5043 from Bidoup–Nui Ba NP, Lam Dong Province, Vietnam; **(C)** dorsal view, **(D)** ventral view, **(E)** plantar view of left foot, **(F)** volar view of left hand, and **(G)** lateral view of the head of an adult female (in life), ZMMU A-7296, from Chu Yang Sin NP, Dak Lak Province, Vietnam. © Photos Nikolay A. Poyarkov.

the width of phalanges; metacarpal tubercles two, both prominent and rounded; tibiotarsal articulation at straightened limb reaching beyond eye but not reaching snout tip; toe webbing basal, formula: I 1½-2½ II 1¾-3 III 2¾-3¾ IV 4-2½ V; both inner and outer metatarsal tubercles present; upper eyelid without supraciliary spines; canthus rostralis with dark lines, top of snout well-differentiated in colour from the brown interorbital bar, which bears a dark spot; dark stripe running from the posterior edge of eye along the supratympanic fold, interrupted above the axilla (Figs. 3G, 4F), and continues to groin as a dark lateral stripe, clearly separating darker flanks and lighter dorsum; an indistinct beige stripe extending from posterior margin of eye to axilla; the axillary region and upper lips bearing numerous bluish-white speckles; light-coloured thin, vertebral stripe present; a small, dark, rounded, middorsal spot, divided by a light-coloured vertebral stripe; dorsal markings formed by dark-brownish lines parallel to vertebral and dorsolateral stripes, narrowly outlined in beige, forming a pattern resembling the grain of pinewood (Figs. 3A–B); chin dark-greyish with orange speckles and a thin light-coloured medial stripe continuing to chest and belly (Figs. 3B,D); two white lines extend along the ventral surfaces of forelimbs reach the chest and meet on the midline of the belly; belly purplish-grey with indistinct whitish mottling.

Description of holotype. See Poyarkov *et al*. (2014). Measurements and morphological characters of the holotype and paratype series of this species are given in Table 3. The brief tadpole description presented by Poyarkov *et al.* (2014: 104–105, Fig. 13) may actually correspond to the larvae of the new species.

Distribution. To date known at elevations from 970 m a.s.l. in Chu Yang Sin National Park (Dak Lak Province) to 1800 m a.s.l. in Bidoup–Nui Ba National Park (Lam Dong Province). This species seems to be restricted to polydominant evergreen montane forests with a predominance of *Pinus krempfii* Lecomte (Family Pinaceae), *Lithocarpus* sp., *Castanopsis* sp., and *Quercus* sp. (all Family Fagaceae); and dry monodominant pine forests formed mostly by *P. kesiya* Royle ex Gordon (Family Pinaceae) on the Langbian Plateau (see Poyarkov *et al*. 2014). Based on known distribution, habitat and elevation preferences, *Microhyla pineticola* is likely endemic to the Langbian Plateau, southern Vietnam (Fig. 1).

Microhyla neglecta sp. nov.

[urn:lsid:zoobank.org:act:22E3B2D0-A6BB-45C7-BA7A-87ADF2B17E9E]

(Figs. 4A–E; Tables 3, 4)

Microhyla "sp. 1" — Poyarkov [Paiarkov] & Vassilieva 2011: Fig. 5.8.
Microhyla pineticola — Poyarkov *et al.* 2014 [*partim*]

Holotype. Adult male, ZMMU A-7303 (field number NAP-00553, formerly part of ZMMU A-4331 and a member of *M. pineticola* type series), collected from Da Nhim River Valley (12.170838° N, 108.697765° E; alt. 1,500 m a.s.l.), Bidoup–Nui Ba National Park, Lam Dong Province, Vietnam by N.A. Poyarkov and A.B. Vassilieva on 26 June 2010.

Paratypes (*n*=14): Six adult males, the former members of ZMMU A-4331 and members of *M. pineticola* type series with the following new collection numbers: ZMMU A-7297 (field number NAP-00413), ZMMU A-7298 (field number NAP-00415), ZMMU A-7299 (field number NAP-00416), ZMMU A-7300 (field number NAP-00417), and ZMMU A-7301 (field number NAP-00523), collected from Da Nhim River Valley (12.180525° N, 108.681983° E; alt. 1,450 m a.s.l.), Bidoup–Nui Ba National Park, Lam Dong Province, Vietnam by N.A. Poyarkov on 5 May 2009; ZMMU A-7302 (field number NAP-00552), collected from Da Nhim River Valley (12.170838° N, 108.697765° E; alt. 1,500 m a.s.l.), Bidoup–Nui Ba National Park, Lam Dong Province, Vietnam, by N.A. Poyarkov and A.B. Vassilieva collected on 26 June 2010. Three adult males, the former members of ZMMU A-5080 with the following new collection numbers: ZMMU A-7304 (field number NAP-01800), and ZMMU A-7305–7306 (field numbers NAP-01884–01885) collected from Giang Ly ranger station (12.185416° N, 108.689419° E; alt. 1,480 m a.s.l.), Bidoup–Nui Ba National Park, Lam Dong Province, Vietnam by N.A. Poyarkov, A.B. Vassilieva and E.A. Galoyan on 07 July 2011. Four adult females, the former members of ZMMU A-4331 with the following new collection numbers: ZMMU A-7307 (field number NAP-09900) collected from the northern slope of Mt. Bidoup (12.116070° N, 108.660232° E; alt. 1,800 m a.s.l.), Bidoup–Nui Ba National Park, Lam Dong Province, Vietnam by N.A. Poyarkov on 9 May 2009; ZMMU A-7308–7309 (field numbers NAP-00418–00419) collected from Da Nhim River Valley (12.180525° N, 108.681983° E; alt. 1,450 m a.s.l.), Bidoup–Nui Ba National Park, Lam Dong Province, Vietnam by N.A. Poyarkov on 5 May 2009; and ZMMU A-7310 (field number NAP-01422) collected from Giang Ly ranger station (12.185416° N, 108.689419° E; alt. 1,480 m a.s.l.), Bidoup–Nui Ba National Park, Lam Dong Province, Vietnam by N.A. Poyarkov and A.B. Vassilieva on 26 June 2010.

Diagnosis: The new species is allocated to the genus *Microhyla* Tschudi, 1838 based on the following combination of diagnostic characters (Parker 1934; Poyarkov *et al.* 2014, 2019a, 2020b): small body size; head comparatively narrow; eyes small with circular pupil; spine-like projection of skin at heel and elbow absent; maxillary and vomerine teeth absent; snout less than twice the diameter of the eye; tongue obovate, entire, and free posteriorly; webbing on fingers absent; webbing on toes basal; palmar tubercles distinct; inner and outer metatarsal tubercles prominent; supratympanic fold present; tympanum hidden under the skin.

Microhyla neglecta sp. nov. is allocated to the *Microhyla achatina* species group (see Garg *et al.* 2018; Gorin *et al.* 2020) and is diagnosed from all other congeners by the following combination of morphological characters: body moderately slender, small, male SVL 17.2–19.5 mm (males), 17.8–23.0 mm (females); dorsum smooth with evenly scattered small flat, tubercles; snout sharply acuminate in lateral profile, nostrils on the lateral sides of snout; finger I longer than one-half the length of finger II; tips of three outer fingers weakly dilated forming weak discs, with median, dorsal, longitudinal grooves; tips of all toes distinctly dilated into discs, with median, dorsal longitudinal grooves; expanded toe discs ca. two times wider than width of penultimate phalanges; metacarpal tubercles two, outer round, inner tubercle oval and prominent; tibiotarsal articulation of a straightened limb reaching well beyond snout; toe webbing basal, formula: I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V; metatarsal tubercles two, prominent, inner elongate, outer round; upper eyelid lacking supraciliary spines or tubercles; a dark line extends along canthus rostralis; dorsal surface of snout light-grey, well-differentiated in colour from the dark-brown interorbital bar, which bears an 8-shaped, dark, medial blotch; a narrow, continuous, black stripe running from the posterior margin of the eye, along the supratympanic fold, transforming into a dark dorsolateral stripe reaching the groin; a distinct, narrow, cream-white stripe extending from the posterior margin of the eye to the axilla; the axillary region and upper lips lack bluish-white speckles; dorsal pattern formed by a weak light-coloured, thin, vertebral stripe; small, dark, middorsal oval marking; a light-brown chevron-shaped marking or “teddy-bear” edged with beige; the lateral sides of dorsum may have indistinct, thin, brownish lines forming nested reverse V-shaped figures; centre of chin grey, sides dark-brown to black, with a thin, light-coloured medial stripe not reaching the chest; belly yellowish with indistinct greyish marbling laterally.

