

The first record of *Kurixalus yangi* Yu, Hui, Rao and Yang, 2018 (Anura: Rhacophoridae) from Mizoram State, India, with a reassessment of previous records of its congeners from Mizoram

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Abstract

Based on a collection of *Kurixalus* specimens collected from different localities in Mizoram State, we report the occurrence of *Kurixalus yangi* from the State. Species identification was confirmed based on morphology and molecular data (mitochondrial 16S rRNA marker gene sequence). In addition, we confirm the previous record of *Kurixalus naso* from the same region to be erroneous as it is in fact *K. yangi*. Herein, we reassess the systematic status of this montane population of *Kurixalus* from Northeast India and provide evidence for its distinction from *Kurixalus naso* sensu stricto, thereby reporting *K. yangi* as an addition to the amphibian fauna of Mizoram. This record represents the southernmost distribution of the species.

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Key words: First record, Northeast India, range extension, re-identification, 16S rRNA gene, taxonomy

Introduction

The family Rhacophoridae (Amphibia: Anura) comprises 442 species belonging to 22 genera and the genus *Kurixalus* Ye, Fei and Dubois, 1999 consists of 20 species of tree frogs, distributed in Myanmar, India, China, southern Cambodia, Vietnam, Thailand, Peninsular Malaysia, Sumatra, Borneo and the Philippines (Frost, 2021). However, cryptic species diagnoses on the basis of their morphology is challenging in *Kurixalus* (Yu et al., 2018). Studies indicate that this genus originated on mainland Asia and subsequently dispersed to the continental islands of East Asia and Southeast Asia by multiple colonization events (Yu et al., 2020).

Contiguous land connection between Borneo and mainland Southeast Asia existed throughout much of the Neogene Period (during times of lowered sea levels), and might have facilitated migration of terrestrial biotas (Moss and Wilson, 1998). *Kurixalus yangi* was first described by Yu et al. (2018) from Nabang, Yingjiang County, Dehong Autonomous Prefecture, western Yunnan in China. Its distribution

ranges from the vicinity of the type locality into adjacent northern Myanmar on the border region and Nagaland of northeastern India (Frost, 2021). Previously, two species in the same genus, *Kurixalus appendiculatus* (Günther, 1858) and *Kurixalus naso* (Annandale, 1912) were reported from Arunachal Pradesh State of Northeast India (Dinesh et al., 2020). Recently, *Kurixalus yangi* was reported from Nagaland, northeastern India by Humtsoe et al. (2020).

In this paper, we report the occurrence of *Kurixalus yangi* from Mizoram of northeastern India, confirmed on the basis of morphological and molecular data and also re-assess the validity of early records of *Kurixalus naso* from the same region.

Material and Methods

Surveys were conducted in Mizoram State to explore the local herpetofauna between 2010 and 2020, employing Visual Encounter Survey (VES) and Acoustic Encounter Survey (AES) techniques. We observed and collected several specimens of *Kurixalus* individuals from Mizoram. Specimens were identified

using Yu et al. (2018) at the Laboratory of Developmental Biology and Herpetology, Department of Zoology, Mizoram University. Specimens were preserved in 70% ethanol, and liver tissues extracted for genetic analysis; voucher specimens were

deposited in the Department Museum of Zoology, Mizoram University (MZMU) for further studies. Specimens were collected from seven localities (Table 1). The distribution map was created using an open source QGIS version 3.10.8 (Fig. 1).

