Supplementary Materials Supplementary Methods

Molecular analyses

Total genomic DNA was extracted from liver tissues. Tissue samples were digested using proteinase K, and subsequently purified following standard phenol/chloroform isolation and ethanol precipitation. Fragments encoding partial 16S rRNA (16S) and cytochrome c oxidase subunit I (COI) genes were amplified using primer pairs 16Sar/16Sbr (Palumbi et al., 1991) and Chmf4/Chmr4 (Che et al., 2012), respectively. Polymerase chain reaction (PCR) amplifications were performed in 50 µL reactions using the following cycling conditions: initial denaturing step at 95 °C for 4 min; 35 cycles of denaturing at 94 °C for 60 s, annealing at 46-51 °C for 60 s (46 °C for COI and 51 °C for 16S), and extending at 72 °C for 60 s; and a final extension step of 72 °C for 10 min. Sequencing was conducted directly using the corresponding PCR primers. All new sequences were deposited in GenBank under accession Nos. MT509809, MT509810, and MT522176 (Supplementary Table S1). Available homologous sequences of members of Theloderma were obtained from GenBank (Supplementary Table S1). Four rhacophorid species were selected as outgroups according to Qi et al. (2018) and their sequences were also downloaded from GenBank.

Sequences were aligned using MUSCLE with default parameters in MEGA 7 (Kumar et al., 2016). Uncorrected pairwise distances between species were calculated in MEGA 7. The best substitution models of *16S* and *COI* were selected using the corrected Akaike Information Criterion (AICc) in jMODELTEST v2.1.10 (Darriba et al., 2012). Bayesian inferences were performed in MRBAYES v3.2.6 (Ronquist et al., 2012) under the selected substitution models for *16S* (TIM2 + I + G) and *COI* (TIM2 + I + G). Two runs were performed simultaneously with four Markov chains starting from random tree. The chains were run for 3 000 000 generations and sampled every 100 generations. The first 25% of the sampled tree was discarded as burn-in after the standard deviation of split frequencies of the two runs was less than 0.01. The remaining trees were then used to create a consensus tree and to estimate Bayesian

posterior probabilities (BPPs).

Morphology

Measurements were taken with a digital caliper to the nearest 0.1 mm. Morphological terminology followed Fei et al. (2009). Measurements included: snout-vent length (SVL, from tip of snout to vent); head length (HL, from tip of snout to rear of jaw); head width (HW, width of head at widest point); snout length (SL, from tip of snout to anterior border of eye); internarial distance (IND, distance between nares); interorbital distance (IOD, minimum distance between upper eyelids); upper eyelid width (UEW, maximum width of upper eyelid); eye diameter (ED, diameter of exposed portion of eyeball); tympanum diameter (TD, greater of tympanum vertical and horizontal diameters); distance from nostril to eye (DNE, from nostril to anterior border of eye); forearm and hand length (FHL, from elbow to tip of third finger); tibia length (TL, distance from knee to heel); foot length (FL, from proximal end of inner metatarsal tubercle to tip of fourth toe); and length of foot and tarsus (TFL, distance from tibiotarsal joint to tip of fourth toe). Webbing formula followed Myers & Duellman (1982).

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Species	Voucher	Locality	16S	COI
Buergeria oxycephala	MVZ 230425	Hainan, China	KU244359	KU244459
Nyctixalus pictus	MVZ 239460	Bengkulu, Indonesia	KU561880	-
Gracixalus jinxiuensis	KIZ 0612210YP	Guangxi, China	EU215525	-
Liuixalus hainanus	LJT V15	Hainan, China	KC465826	-
Theloderma albopunctatum	Tal	Kon Tum, Vietnam	KT461884	-
Theloderma albopunctatum	VNMN JR2887	Tam Dao, Vinh Phuc, Vietnam	KU244375	KU244431
Theloderma annae	IEBR 3732	Hoa Binh, Vietnam	LC168170	-
Theloderma asperum	ZRC 1.1.9321	Fraser Hill, Malaysia	GQ204725	-
Theloderma auratum	ZMMU NAP 064022	Kon Tum, Vietnam	MG917772	-
Theloderma baibengense	YPX 31940	Motuo, Xizang, China	KU981089	-
Theloderma baibengense	YPX37270	Motuo, Xizang, China	KU243080	-
Theloderma bicolor	YPX31244	Jingdong, Yunnan, China	KY495634	-
Theloderma corticale	MVZ 223905	Tam Dao, Vinh Phuc, Vietnam	KU244364	KU244452
Theloderma gordoni	MVZ 226469	Tam Dao, Vinh Phuc, Vietnam	KU244363	KU244451
Theloderma horridum	KUHE 52582	Negeri Sembilan, Malaysia	LC012861	-
Theloderma lacustrinum	NCSM 84682	Vientiane, Laos	KX095245	-
Theloderma laeve	VNMN 4403	Gia Lai, Vietnam	LC012846	-
Theloderma lateriticum	VNMN 1216	Tay Yen Tu, Bac Giang, Vietnam	LC012851	-
Theloderma leporosum	LJT W46	Malaysia	KC465841	-
Theloderma licin	MVZ 9458	Indonesia	KU244368	KU244447
Theloderma moloch	YPX 31941	Motuo, Xizang, China	KU243081	-
Theloderma moloch	GXNU YU000115	Yingjiang, Yunnan, China	MT509809	-
Theloderma nebulosum	ROM 39588	Kon Tum, Vietnam	LC012845	-
Theloderma palliatum	NAP02516	Lam Dong, Vietnam	KT461895	-
Theloderma petilum	HNUE MNA.2012.0001	Dien Bien, Vietnam	KJ802925	-
Theloderma phrynoderma	CAS247910	Tanintharyi, Myanmar	KJ128283	KU244449
Theloderma rhododiscus	CIB GX200807017	Guangxi, China	LC012842	-
Theloderma ryabovi	VNMN 3924	Kon Tum, Vietnam	LC012860	-
Theloderma stellatum	ZMMU NAP 03961	Nakhonnayok, Thailand	KT461917	-
Theloderma truongsonense	VNMN 4402	Khanh Hoa, Vietnam	LC012847	-
Theloderma vietnamense	AMS R174047	Mondol Kiri, Cambodia	JN688171	KU244460
Theloderma pyaukkya	CAS 226113	Putao District, Kachin, Myanmar	KU244361	KU244443
Theloderma pyaukkya	CAS 236133	Mohynyin Township, Kachin, Myanmar	KU244360	KU244444
Theloderma pyaukkya	GXNU YU000116	Yingjiang, Yunnan, China	MT509810	MT522176
Theloderma pyaukkya	CAS 234869	Mintatt Township, Chin, Myanmar	KU244370	KU244445
Theloderma pyaukkya	CAS 234857	Mindat Township, Chin, Myanmar	KU244371	KU244446
Theloderma albopunctatum	AMS R173734	Kon Tum, Vietnam	KU244374	KU244436
Theloderma albopunctatum	AMS R173794	Kon Tum, Vietnam	KU244373	KU244435

Supplementary Table S1 Species used for molecular phylogenetic analysis.