Description of holotype: A small-sized, SVL 18.1 mm, adult male specimen in a generally good state of preservation (slightly dehydrated); body habitus moderately slender; head comparatively large, almost as long as wide (HL/HW 1.01); snout truncate in dorsal view, sharply acuminate in lateral profile, slightly protruding beyond lower jaw, longer than eye diameter (EL/SL 0.86); eye rounded, comparatively small, slightly protuberant in dorsal view and not protruding in lateral view, pupil horizontal; dorsal surface of head slightly convex, canthus rostralis sharp; loreal region distinctly concave; nostrils rounded, placed more on the sides of the snout, located closer to the tip of snout than to the eye; tympanum hidden under skin of temporal region; supratympanic fold weak, becoming indistinct above the axilla; maxillary and vomerine teeth absent; vocal sac single, subgular; tongue obovate, entire, and free posteriorly, lacking papillae.

Forelimbs short, ca. one-third of hindlimb length (FLL/HLL 0.34); hand short (HAL/LAL 0.55; HAL/FLL 0.44); fingers comparatively thin, rounded in cross-section, first finger slightly longer than half of second finger length (1FL/2FL 0.53); relative length of fingers: I<IV<II<III. Webbing absent between all fingers; dermal fringes absent; tips of all fingers rounded, tip of finger I not enlarged, tips of fingers II–IV notably widened forming discs, with median, dorsal, longitudinal grooves and dorso-terminal grooves; third finger disc largest; subarticular tubercles on volar surface of fingers barely distinct, flattened, subarticular tubercle formula: 1:1:2:2; nuptial pad absent; two metacarpal (palmar) tubercles, both distinct, inner tubercle round, outer tubercle elongate, slightly larger than inner one (IPTL/OPTL 0.79); area between

Plate 47

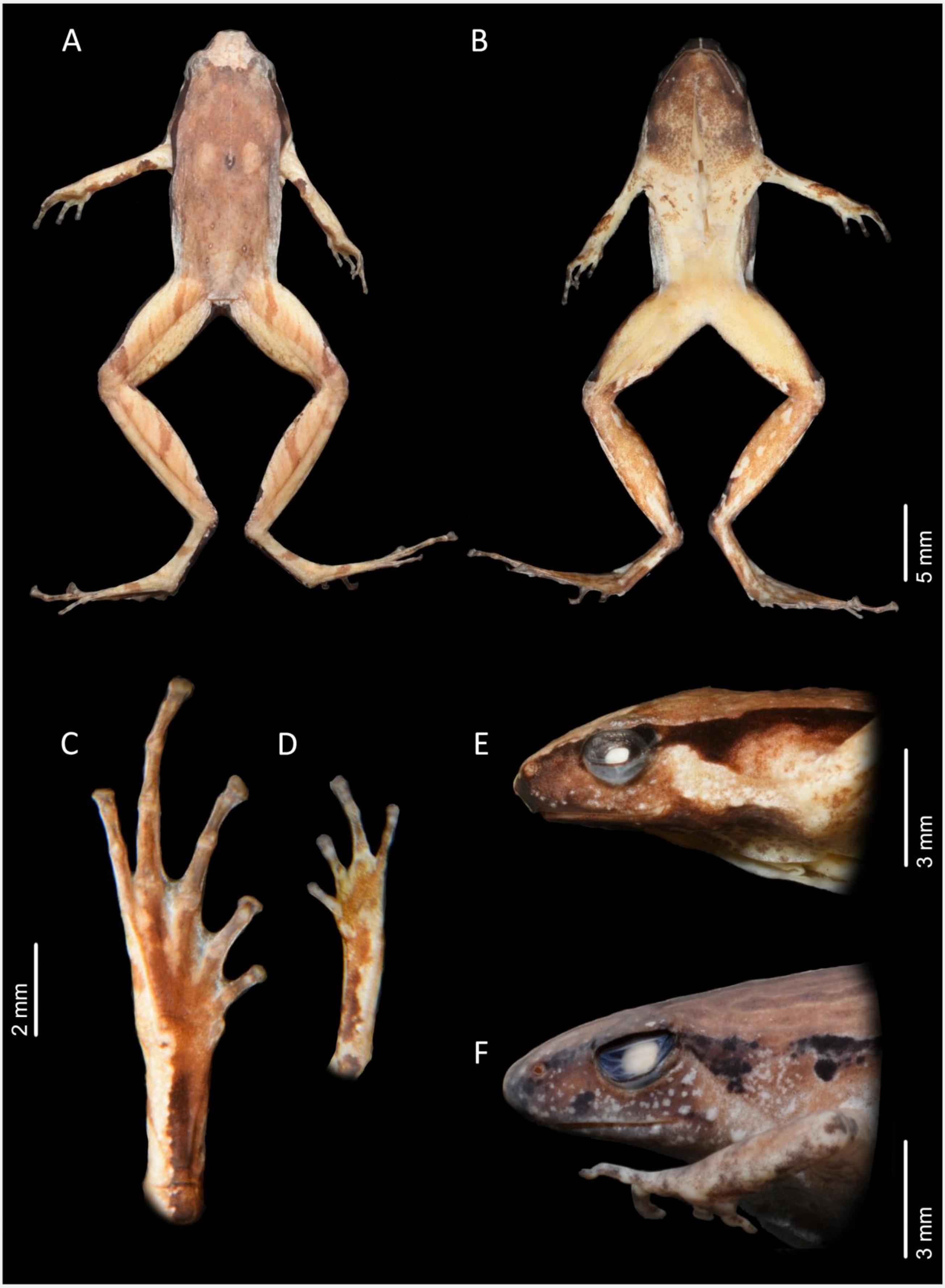

Figure 4. **(A)** dorsal view, **(B)** ventral view, **(C)** plantar view of right foot, **(D)** volar view of left hand, and **(E)** lateral view of the head of *Microhyla neglecta* sp. nov., holotype, adult male, ZMMU A-7303; and **(F)** lateral view of the head of *M. pineticola*, holotype, adult female, ZMMU A-5043. Both holotypes are from Bidoup–Nui Ba NP, Lam Dong Province, Vietnam. © Photos Nikolay A. Poyarkov.

Plate 48

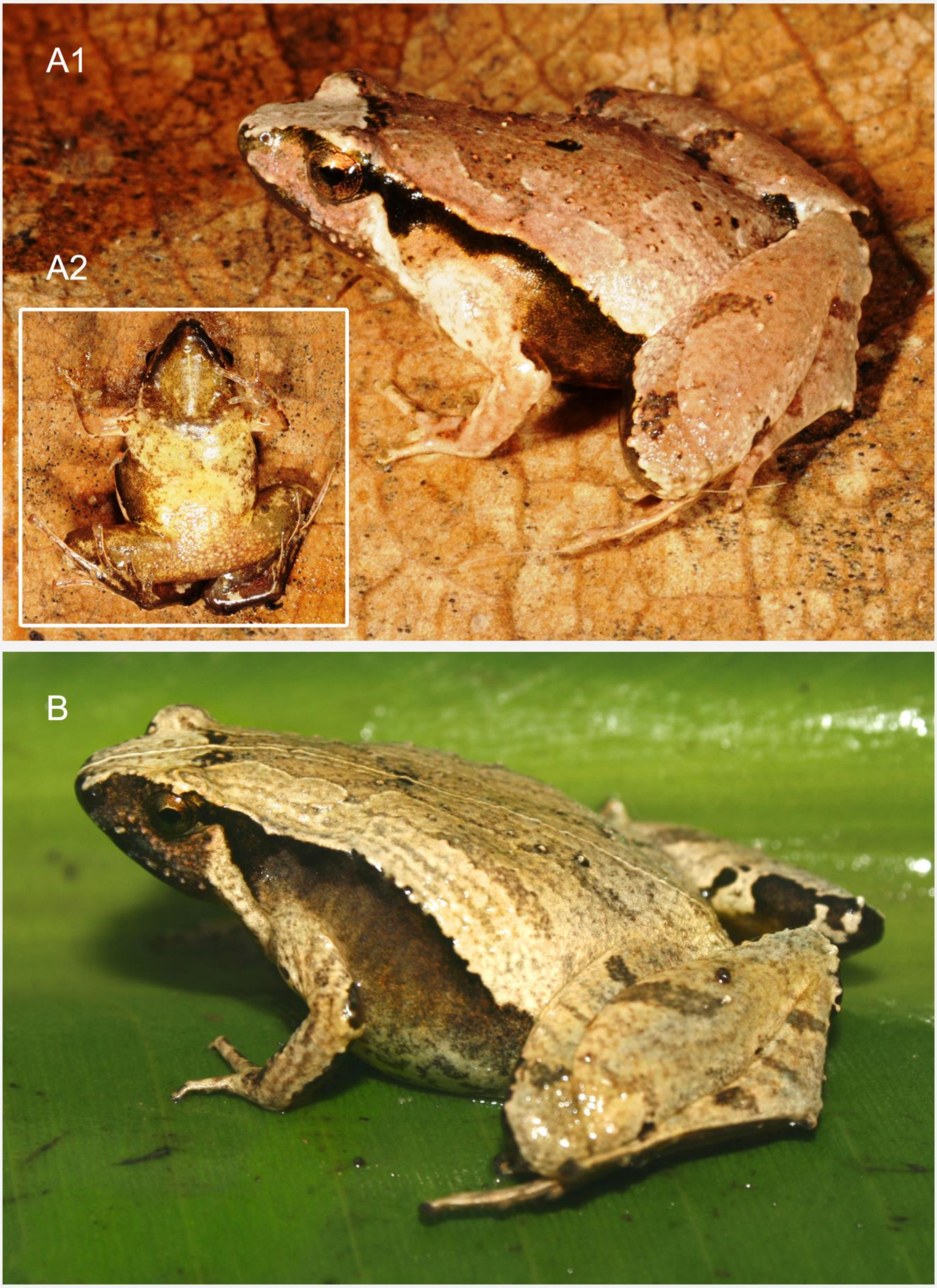

Figure 5. *Microhyla neglecta* sp. nov. in life **(A1)** dorsolateral view, **(A2)** ventral view of paratype, adult male, ZMMU A-7302; and **(B)** dorsolateral view of paratype, adult female, ZMMU A-7307. Both paratypes are from Bidoup–Nui Ba NP, Lam Dong Province, Vietnam. © Photos Nikolay A. Poyarkov.

inner and outer palmar tubercles flat and lacking medial or supernumerary palmar tubercles.