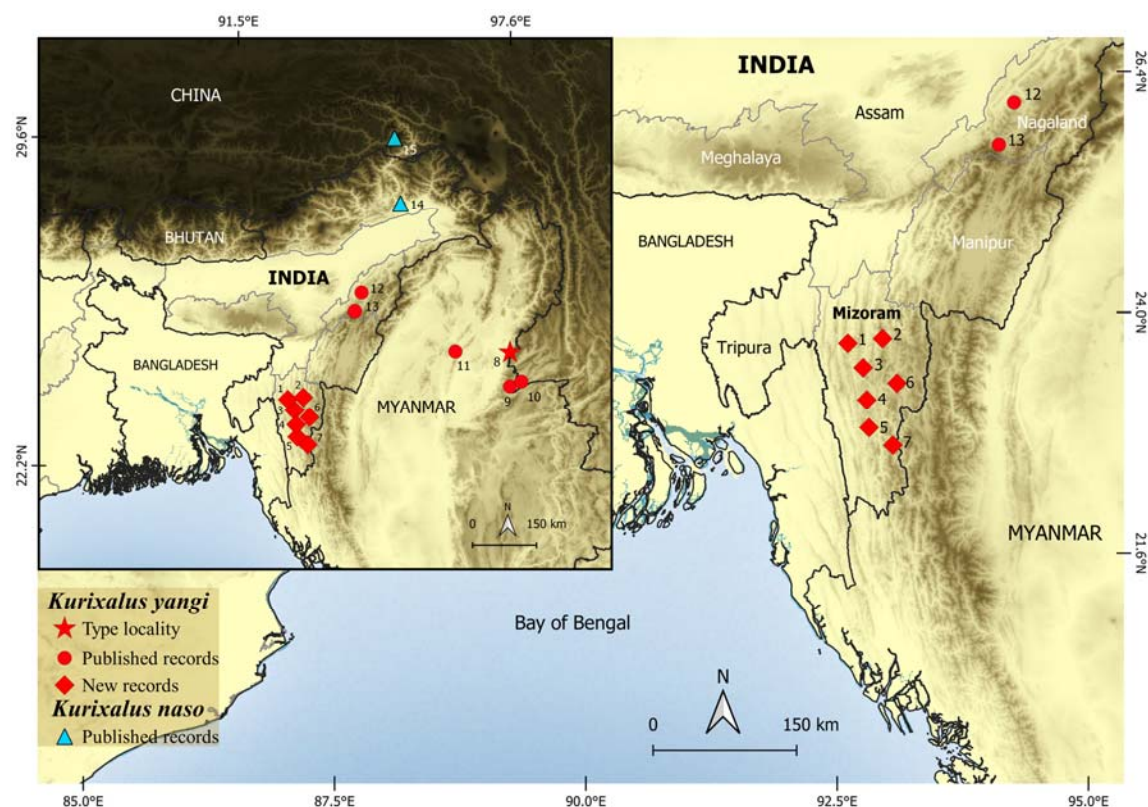


Figure 1: Map showing the distribution of *Kurixalus yangi* (type locality in red star, published records in red circles, and new records in red diamonds) and previous records of *Kurixalus naso* (in blue triangles): 1. Reiek Community Reserved Forest, 2. Tamdil National Wetland, 3. Hmuifang Community Reserved Forest, 4. Bualpui V, 5. District Park (Lunglei), 6. Sialhawk, 7. Phawngpui National Park, 8. Nabang, 9. Dengga, 10. Nanjingli, 11. Mohynin, 12. Wokha, 13. Kohima, 14. Egar, and 15. Muotuo.

Mensural data were taken by using a digital calliper (Mitutoyo™ 505-507) to the nearest 0.01 mm. Abbreviations used in this study for morphometric measurements are: snout-vent length (SVL); head width (HW); head length (HL); distance from the back of the mandible to the nostril (MN); distance from the back of the mandible to the front of the eye (MFE); distance from the back of the mandible to the back of the eye (MBE); distance between the front of the eye (IFE); distance between the back of the eye (IBE); inter-narial distance (IN); distance from the eye to nostril (EN); eye length (EL); snout to nostril distance (SN); snout length (SL, distance from the nostril to the tip of the snout); greatest tympanum diameter (TYD); distance from tympanum to the back of the eye (TYE); inter-orbital distance (IO); upper eyelid width (UEW); forelimb length (FLL, distance from upper arm insertion to the tip of the longest finger); hand length (HAL, distance from the

proximal end of the outer palmar tubercle to the tip of the longest finger); finger length (F, distance from wrist-metacarpal joint to tip of finger); femur length (FL); tibia length (TL); length of tarsus and foot together (TFOL); foot length (FOL); fourth toe length (FTL); toe length (T, distance from tarsus-metatarsal joint to tip of finger); VA/ERS/ZSI (Vouchered Amphibians/Eastern Regional Station/Zoological Survey of India). Detailed morphological data of the specimens are provided in Table 2.