Hindlimbs comparatively long, tibia length much longer than half of snout-vent length (TL/SVL 0.61), hindlimb length over 1.5 times longer than snout-vent length (HLL/SVL 1.80); tibiotarsal articulation of adpressed limb reaching well beyond snout (checked prior to preservation); tibia slightly longer than foot (FL/TL 0.98); relative toe lengths: I<II<V<III<IV; tarsal fold on inner surface of tarsus absent; tips of all toes rounded and widened, forming broad, terminal discs; all toe discs having distinct dorso-terminal groves; discs on toes II–V having distinct median, distal, dorso-longitudinal grooves not reaching over one-half of disc length and producing the appearance of two scutes; toes long, thin, slightly flattened in cross-section; toe webbing basal, formula: I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V; toe subarticular tubercles distinct, round, slightly protruding, subarticular tubercle formula: 1:1:2:3:2; two metatarsal tubercles: inner metatarsal tubercle elongate, oval, slightly prominent; outer metatarsal tubercle small, round, shorter than the inner tubercle (OMTL/IMTL 0.74), slightly protruding.

Skin on dorsal surface of head and body smooth with small, flat tubercles irregularly scattered along the medial part of dorsum; supratympanic fold slightly swollen, becoming indistinct posteriorly at level of the axilla; upper eyelid without supraciliary spines or tubercles; lateral head and body smooth, forelimbs dorsally smooth, hindlimbs with few small, flat, dorsal tubercles; ventral surfaces of body and limbs smooth, ventral surfaces of thighs with numerous flat, glandular pustules, cloacal region smooth with few tubercles. Cloacal opening unmodified, directed posteriorly, at the lower level of thighs.

Colouration of holotype. In life, dorsally light-brown, with a distinct slightly darker brownish "teddy-bear"-shaped pattern (*sensu* Rakotoarison *et al.* 2017) edged with beige. Anterior parts of head and snout light-grey above, well-differentiated in colour from the darker dorsum. A distinct dark-brown interorbital transverse bar between most medial edges of upper eyelids, extending anterolaterally, covering almost all the posterior two thirds of eyelid; an 8-shaped, medial, dark blotch within the interorbital bar. A weak, thin, light-coloured vertebral stripe runs from the tip of the snout to the vent. A small, elongate, U-shaped, black spot at middorsum. Small tubercles on dorsum edged with brown; two series of three, black sacral spots on each side of body. Dorsolateral surfaces of trunk and upper arm light-brown with indistinct greyish pattern; forelimbs lacking darker dorsal cross-bars, hindlimbs with a single, brown, dorsal cross-bar on proximal part of thighs and middle part of shanks; fingers and toes light-brown above with indistinct, brownish cross-bars. Lateral head brownish, a dark-brown lateral stripe running from tip of snout to nostril, and curving along the edge of the canthus rostralis towards the anterior margin of the eye; upper and lower lips dark-brown with a few light-coloured speckles. A black stripe extends from the posterior margin of the eye along the supratympanic fold to above the axilla along a dorsolateral line reaching the groin and separating the light-brown colouration of dorsum from the dark-brown colour of flanks; the stripe fades ventrally towards the groin. A distinct, narrow, cream-white stripe extends from the posterior margin of the eye to the axilla. Centre of chin grey, sides dark-brown to black with a thin, light-coloured medial stripe not reaching the chest; chest and belly yellowish with indistinct greyish marbling laterally; limbs greyish-pink below with creamy or yellowish irregularly shaped blotches. Iris bronze with dense black dusting at the anterior and posterior edges; pupil horizontal, black, outlined with a golden circle.

In preservative, after ten years of preservation in ethanol, the colours have significantly faded (Fig. 4). The ground colouration of dorsum faded to greyish-brown, black spots and stripes fade to dark-brown, colouration of iris and the yellowish tint of ventral colouration faded completely. However, the overall pattern on dorsum, flanks, and venter remained unchanged.

Variation. Morphometric variation of the type series is presented in Table 3. Paratypes are generally similar to the holotype in body proportions and colouration, with only slight variation is observed in shape of the dorsal pattern. All specimens have a continuous black stripe running from the posterior margin of the eye to the groin. Males (SVL 17.2–19.5 mm, mean 18.3±0.8 mm; *n*=10) were slightly smaller than females (SVL 17.8–23.0 mm, mean 19.5±2.1 mm; *n*=5). Colouration also differed little between the sexes. In males, the dorsal pattern is generally represented by indistinct 'teddy-bear' or chevron-shaped brownish markings with weak, beige edging (Fig. 5A), while in females, like in ZMMU A-7307 (see Fig. 5B), the lateral body has indistinct, thin, brownish lines forming nested reverse V-shaped figures resembling that of *M. pineticola*. Female ZMMU A-7307 was swollen with yellowish-white eggs with a dark-brown animation pole, ca. 1.1–1.2 mm in diameter (*n*=10).

Etymology. Specific epithet "*neglecta*" is a Latin adjective in nominative singular, feminine form of "*neglectus*", Latin for "having been overlooked". The name is given in reference to the complicated taxonomic history of the new species, which remained unnoticed until recently and was even included in the type series of its sister species *M. pineticola*. We recommend "*Neglected narrow-mouth frog*" as the common English name, "*Nezamechennyi Uzkorot*" as the name in Russian, and "*Nhái bầu quên lãng*" in Vietnamese.

Comparison. The differences of the new species from all other congeners are summarized in Table 4. In general morphology, *Microhyla neglecta* sp. nov. superficially most resembles its sister species *M. pineticola* s. str., however the new species can be readily distinguished from the latter by having the following suite of morphological characters: (1) a moderately slender body (Fig. 4A) (*vs* stocky, triangular, see Figs. 3A,C); (2) a thick continuous black stripe running from the posterior edge of eye to the groin (see Fig. 4E, Fig. 5A1) (*vs* thin and interrupts above the axilla, see Fig. 3G, Fig. 4F); (3) a yellowish belly with indistinct greyish marbling laterally (see Fig. 4B, Fig. 5A2) (*vs* purplish-grey with indistinct whitish mottling, Fig. 3B,D); (4) medially grey throat laterally dark brown to black, with a thin white medial line running from chin upto the posterior edge of throat (Fig. 4B, Fig. 5A2) (*vs* dark-greyish laterally orange speckles, with a thin light-colour medial line running from chin upto the chest and belly, and also connects to the two white lines continuing to the ventral surface of forelimbs, see Fig. 3D); (5) a distinct thin cream-white stripe from posterior eye to axilla and uniform lips and axilla (Fig. 4E) (*vs* an indistinct beige stripe, and the upper lips and axilla with numerous bluish-white speckles, see Fig. 3G, Fig. 4F); (6) first finger longer than one half of the second finger (*vs* shorter); (7) an oval shaped, elongated outer metacarpal tubercle (*vs* rounded); (8) comparatively longer hindlimbs, with a tibiotarsal articulation of straightened limb projecting well beyond snout (*vs* shorter than snout); (9) slightly less developed foot webbing I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V (*vs* I 1½-2½ II 1¾-3 III 2¾-3¾ IV 4-2½ V); and (10) sharply acuminate snout in lateral profile (*vs* rounded).

Based on morphological characteristics and the phylogenetic position, *Microhyla neglecta* sp. nov. can be assigned to the *M. achatina* species group, and its comparison to other members of this group are the most pertinent; we present it below. The new species differs from (1) *M. achatina* by having a smaller body SVL 17.2–19.5 mm in males and 17.8–23.0 mm in females (*vs* 19.7–23.0 mm in males and 24.0–26.1 mm in females), first finger longer than one half of the second finger (*vs* shorter), a black spot on the middorsum (*vs* absent), a comparatively less developed foot webbing I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V (*vs* I 2-2½ II 2-3¼ III 3-4 IV 4-3 V), and a continuous dark line above the axilla (*vs* interrupted); (2) from *M. borneensis* by having a larger body SVL 17.2–19.5 mm in males and 17.8–23.0 mm in females (*vs* 11.0–13.0 mm in males and 18.0–19.0 mm in females), a well-developed first finger (*vs* greatly reduced to a nub), a light vertebral line (*vs* absent), tibiotarsal articulation reaching well beyond snout (*vs* not reaching the snout); (3) from *M. fodiens* by having a moderately slender body habitus (*vs* stout), snout acuminate in lateral profile (*vs* rounded), first finger longer than one half of the second finger (*vs* shorter), longitudinal grooves on the dorsal surface of fingers and toes (*vs* absent), a light vertebral line (*vs* absent), and tibiotarsal articulation reaching well beyond snout (*vs* not reaching the eye); (4) from *M. gadjahmadai* by having a moderately slender habitus (*vs* stout), snout acuminate in lateral profile (*vs* rounded), a strong continuous dark stripe above the axilla (*vs* thin and interrupted), and a comparatively less developed foot webbing I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V (*vs* I 2-2¼ II 1¾-3 III 3-4 IV 4-2¾ V); (5) from *M. heymonsi* by having two lower metacarpal tubercles and no supernumerary tubercles on palm (*vs* three distinct prominent metacarpal tubercles and supernumerary tubercles), snout acuminate in lateral profile (*vs* obtusely pointed), tibiotarsal articulation reaching well beyond snout (*vs* not reaching the snout), and a comparatively less developed foot webbing I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V (*vs* I 2-2½ II 2-3 III 3-4 IV 4⅓-3 V); (6) from *M. irrawaddy* by having a larger body SVL 17.2–19.5 mm in males (*vs* 12.3–17.1 mm), a smooth dorsum with few small tubercles (*vs* granular), longitudinal grooves on the dorsal surface of fingers and toes (*vs* absent), supratympanic fold distinctly edged with black (*vs* absent), tibiotarsal articulation reaching well beyond snout (*vs* not reaching the snout), and a comparatively less developed foot webbing I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V (*vs* I 2-3 II 2-3 III 3-4½ IV 4½-2¾ V); (7) from *M. kodial* by having snout acuminate in lateral profile (*vs* rounded), canthus rostralis distinct (*vs* indistinct), a vertebral line (*vs* absent), and a lateral dark stripe from eye to groin (*vs* absent); (8) from *M. malang* by having snout acuminate in lateral profile (*vs* rounded), first finger longer than one half of the second finger (*vs* shorter), a dark continuous line above the axilla (*vs* interrupted), a light-colour vertebral line (*vs* absent), and a comparatively less developed foot webbing I 1½-2½ II 1¾-3 III 2¾-3¾ IV 3¾-2½ V (*vs* I 1-2 II 1-2⅔ III 1⅔-3 IV 3-1 V); (9) from *M. mantheyi* by having first finger longer than one half of the second finger (*vs* shorter), a smooth dorsum with few small tubercles (*vs* granular with regularly scattered pustules), a dark continuous line above the axilla (*vs* interrupted); (10) from *M. minuta* by having a larger body SVL 17.2–19.5 mm in males and 17.8–23.0 mm in females (*vs* 14.7–15.9 mm in males and 15.7–17.2 mm in females), smooth dorsum with few small tubercles (*vs* granular with regularly scattered pustules), a dark dorsolateral stripe (*vs* absent), a light-colour vertebral line (*vs* absent), and tibiotarsal articulation reaching well beyond snout (*vs* not reaching the snout); (11) from *M. orientalis* by having a larger body SVL 17.2–19.5 mm in males and 17.8–23.0 mm in females (*vs* 15.8–17.4 mm in males and 15.8–17.4 mm in females), first finger longer than one half of the second finger (*vs* shorter), tibiotarsal articulation reaching well beyond snout (*vs* not reaching reaching the snout), and a distinct light vertebral line (*vs* faint).

Distribution. To date, the new species is known exclusively from three localities within the eastern portion of the Bidoup–Nui Ba National Park in Lam Dong Province, southern Vietnam. *Microhyla neglecta* was observed at elevations from 1,450 m a.s.l. (in the environs of the Giang Ly ranger station) to 1,800 m a.s.l. (on the northern slope of Mt. Bidoup). All three known localities are located within a narrow area (approximately 20 km^2) within the Da Nhim River Valley.

Natural history. All the *Microhyla neglecta* specimens were found on the ground (both during day and night) in mixed montane tropical forests with a predominance of *Lithocarpus* sp., *Castanopsis* sp., and *Quercus* sp. (Family Fagaceae), *Pinus krempfii* (Family Pinaceae), and with a dense understory comprised of *Pandanus* sp. (Family Pandanaceae) and various bushes and small trees.

In all localities surveyed, *M. neglecta* was recorded in sympatry with *M. pineticola*, though the specimens of the new species were usually found within mixed montane forest, while *M. pineticola* specimens were often recorded in open areas and dry monodominant pine forests comprised of *Pinus kesiya*. Other syntopic amphibian species were *M. annamensis* Smith, 1923; *M. berdmorei* (Blyth, 1856); *M. pulchella* Poyarkov, Vassilieva, Orlov *et al*., 2014; *Ingerophrynus galeatus* (Günther, 1864); *Feihyla palpebralis* (Smith, 1924); *Rhacophorus calcaneus* Smith, 1924; *R. vampyrus* Rowley, Le, Tran *et al*. 2010; and *Polypedates megacephalus* Hallowell, 1861.

The reproduction of the new species is insufficiently studied due to the earlier confusion with the sympatric and superficially similar species *M. pineticola*. Further morphological and genetic studies are required to clarify the differences in larval morphology between these two species.

Conservation status. To date, *Microhyla neglecta* is known only from a narrow area within Bidoup–Nui Ba National Park (Lam Dong Province), Langbian Plateau, southern Vietnam. Our intensive surveys in several other forested areas on the Langbian Plateau within Lam Dong, Khanh Hoa, and Dak Lak Provinces failed to discover new populations of *M. neglecta*. Thus the actual extent of distribution of the new species and its population trends remain unknown.

The application of the IUCN Red List criteria (2019: version 14) shows that *Microhyla neglecta* is restricted to an extent of occurrence (EOO) of 70–100 km^2 where 15 individuals were recorded within 10 km distance. Given the relatively narrow distribution range and the rapid montane forest fragmentation accelerated by the high human population density within the range, we suggest *M. neglecta* to be considered a Near Threatened (NT) species.

Table 3. Measurements of the type series of *Microhyla pineticola* and *M. neglecta* sp. nov.; H, holotype; Continue on next page.

Cat. No	SVL	HL	SL	EL	N-EL	HW	IND	IOD	UEW	FLL	LAL
Microhyla pineticola s. str.											
males											
1. ZMMU-A5080	17.5	6.3	2.3	2.2	1.5	5.5	1.6	2.5	1.2	10.0	8.1
2. ZMMU-A6029	17.4	6.4	2.4	2.5	1.4	6.6	1.8	2.4	1.4	9.9	7.3
3. ZMMU-A4331	18.6	6.0	2.2	2.0	1.6	6.5	1.7	2.1	1.1	11.6	7.9
Mean±SD	17.9±0.7	6.2±0.2	2.3±0.1	2.3±0.2	1.5±0.1	6.2±0.6	1.7±0.1	2.3±0.2	1.2±0.1	10.5±1.0	7.8±0.4
Range	17.4–18.6	6.0–6.4	2.2–2.4	2.0–2.5	1.4–1.6	5.5–6.6	1.6–1.8	2.1–2.5	1.1–1.4	9.9–11.6	7.3–8.1
females											
4. ZMMU-A4331	20.0	6.5	2.7	2.3	1.2	7.1	1.8	2.5	1.3	10.8	9.3
5. ZMMU-A5043[H]	22.3	7.3	2.8	2.4	1.8	7.0	2.2	2.5	1.6	12.1	8.7
6. ZMMU-A7296	22.0	6.9	2.8	2.5	1.6	7.3	2.1	2.4	2.2	11.5	9.2
Mean±SD	21.4±1.2	6.9±0.4	2.8±0.1	2.4±0.1	1.5±0.3	7.1±0.1	2.0±0.2	2.5±0.1	1.7±0.5	11.5±0.7	9.1±0.3
Range	20.0–22.3	6.5–7.3	2.7–2.8	2.3–2.5	1.2–1.8	7.0–7.3	1.8–2.2	2.4–2.5	1.3–2.2	10.8–12.1	8.7–9.3
Microhyla neglecta sp. nov.											
males											
1. ZMMU-A7297	18.7	5.5	2.5	2.0	1.6	6.3	1.9	2.5	1.2	12.1	7.9
2. ZMMU-A7298	19.0	6.2	2.8	2.2	1.5	6.5	1.9	2.2	1.0	10.9	8.1
3. ZMMU-A7299	19.5	6.6	2.7	2.3	1.6	6.2	1.9	2.3	1.1	11.1	8.5
4. ZMMU-A7300	17.9	5.6	2.3	2.0	1.3	6.4	1.9	2.2	1.2	11.5	8.8
5. ZMMU-A7301	18.0	6.5	2.3	2.1	1.6	6.2	1.9	2.5	1.3	10.7	8.4
6. ZMMU-A7302	19.2	6.1	2.5	1.9	1.7	5.8	1.8	2.3	1.1	11.0	8.2
7. ZMMU-A7303[H]	18.1	6.1	2.5	2.1	1.7	6.0	1.8	2.3	1.0	11.0	8.0
8. ZMMU-A7304	17.2	5.9	2.5	2.2	1.3	5.9	2.0	2.8	1.3	10.6	7.5
9. ZMMU-A7305	18.2	5.6	2.5	2.3	1.5	6.5	1.7	2.5	1.3	10.5	7.6
10. ZMMU-A7306	17.4	5.2	2.5	1.8	1.3	6.4	1.7	2.1	1.2	9.5	7.4
Mean±SD	18.3±0.8	5.9±0.4	2.5±0.2	2.1±0.2	1.5±0.2	6.2±0.2	1.9±0.1	2.4±0.2	1.2±0.1	10.9±0.7	8.0±0.4
Range	17.2–19.5	5.2–6.6	2.3–2.8	1.8–2.3	1.3–1.7	5.8–6.5	1.7–2.0	2.1–2.8	1.0–1.3	9.5–12.1	7.4–8.8
females											
11. ZMMU-A7307	23.0	6.9	3.0	2.4	1.8	7.2	2.1	2.6	1.3	11.1	9.9
12. ZMMU-A7308	18.7	6.1	2.7	2.5	1.2	6.3	1.9	2.4	1.2	10.6	8.0
13. ZMMU-A7309	19.7	6.4	3.1	2.3	2.1	7.1	1.9	2.4	1.0	11.9	8.9
14. ZMMU-A7310	18.0	6.7	2.5	2.2	1.8	6.9	1.8	2.8	1.3	11.5	8.2
15. ZMMU-A7311	17.8	5.8	2.2	2.0	1.6	5.6	1.7	2.8	1.1	10.5	7.6
Mean±SD	19.5±2.1	6.4±0.4	2.7±0.4	2.3±0.2	1.7±0.3	6.6±0.7	1.9±0.1	2.6±0.2	1.2±0.1	11.1±0.6	8.5±0.9
Range	17.8–23.0	5.8–6.9	2.2–3.1	2.0–2.5	1.2–2.1	5.6–7.2	1.7–2.1	2.4–2.8	1.0–1.3	10.5–11.9	7.6–9.9