Genomic DNA was extracted from the liver tissues of adult amphibians according to manufacturer's protocol using a QIAamp DNA Mini Kit (Cat No. ID: 51306). PCR reaction was prepared for 20 µL reaction mixture contained 1X amplification buffer, 2.5 mM MgCl₂, 0.25 mM dNTPs, 0.2 pM each forward and reverse primer, 1 µL genomic DNA, and 1U Taq DNA polymerase with a pair of partial 16S

rRNA primers: forward (L02510- CGC CTG TTT ATC AAA AAC AT) (Palumbi, 1996) and reverse (H03063- CTC CGG TTT GAA CTC AGA TC) (Rassmann, 1997). The PCR thermal regime for amplification was 5 min at 95 °C for initial denaturation, followed by 35 cycles of 1 min at 95 °C for denaturation, 30s for annealing at 50.3 °C, elongation for 1 min at 72 °C, and a final elongation for 5 min at 72 °C. PCR products were checked by gel electrophoresis on a 1.5% agarose gel containing ethidium bromide. Samples were sequenced using Sanger's dideoxy method and sequencing reactions were carried out in both directions on a sequencer (Agrigenome Labs Pvt Ltd., Kochin, India). The generated partial 16S rRNA sequence was deposited in GenBank (595 base pairs; accession number MT808303.1).

For the analysis of our dataset of 16S rRNA, we included 15 congener sequences obtained from NCBI database and one sequence of *Odorrana chloronata* (MZMU1842) was used as an outgroup. All sequences were aligned by using MUSCLE algorithm in MEGA

7 (Kumar et al., 2016), the Kimura 2 (K2P) and genetic distances (Kimura, 1980) were calculated using MEGA 7 (Kumar et al., 2016).

The Bayesian Inference (BI) phylogenetic tree was constructed in MrBayes 3.2.5 using GTR+I+G model. The MCMC (one cold and three hot chains) was run for 100,000 generations by sampling every 100 generations and set the burn-in to 25%. The analysis was terminated when the standard deviation of split frequencies was less than 0.01. The percentage of trees in which the associated taxa clustered together is shown next to the branches (Ronquist and Huelsenbeck, 2003). The generated phylogenetic tree was further modified using web-based iTOL software (Letunic and Bork, 2019).

Results and Discussion

The present study confirmed the first documentation of *Kurixalus yangi* from the Mizoram State of India (Fig. 2).

All specimens were collected during the monsoon season from undisturbed riparian forests (Fig. 3).

Table 1: Collection data of the present specimens and Mathew and Sen (2008; 2010) of *Kurixalus yangi* based on seven different localities in Mizoram state, India. 1- Reiek Community Reserved Forest, 2- Tamdil National Wetland, 3- Hmuifang Community Reserved Forest, 4- Bualpui V, 5- District Park, Lunglei, 6- Sialhawk, 7- Phawngpui National Park. Elevations are above the sea level (a.s.l.).

Locality No.	1		2		3		4		5		6		7		District Park, Lunglei (Mathew and Sen 2008; 2010)		
Museum No. (MZMU)	243	615	1014	1022	1016	1018	1815	1816	1924	2048	618	621	1013	1017	617	V A/ERS/ZSI/769	V A/ERS/ZSI/728
Collection date	30/7/2010	1/6/2014	29/5/2016	2/9/2016	25/5/2016	3/7/2016	14/5/2017	5/6/2018	27/4/2019	7/8/2020	4/8/2014	23/6/2015	19/6/2016	12/6/2016	21/7/2014	22/9/2005	4/6/2006
Coordinate	23°41'36.48"N 92°36'21.93"E		23°44'30.35"N 92°57'2.23"E		23°27'15.03"N 92°45'7.71"E		23°7'12.42"N 92°47'39.32"E		22°50'52.60"N 92°49'3.54"E		23°17'43.39"N 93°5'30.89"E		22°37'19.79"N 93°1'56.03"E		22°50' N 92°49' E		
Elevation	1232 m		764 m		1484 m		925 m		1128 m		1292 m		1452 m		1128 m		