Table 3 continued. Measurements of the type series of *Microhyla pineticola* and *M. neglecta* sp. nov.; H, holotype; Continue on next page.

	HAL	1FL	IPTL	OPTL	3FDD	HLL	TL	FL	IMTL	1TOEL	OMTL	4TDD
Microhyla pineticola s. str.												
males												
1. ZMMU-A5080	4.5	0.9	0.6	0.9	0.6	30.0	10.1	10.3	0.7	1.9	0.5	0.7
2. ZMMU-A6029	4.4	0.9	0.6	0.8	0.6	30.8	11.1	10.4	0.7	1.7	0.5	0.8
3. ZMMU-A4331	4.2	1.0	0.5	0.7	0.5	31.6	12.0	10.5	0.7	1.4	0.5	0.9
Mean±SD	4.4±0.1	0.9±0.1	0.5±0.1	0.8±0.1	0.5±0.1	30.8±0.8	11.1±1.0	10.4±0.1	0.7±0.0	1.6±0.2	0.5±0.0	0.8±0.1
Range	4.2–4.5	0.9–1.0	0.5–0.6	0.7–0.9	0.5–0.6	30.0–31.6	10.1–12.0	10.3–10.5	0.7–0.7	1.4–1.9	0.5–0.5	0.7–0.9
females												
4. ZMMU-A4331	5.2	1.0	0.6	0.9	0.6	34.5	12.8	12.2	0.8	2.1	0.6	0.9
5. ZMMU-A5043[H]	5.4	1.3	0.8	1.0	0.8	35.6	12.7	12.9	0.9	2.2	0.8	1.1
6. ZMMU-A7296	5.5	1.2	0.9	1.1	0.7	36.3	13.3	12.1	1.0	2.0	0.5	1.0
Mean±SD	5.4±0.1	1.2±0.1	0.8±0.2	1.0±0.1	0.7±0.1	35.5±0.9	12.9±0.3	12.4±0.5	0.9±0.1	2.1±0.1	0.6±0.2	1.0±0.1
Range	5.2–5.5	1.0–1.3	0.6–0.9	0.9–1.1	0.6–0.8	34.5–36.3	12.7–13.3	12.1–12.9	0.8–1.0	2.3–2.2	0.5–0.8	0.9–1.1
Microhyla neglecta sp. nov.												
males												
1. ZMMU-A7297	5.0	1.2	0.5	0.7	0.4	33.6	11.1	11.3	0.7	1.7	0.5	0.8
2. ZMMU-A7298	4.5	1.1	0.6	0.9	0.4	32.6	11.2	11.7	1.0	1.8	0.6	0.8
3. ZMMU-A7299	4.9	1.1	0.6	1.0	0.5	35.4	11.7	11.4	0.8	2.0	0.5	0.8
4. ZMMU-A7300	4.8	1.2	0.7	0.8	0.5	34.8	11.5	11.7	0.9	1.9	0.7	0.7
5. ZMMU-A7301	5.0	1.0	0.7	1.0	0.6	32.6	11.1	11.6	0.7	1.8	0.5	0.7
6. ZMMU-A7302	4.7	1.3	0.8	1.0	0.4	34.0	11.2	11.5	0.7	1.8	0.4	0.8
7. ZMMU-A7303[H]	4.4	1.0	0.6	0.8	0.4	32.6	11.0	10.8	0.6	1.7	0.5	0.7
8. ZMMU-A7304	4.3	0.9	0.7	0.9	0.4	32.2	11.4	10.6	0.7	1.7	0.6	0.8
9. ZMMU-A7305	4.6	1.1	0.6	0.7	0.5	32.1	11.2	11.3	0.9	1.8	0.7	0.9
10. ZMMU-A7306	4.2	0.9	0.5	0.8	0.4	32.0	11.1	10.2	0.7	1.3	0.4	0.8
Mean±SD	4.6±0.3	1.1±0.1	0.6±0.1	0.8±0.1	0.4±0.1	33.2±1.2	11.3±0.2	11.2±0.5	0.8±0.1	1.7±0.2	0.5±0.1	0.8±0.1
Range	4.2–5.0	0.9–1.3	0.5–0.8	0.7–1.0	0.4–0.6	32.0–35.4	11.0–11.7	10.2–11.7	0.6–1.0	1.3–2.0	0.4–0.7	0.7–0.9
females												
11. ZMMU-A7307	5.3	1.3	0.8	0.9	0.6	37.6	14.4	13.6	0.8	2.4	0.6	1.2
12. ZMMU-A7308	4.9	1.2	0.9	1.0	0.5	37.5	11.6	11.3	0.7	1.6	0.5	1.1
13. ZMMU-A7309	5.0	1.4	0.6	0.9	0.5	36.5	13.4	11.8	0.7	1.8	0.6	0.7
14. ZMMU-A7310	4.8	1.2	0.8	1.0	0.4	34.2	11.5	12.1	0.8	2.0	0.4	0.9
15. ZMMU-A7311	4.5	1.2	0.6	0.8	0.5	31.4	10.7	10.2	0.8	1.7	0.8	0.8
Mean±SD	4.9±0.3	1.2±0.1	0.7±0.1	0.9±0.1	0.5±0.1	35.5±2.7	12.3±1.5	11.8±1.3	0.8±0.1	1.9±0.3	0.6±0.1	0.9±0.2
Range	4.5–5.3	1.2–1.4	0.6–0.9	0.8–1.0	0.4–0.6	31.4–37.6	10.7–14.4	10.2–13.6	0.7–0.8	1.6–2.4	0.4–0.8	0.7–1.2

Table 4. Morphological comparison between *Microhyla neglecta* sp. nov with 52 currently recognized species of genus *Microhyla*. Members of the *M. achatina* species group are highlighted; ? = no data.

Species	**SVL (males)**	**SVL (females)**	**Body habit**	**Snout in lateral profile**
***M. neglecta* sp. nov.**	17.2–19.5	17.8–23.0	Moderately slender	Acuminate
M. achatina	21.7–24.3	20.6–28.0	Slender	Obtusely pointed
M. annamensis	15.2–19.8	18.2–22.6	Moderately stocky	Bluntly rounded
M. annectens	14.4–15.6	18.2–18.4	Slender	Rounded
M. arboricola	13.2–15.0	15.9–17.0	Moderately slender	Pointed
M. aurantiventris	25.2–27.0	30.5	Moderately stocky	Rounded
M. beilunensis	19.1–23.7	26.4–28.3	Moderately slender	Bluntly rounded
M. berdmorei	23.8–32.5	26.2–45.6	Slender	Obtusely pointed
M. borneensis	11–13	18–19	Stocky	Obtusely pointed
M. butleri	20.0–25.0	21.0–26.0	Slender	Rounded
M. chakrapanii	22	?	Moderately stout	Obtusely rounded
M. darevskii	27.0–32.6	?	Stocky, flattened	Rounded
M. darreli	15.0–15.7	?	Rather slender	Sub ovoid
M. eos	21.5	26.9–27.8	Stout	Rounded
M. fanjingshanensis	19.0–22.7	22.5–23.0	Slender	Rounded
M. fissipes	18.0–27.5	20.0–28.0	Moderately slender	Rounded
M. fodiens	20.1–29.1	20.0–30.0	Stout	Rounded
M. gadjahmadai	18.2–21.3	20.4–25.5	Stout	Rounded
M. heymonsi	16.5–22.0	18.0–26.5	Stocky	Obtusely pointed
M. hongiaoensis	13.6–14.7	18.3–18.6	Slender	Bluntly rounded
M. irrawaddy	12.3–17.1	16.7–20.9	Very slender	Acuminate
M. karunaratnei	15.8–19.1	19.6–21.0	Moderately stocky	Rounded
M. kodial	16.9–17.4	18.0–20.4	Slender	Rounded
M. kuramotoi	23.8–27.8	28.8–34.6	Moderately slender	Rounded
M. laterite	15.3–16.6	18.4	very small sized	Obtuse
M. maculifera	12.0–13.3	11.8	Moderately stout	Bluntly rounded
M. malang	18.7–22.2	19.0–23.4	Stocky	Rounded
M. mantheyi	15.0–29.2	14.8–24.1	Stocky	Pointed
M. marmorata	18.8–21.5	21.1–23.2	Moderately stocky	Bluntly rounded
M. mihintalei	21.7–27.3	24.4	Slender	Sub-ovoid
M. minuta	14.7–15.9	15.7–17.2	Slender	Bluntly rounded
M. mixtura	18.8–25.2	24.8–26.2	Stout	Rounded
M. mukhlesuri	16.5–21.0	17.3–18.4	Moderately slender	Rounded
M. mymensinghensis	14.2–17.6	15.2–21.3	Stocky	Truncated
M. nanapollexa	13.5	16.6	Slender	Rounded
M. nepenthicola	10.6–12.8	177.9–18.8	Slender	Obtusely pointed
M. nilphamariensis	14.8–20.0	18.7–21.0	Stout	Rounded
M. okinavensis	20.8–25.6	26.5–30.8	Moderately slender	Rounded
M. orientalis	15.8–17.4	15.8–17.4	Moderately slender	Rounded
M. ornata	13.4–24.9	24.9–26.2	Moderately slender	Rounded
M. palmipes	16	21.8	Slender	Rounded
M. perparva	10.5–11.9	12.4–14.5	Moderate	Obtusely pointed
M. petrigena	13.9–16.2	15.1–17.8	Moderately stout	Obtusely pointed
M. picta	25.2–30.1	27.2–33.4	Stout	Rounded
***M. pineticola* s. str.**	17.4–18.6	20.0–22.3	Stocky	Rounded
M. pulchella	14.7–21.6	18.1–25.8	Moderately stocky	Bluntly rounded
M. pulchra	23.0–32.0	28.0–36.5	Stocky	Obtusely pointed
M. rubra	20.0–27.5	20.5–29.5	Stout	Rounded
M. sholigari	15.9–16.2	15.9–19.2	Moderately slender	Truncated
M. superciliaris	12.7	12	Slender	Rounded
M. taraiensis	19.9–20.9	22.1–24.9	Stout	Rounded
M. tetrix	10.1–13.7	15.2–17.6	Slender	Rounded
M. zeylanica	14.4–18.3	15.8–20.0	Moderately slender	Rounded

Table 4 continued. Morphological comparison between *Microhyla neglecta* sp. nov with 52 currently recognized species of genus *Microhyla*. Members of the *M. achatina* species group are highlighted; ? = no data.

Species	Skin on dorsum	F1 *vs* F2	Disks on distal end of fingers
***M. neglecta* sp. nov.**	Smooth with few tubercles	F1>½F2	present
M. achatina	Smooth or feebly tubercular	F1<½F2	present
M. annamensis	Warty, strongly tubercular	F1<½F2	present
M. annectens	Smooth	F1<½F2	present
M. arboricola	Feebly granular	F1<½F2	present
M. aurantiventris	Shagreened, tiny tubercles	F1>½F2	present
M. beilunensis	Smooth, small tubercles	F1<½F2	present (weak)
M. berdmorei	Smooth, small tubercles	F1<½F2	present (weak)
M. borneensis	Smooth, small tubercles	nub / bulge	weak / absent
M. butleri	Smooth or tubercular	F1>½F2	present (weak)
M. chakrapanii	Smooth	F1>½F2	absent
M. darevskii	Slightly tubercular or pustulate	F1>½F2	absent
M. darreli	Shagreened to sparsely granular	F1>½F2	present (weak)
M. eos	Smooth to shagreened	?	present
M. fanjingshanensis	Roughish with tiny tubercles	F1>½F2	absent
M. fissipes	Smooth or slightly tubercular	F1>½F2	absent
M. fodiens	Feebly tubercular	F1<½F2	absent
M. gadjahmadai	Low tubercles	F1>½F2	present (weak)
M. heymonsi	Smooth	F1≤½F2	present
M. hongiaoensis	Low tubercles	F1<½F2	present
M. irrawaddy	Granular	F1>½F2	present
M. karunaratnei	Smooth	F1>½F2	present
M. kodial	Tuberculated	F1>½F2	present
M. kuramotoi	Smooth or slightly tubercular	F1≤½F2	absent
M. laterite	Smooth	F1>½F2	present
M. maculifera	Tuberculated	F1>½F2	absent
M. malang	Smooth	F1<½F2	present
M. mantheyi	Granular, feebly pustular	F1<½F2	present
M. marmorata	Smooth or feebly pustular	F1<½F2	present
M. mihintalei	Smooth	F1≤½F2	absent
M. minuta	Granular, feebly pustular	F1≤½F2	present
M. mixtura	Smooth, with tubercles	F1<½F2	present (weak)
M. mukhlesuri	Smooth	F1>½F2	absent
M. mymensinghensis	Smooth	F1>½F2	absent
M. nanapollexa	Smooth	nub / bulge	present
M. nepenthicola	Smooth, small tubercles	nub / bulge	weak / absent
M. nilphamariensis	Smooth	F1>½F2	absent
M. okinavensis	Smooth or slightly tubercular	F1≤½F2	absent
M. orientalis	Smooth or slightly tubercular	F1<½F2	weak
M. ornata	Smooth or slightly tubercular	F1≤½F2	absent
M. palmipes	Smooth or slightly tubercular	nub / bulge	present
M. perparva	Smooth	nub / bulge	present
M. petrigena	Smooth, tubercles posteriorly	nub / bulge	present
M. picta	Smooth or slightly warty	F1<½F2	absent
***M. pineticola* s. str.**	Feebly granular	F1≤½F2	present
M. pulchella	Smooth	F1<½F2	present
M. pulchra	Smooth, feebly granular	F1<½F2	absent
M. rubra	Smooth, feebly tuberculated	F1 ≤½F2	absent
M. sholigari	Smooth	F1>½F2	present
M. superciliaris	Smooth	F1<½F2	present
M. taraiensis	granular	F1>½F2	absent
M. tetrix	Smooth	F1=½F2	present
M. zeylanica	Smooth or slightly tubercular	F1>½F2	absent

Table 4 continued. Morphological comparison between *Microhyla neglecta* sp. nov with 52 currently recognized species of genus *Microhyla*. Members of the *M. achatina* species group are highlighted; ? = no data.