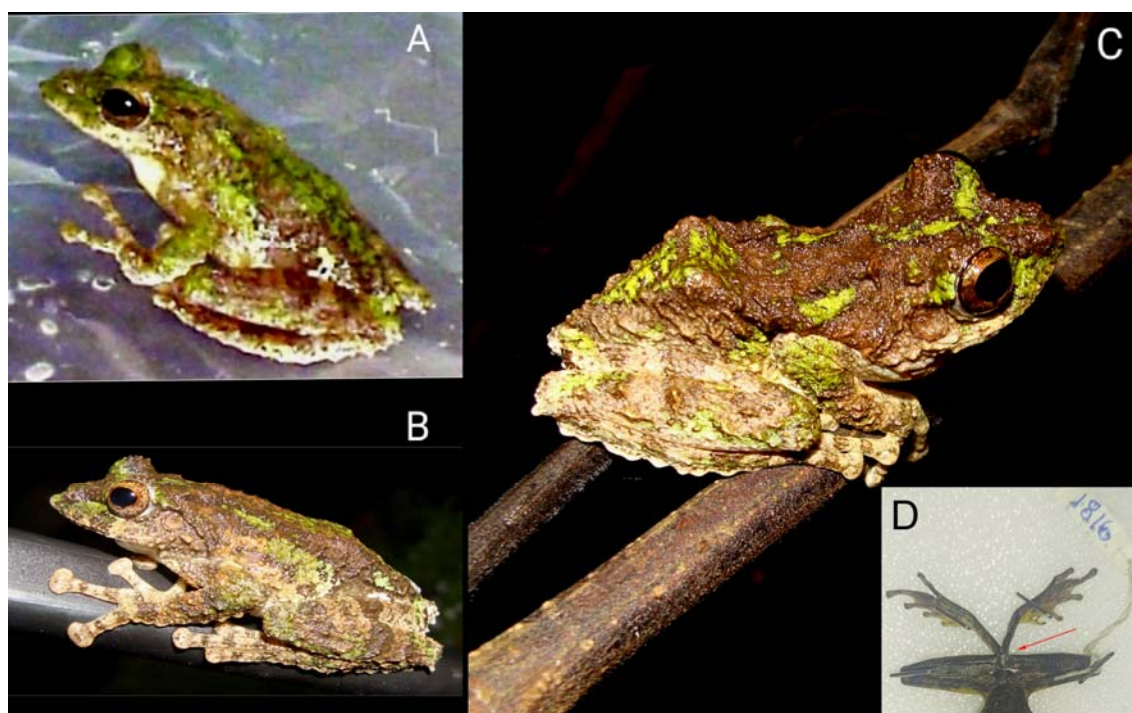


Figure 2: Adult males of *Kurixalus yangi* from (A) District Park, Lunglei (adopted from Mathew and Sen, 2010), (B) District Park, Lunglei (MZMU 1013), (C) Hmuifang Community Reserved Forest, Mizoram State, India (MZMU 615) and (D) an individual (MZMU 1816) showing heels overlapping when hind limbs folded at right angles to body.

Morphometric measurements of the specimens are given in Table 2. SVL ranges of the series were 29.4–44.1 mm with all adult males being greater than 30 mm in SVL. This species has a distinctly pointed snout when viewed laterally; head longer than wide; snout as long as the diameter of eye; iris golden-colored; canthus rostralis obtuse in dorsal view and acute in lateral view, loreal region concave; nostril closer to snout than eye; interorbital space broader than upper eyelid width; tympanum distinct, half the diameter of eye; male with single internal vocal sac; vomerine teeth in two oblique series touching inner edge of each side of choanae; head with small warts; body with coarse dorsal and lateral warts intermixed with small, irregular tubercles; dorsal color not uniform, generally green and brown colored with dark markings; belly granulated; chin, throat and breast smooth; ventral surface shaded posteriorly with dark spots; irregular dark cross-bars on limbs; serrated dermal fringes along outer edge of forearm and tibia; fingers with rudimentary web; tips of digits enlarged to form discs, bearing circum-marginal grooves; finger discs more or less similar to the size of toes; nuptial pad weakly developed; supernumerary and outer metacarpal tubercles present; relative finger

and toe lengths are $\text{III} > \text{IV} > \text{II} > \text{I}$ and $\text{IV} > \text{V} > \text{III} > \text{II} > \text{I}$, respectively; few enlarged tubercles present just below the cloacal opening; inner and outer metatarsal tubercle small; heels overlapping when hind limbs folded at right angles to body (Fig. 2D); tibio-tarsal articulation reaches between eye and nostril when adpressed.