Species	Median longitudinal grooves on dorsal finger disks	Disks at the distal end of toes	Dorsal peripheral grooves on toe disks	metatarsal tubercles	Superciliary tubercles
***M. neglecta* sp. nov.**	present	present	present (weak)	2	absent
M. achatina	present	present	present	2	absent
M. annamensis	present	present	present	2	absent
M. annectens	present	present	present	1	absent
M. arboricola	present (weak)	present	present	1	absent
M. aurantiventris	present (weak)	present	present	2	absent
M. beilunensis	absent	present	present	2	absent
M. berdmorei	present	present	present	2	absent
M. borneensis	present	present	present	2	absent
M. butleri	present	present	present	2	absent
M. chakrapanii	absent	present	absent	2	absent
M. darevskii	absent	weak	present	2	absent
M. darreli	absent	present (weak)	present	2	absent
M. eos	absent	present	present	2	absent
M. fanjingshanensis	absent	present	present	2	absent
M. fissipes	absent	absent	absent	2	absent
M. fodiens	absent	absent	absent	2	absent
M. gadjahmadai	present	present	present	2	absent
M. heymonsi	present	present	present	2	absent
M. hongiaoensis	absent	present	present (weak)	2	absent
M. irrawaddy	absent	absent	present (weak)	?	absent
M. karunaratnei	present	present	present	2	absent
M. kodial	absent	present	absent	2	absent
M. kuramotoi	absent	absent	absent	2	absent
M. laterite	present	present	present	2	present
M. maculifera	absent	present (weak)	absent	1	absent
M. malang	present	present	present	2	absent
M. mantheyi	present	present	present	2	absent
M. marmorata	present	present	present	2	absent
M. mihintalei	absent	absent	absent	2	present
M. minuta	present (weak)	present	present	2	absent
M. mixtura	absent	present	present	2	absent
M. mukhlesuri	absent	absent	absent	2	absent
M. mymensinghensis	absent	absent	absent	2	absent
M. nanapollexa	present	present	present	1	absent
M. nepenthicola	present	present	present	2	absent
M. nilphamariensis	absent	absent	absent	2	absent
M. okinavensis	absent	absent	absent	2	absent
M. orientalis	present	present	present	2	absent
M. ornata	absent	absent	absent	2	absent
M. palmipes	absent	present	absent	2	absent
M. perparva	absent	present	present	1	present
M. petrigena	present (weak)	present	present	1	absent
M. picta	absent	absent	absent	2	absent
***M. pineticola* s. str.**	present	present	present (weak)	2	absent
M. pulchella	present (weak)	present	present (weak)	1 (2)	absent
M. pulchra	absent	absent	absent	2	absent
M. rubra	absent	absent	absent	2	absent
M. sholigari	absent	present	present	2	absent
M. superciliaris	absent	present	present (weak)	2	present
M. taraiensis	absent	absent	absent	2	absent
M. tetrix	absent	present	present (weak)	2	absent
M. zeylanica	absent	present	absent	2	absent

Table 4 continued. Morphological comparison between *Microhyla neglecta* sp. nov with 52 currently recognized species of genus *Microhyla*. Members of the *M. achatina* species group are highlighted; ? = no data.

Species	Light dorsomedial (vertebral) line	Tibiotarsal articulation reaches	Toe webbing formula
***M. neglecta* sp. nov.**	present	Well beyond snout	I1½-2½II1¾-3III2¾-3¾IV3¾-2½V
M. achatina	present	To snout or just beyond	I2-2½II2-3¼III3-4IV 4- 3V
M. annamensis	absent	Well beyond snout	I1-2¼II1-2½III1½-2¾IV3-1V
M. annectens	absent	Well beyond eye	I1-1II1-1III1-3IV3-1V
M. arboricola	absent	Well beyond snout	I1⅔-2¼II2-3III2½-3½IV3-1½V
M. aurantiventris	absent	Slightly beyond snout	I1¾-2II1½-2¾III2-3⅓IV3¼-1½V
M. beilunensis	absent	To the eye	Basal
M. berdmorei	absent	Well beyond snout	I1-1II1-2III1-2IV2-1V
M. borneensis	absent	Shorter than snout	I1-2II1-3III2½-3⅓IV3½-2V
M. butleri	absent	Shorter than snout	I2-2½II1¾-3III2⅓-3½IV3½-2¼V
M. chakrapanii	absent	Beyond snout (?)	Basal
M. darevskii	absent	Well beyond snout	I1-1II1-1III1-1IV1-1V
M. darreli	absent	Shorter than eye	I2-2¼II1¾ -3III2-3IV3-2¼V
M. eos	absent	?	I1½-2^+II1⅔-3^-III2½-IV4^--1½V
M. fanjingshanensis	present	Between eye to nostril	Basal
M. fissipes	absent	Shorter than snout	I2-2½II2-3½III3-4IV4-3V
M. fodiens	absent	Shorter than eye	I1-2II1¾-3III2¾-3¾IV 4-2¾V
M. gadjahmadai	present	Well beyond snout	I2-2¼II1¾-3III3-4IV4-2¾V
M. heymonsi	present	Shorter than snout	I2-2½II2-3III3-4IV4⅓-3V
M. hongiaoensis	absent	Well beyond snout	I1-2II1-2½III1-2½IV2½-1V
M. irrawaddy	absent	To the eye	I2-3II2-3III3-4½IV4½-2¾V
M. karunaratnei	absent	Beyond snout (?)	I2-2½ II2-3½ III2½-3¾IV4-2V
M. kodial	absent	Well beyond snout	Basal
M. kuramotoi	absent	To the eye	I2-2II2-3III3-4IV4-2⅘V
M. laterite	absent	Well beyond snout	I1-2II1-2III1⅔-2IV3-1V
M. maculifera	absent	To snout or just beyond	Basal
M. malang	absent	To snout or just beyond	I1-2II1-2⅔III1⅔-3IV3-1V
M. mantheyi	absent	Well beyond snout	I1-2II1-2III2-3IV3-1½V
M. marmorata	absent	Well beyond snout	I1-2II1-1¾III1½-2¾IV2¾-1V
M. mihintalei	absent	To snout	Basal
M. minuta	absent	Shorter than snout	In.a.-n.a.II2-3½III3-4IV4-3V
M. mixtura	absent	Shorter than snout	I2-2½II1¾-3¼III3-4IV4¼-2¾V
M. mukhlesuri	absent	To snout	I2-2½II2-3½III3-4IV4-2¾V
M. mymensinghensis	absent	To snout	I2-2½II2-3½III3-4IV4¼-2¾V
M. nanapollexa	absent	Well beyond snout	I1-2II1-2½III2½-2½IV2½-1V
M. nepenthicola	absent	Shorter than snout	?
M. nilphamariensis	absent	To snout	Basal
M. okinavensis	absent	Beyond eye	I1½-2II1½-3¼III2¾-4IV4-2½V
M. orientalis	present	To the eye	In.a.-n.a.II2-3¼III3-4¼IV4¼-3V
M. ornata	absent	Shorter than snout	I2-2½II1¾-3½III3-4IV4-2¾V
M. palmipes	absent	To snout or just beyond	In.a.-n.a.II2⅓-3¾III3¼-4IV4-3V
M. perparva	absent	Well beyond snout	I1-1II1-1III1-2IV2-1V
M. petrigena	absent	Well beyond snout	I1-1II1-1III1-2IV2-1V
M. picta	absent	Shorter than eye	I2-2¾II1¾-2¾III2¾-3¾IV4-2½V
***M. pineticola* s. str.**	present	Shorter than snout	I1½-2½II1¾-3III2¾-3¾IV4-2½V
M. pulchella	absent	Well beyond snout	I1½-2II1-2III1-2½IV2¼-1V
M. pulchra	absent	To snout or just beyond	I1½-2II1-3III2-3¼IV3½-2V
M. rubra	absent	Shorter than snout	I1½-2II1½-3III2½-3IV4-2½V
M. sholigari	present	Shorter than snout	I1½-2II2½-3½III2½-3½IV3¾-2V
M. superciliaris	absent	To snout or just beyond	I1-1II1-1III1-2IV2-1V
M. taraiensis	absent	To the snout	I2-3II2¾-3¾III3-4¼IV4-2¾V
M. tetrix	absent	Well beyond snout	I1-2II1-2III1-2½IV2½-1V
M. zeylanica	absent	To the eye	I2-2¼II1¾-3½III2¼-3¾IV4-2V

Table 4 continued. Morphological comparison between *Microhyla neglecta* sp. nov with 52 currently recognized species of genus *Microhyla*. Members of the *M. achatina* species group are highlighted; ? = no data.

Species	Distribution	Sources
***M. neglecta* sp. nov.**	Vietnam (Langbian pl.)	our data
M. achatina	Indonesia (Java)	Poyarkov *et al.* 2014; Atmaja *et al.* 2018
M. annamensis	Vietnam (Langbian pl.)	Poyarkov *et al.* 2014; our data
M. annectens	Thailand, Malaysia	Parker 1928; Poyarkov *et al.* 2014; our data
M. arboricola	Vietnam (Langbian pl.)	Poyarkov *et al.* 2014
M. aurantiventris	Vietnam (Kon Tum pl.)	Nguyen *et al.* 2019
M. beilunensis	China	Zhang *et al.* 2018
M. berdmorei	Indo-Burma and Sundaland	Poyarkov *et al.* 2014; Garg *et al.* 2018; our data
M. borneensis	Malaysia (Borneo)	Das & Haas 2010; Matsui 2011
M. butleri	Indo-Burma and Sundaland	Poyarkov *et al.* 2014, 2020a; our data
M. chakrapanii	India (Andamans)	Pilayi 1977
M. darevskii	Vietnam (Kon Tum pl.)	Poyarkov *et al.* 2014; our data
M. darreli	India	Garg *et al.* 2018
M. eos	India	Biju *et al.* 2019
M. fanjingshanensis	China	Li *et al.* 2019
M. fissipes	China, Vietnam	Poyarkov *et al.* 2014; Garg *et al.* 2018; our data
M. fodiens	Myanmar	Poyarkov *et al.* 2019
M. gadjahmadai	Indonesia (Sumatra)	Atmaja *et al.* 2018
M. heymonsi	Indo-Burma and Sundaland	Poyarkov *et al.* 2014; Garg *et al.* 2018; our data
M. hongiaoensis	Vietnam (Langbian pl.)	Hoang *et al.* 2020
M. irrawaddy	Myanmar	Poyarkov *et al.* 2019
M. karunaratnei	Sri Lanka	Garg *et al.* 2018
M. kodial	India	Vineeth *et al.* 2018
M. kuramotoi	Japan (Yaeyama)	Matsui & Tomiaga 2020
M. laterite	India	Seshadri *et al.* 2016
M. maculifera	Malaysia (Borneo)	Poyarkov *et al.* 2014; our data
M. malang	Malaysia (Borneo)	Matsui 2011
M. mantheyi	Thailand, Malaysia, Singapore	Das *et al.* 2007; our data
M. marmorata	Vietnam, Laos	Bain & Nguyen 2004; our data
M. mihintalei	Sri Lanka	Wijayathilaka *et al.* 2016; Garg *et al.* 2018
M. minuta	Vietnam (Langbian pl.)	Poyarkov *et al.* 2014; our data
M. mixtura	China	Poyarkov *et al.* 2014; Zhang *et al.* 2018
M. mukhlesuri	Bangladesh, Myanmar, Indochina, Thailand	Hasan *et al.* 2014; Garg *et al.* 2018; our study
M. mymensinghensis	Bangladesh, India	Hasan *et al.* 2014; Garg *et al.* 2018
M. nanapollexa	Vietnam (Kon Tum pl.)	Bain & Nguyen, 2004; our data
M. nepenthicola	Malaysia (Borneo)	Das & Haas 2010; Matsui 2011
M. nilphamariensis	Bangladesh, Nepal, India, Pakistan	Howlader *et al.* 2015; Garg *et al.* 2018
M. okinavensis	Japan (Miyako, Okinawa, Amami)	Matsui & Tomiaga 2020
M. orientalis	Indonesia	Matsui *et al.* 2013
M. ornata	Sri Lanka, India	Poyarkov *et al.* 2014; Garg *et al.* 2018
M. palmipes	Indonesia (Sumatra, Nias, Java, Bali)	Poyarkov *et al.* 2014
M. perparva	Malaysia (Borneo)	Poyarkov *et al.* 2014; Inger *et al.* 2017
M. petrigena	Malaysia (Borneo)	Poyarkov *et al.* 2014; Inger *et al.* 2017
M. picta	Vietnam (Low central-souther)	Poyarkov *et al.* 2014; our data
***M. pineticola* s. str.**	Vietnam (Langbian pl.)	Poyarkov *et al.* 2014; our data
M. pulchella	Vietnam (Langbian pl.)	Poyarkov *et al.* 2014
M. pulchra	China, Indochina, Thailand	Poyarkov *et al.* 2014; our data
M. rubra	India	Poyarkov *et al.* 2014; Garg *et al* 2018
M. sholigari	India	Dutta & Ray 2000; Garg *et al.* 2018
M. superciliaris	Thailand, Malaysia, Indonesia	Poyarkov *et al.* 2014, 2020b
M. taraiensis	Nepal	Khatiwada *et al.* 2017; Garg *et al.* 2018
M. tetrix	Thailand	Poyarkov *et al.* 2020b
M. zeylanica	Sri Lanka	Poyarkov *et al.* 2014; Garg *et al.* 2018

Discussion

In this paper we report on a new species of the genus *Microhyla* discovered from the montane forests of Langbian Plateau, southern Vietnam. This discovery underscores the high degree of site-specific endemism in isolated montane regions within the Truong Son, or Annamite mountains (e.g. Orlov *et al.* 2012, Hartmann *et al.* 2013, Geissler *et al.* 2015a–b, Chen *et al.* 2018, Nguyen *et al.* 2018, 2019, Poyarkov *et al.* 2017, 2019b). The Langbian Plateau is widely recognized as the centre of herpetofaunal endemism and diversity in Indochina (e.g. Poyarkov & Vassilieva 2011, Nazarov *et al.* 2012, Vassilieva *et al.* 2014, Poyarkov *et al.* 2014, 2015a, 2015b, 2017, 2018, 2019b, Duong *et al.* 2018, Pauwels *et al.* 2018). Our discovery of *M. neglecta* brings the total number of species in the genus in Vietnam to 17, with the greatest species diversity and highest degree of local endemism occurring in the Central Highlands—also known as Tay Nguyen Region—that encompass the Kon Tum and Langbian plateaus. Based on the recent progress in *Microhyla* taxonomy in Vietnam (Poyarkov *et al.* 2014, Hoang *et al.* 2020, and this study), up to 12 sympatric species of *Microhyla* are known to co-occur in the montane forests of the Langbian Plateau and its surrounding areas, many of which can be recorded in the same biotope. This is the highest known species density for the genus *Microhyla* in the world, which further highlights the importance of the Langbian Plateau for the evolution and ecological differentiation in this group of frogs (for discussion see Gorin *et al.* 2020).

The present description of *M. neglecta* is especially interesting as it was confused with its morphologically similar cryptic sister species *M. pineticola* for more than 10 years. In their review, Poyarkov *et al.* (2014) relied exclusively on morphological characters which they used to distinguish "*M. pineticola*" *sensu lato* from the morphologically similar widespread species *M. heymonsi*. They reported a significant variation in colouration, pattern, and morphometrics within the type series of *M. pineticola*, but due to the lack of genetic data and sympatric co-occurrence of the two species, they misinterpreted it as a high degree of intraspecific variability (Poyarkov *et al.* 2014: 100–111). The integrative taxonomic analysis of the material reported by Poyarkov *et al.* (2014) and the newly collected samples have demonstrated that the diversity hidden within the name "*M. pineticola*" was overlooked. Such situations are rare, but occasionally happen in taxonomic practice. For example, when first discovered, the specimens of a small-sized gecko species *Cnemaspis pseudomcguirei* Grismer, Ahmad, Chan *et al.*, 2009 were confused with juveniles of a larger sympatric species *C. mcguirei* Grismer, Wood & Chan, 2008 (Grismer *et al.* 2008, 2009). This underscores the key importance of integrative approaches, including molecular data for any taxonomic revision. Not only is this paramount for any downstream analyses, it is now also recognized as a cornerstone of biodiversity conservation (Shaffer *et al.* 2015). We further stress that in the age of biodiversity crises and molecular genetics, the systematic collection of tissue samples and application of molecular methods is crucial for taxonomic practice in studies of herpetofaunal diversity in Southeast Asia (Smith *et al.* 2008, Murphy *et al.* 2013, Chomdej *et al.* 2020).

In our study we report on two morphologically highly similar (cryptic) species of *Microhyla* frogs, which co-occur sympatrically within their narrow distribution area restricted to the Langbian Plateau of southern Vietnam. Moreover, our phylogenetic analyses have demonstrated that these two cryptic taxa *M. pineticola* and *M. neglecta* are sister species and their age of divergence likely corresponds to middle Miocene (see Gorin *et al.* 2020). The miniaturized body size of these species (SVL below 23 mm), along with the microendemic pattern of their distribution, suggest that the non-allopatric scenarios for their speciation have to be considered in future (see Wollenberg *et al.* 2011). Though allopatric speciation has been considered the main process leading to species diversity (Mayr 1982), a number of studies demonstrated that species formation may occur in parapatric or sympatric settings as well (Via 2001, 2009, Seehausen *et al.* 2008). In amphibians, sympatric scenarios of speciation have only been rarely discussed (see Steinfartz *et al.* 2007, Vences & Wake 2007, Wollenberg *et al.* 2011, Vences *et al.* 2012). The statistical analysis by Wollenberg *et al.* (2011) suggested that microendemic species of miniaturized frogs tend to speciate more readily and may reject the predominance of allopatric speciation. Interestingly enough, the Langbian Plateau provides further examples of sympatric co-occurrence of sister species in amphibians, such as *Microhyla pulchella* and *M.*

hongiaoensis (Poyarkov *et al.* 2014, Hoang *et al.* 2020), and *Ophryophryne gerti* (Ohler, 2003) and *O. elfina* Poyarkov, Duong, Orlov *et al*. 2017 (Megophryidae; see Poyarkov *et al.* 2017). We recommend that future studies on adaptive speciation and diversification in amphibians should target the Langbian Plateau, as additional pairs of diverging populations and cryptic species are likely to be found, providing further evidence for the possibility of non-allopatric adaptive speciation in the amphibians in this area or a shared historical environmental history resulting in co-occurring speciation events.

Despite the recent increase in species discoveries, many areas of the Annamites have received comparatively little scientific attention and are very likely to harbour additional, previously unknown species (Poyarkov *et al.* 2014). The need for biological exploration in this region is made more urgent given the ongoing loss of natural habitats due to logging, road construction, increasing agricultural pressure and other human activities (Meijer 1973, De Koninck 1999, Laurance 2007, Meyfroidt & Lambin 2008, Kuznetsov & Kuznetsova 2011).

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