The BLAST of the generated partial 16S rRNA gene fragment from the specimen MZMU 1013 which was discovered in this study (GenBank accession no. MT808303.1) matched the database sequence of *Kurixalus yangi* (KX554491.1) sampled from Yunnan, China with 99.82% identity (0% gaps and an e-value of 0.0).

In the present BI phylogenetic tree, our sample (MT808303.1) formed a significant clustering with the specimens from Mohynin, Kachin, Myanmar (GU227333.1); Wokha District, Nagaland State, India (KU589225.2); Longdao, Ruili, Yunnan, China (KX554491.1; KX554493.1); and the sequence submitted as *Kurixalus verrucosus* from Murlen National Park, Mizoram, India (MT632252.1) (Fig. 4).



Figure 3: Microhabitat of *Kurixalus yangi* at Reiek Community Reserved Forest.

From the estimated K2P genetic distances, our sequence (MT808303.1) showed minimal genetic distance (0.3%) with the previous database sequence sampled from Mizoram, India (MT632252.1). Thus, we inferred this individual to be *Kurixalus yangi*; while 0.0% genetic divergence was diagnosed with the conspecific sequence from Mohynin (Myanmar) (GU227333.1), 0.7% each with the two sequences from Longdao (China) (KX554491.1; KX554493.1), and 2.4% with that from Nagaland (India) (KU589225.2). We diagnosed inter-specific genetic divergences of 5.4% each with the two sequences of *Kurixalus naso* from Muotuo, Tibet, China (KX554484.1; KX554485.1). Genetic divergence of 1.4% is also diagnosed with the sequence of unidentified specimen (GU227330.1) from Northern Myanmar (Nagmung, Kachin State) which was previously treated as *Kurixalus verrucosus* by Yu et al. (2010), and we suggested this specimen is also referable to *Kurixalus yangi* according to Yu et al. (2017) (Table 3).

Species diversity of the genus *Kurixalus* appears to be underestimated (Yu et al., 2018). Mathew and Sen (2008) reported a record of *Kurixalus naso*, based on 13 individuals (2 males and 11 females), collected from the District Park, Lunglei district of Mizoram in 2006, in which the identification was solely based on morphological grounds following Annandale (1912).

However, all these specimens, including the specimens (MZMU 612 and MZMU 1013), collected from the same locality mentioned in Mathew and Sen (2008) accord with the description of *Kurixalus yangi* provided by Yu et al. (2018).

In addition, the present identification, which is based on morphology and morphometry is also supported by the molecular analysis. All of our specimens have a shorter head and snout and limb lengths (vs. longer head and snout and limbs in *K. naso*); inter-orbital distance (3.60–6.53 mm) longer than inter-narial distance (2.96–4.50 mm) and upper eyelid width (2.78–4.77 mm) (vs. interorbital distance narrower than internarial distance and upper eyelid width in *K. naso*). In addition, all adult males with SVL greater than 30 mm agree with the morphological features mentioned by Yu et al. (2018). Thus, we suggest that the record of *Kurixalus naso* (then as *Rhacophorus naso*) (Fig. 2A) from Mizoram by Mathew and Sen (2008; 2010) is probably an incorrect identification of *K. yangi* (Fig. 2B, C). Moreover, on the basis of our study, all specimens collected from various areas of Mizoram State in India are diagnosed as *Kurixalus yangi*. The specimen collected from Phawngpui National Park (MZMU 617) represents the southernmost distribution of *Kurixalus yangi* being about 341 km further south than the previous record in Kohima of Nagaland State in India.

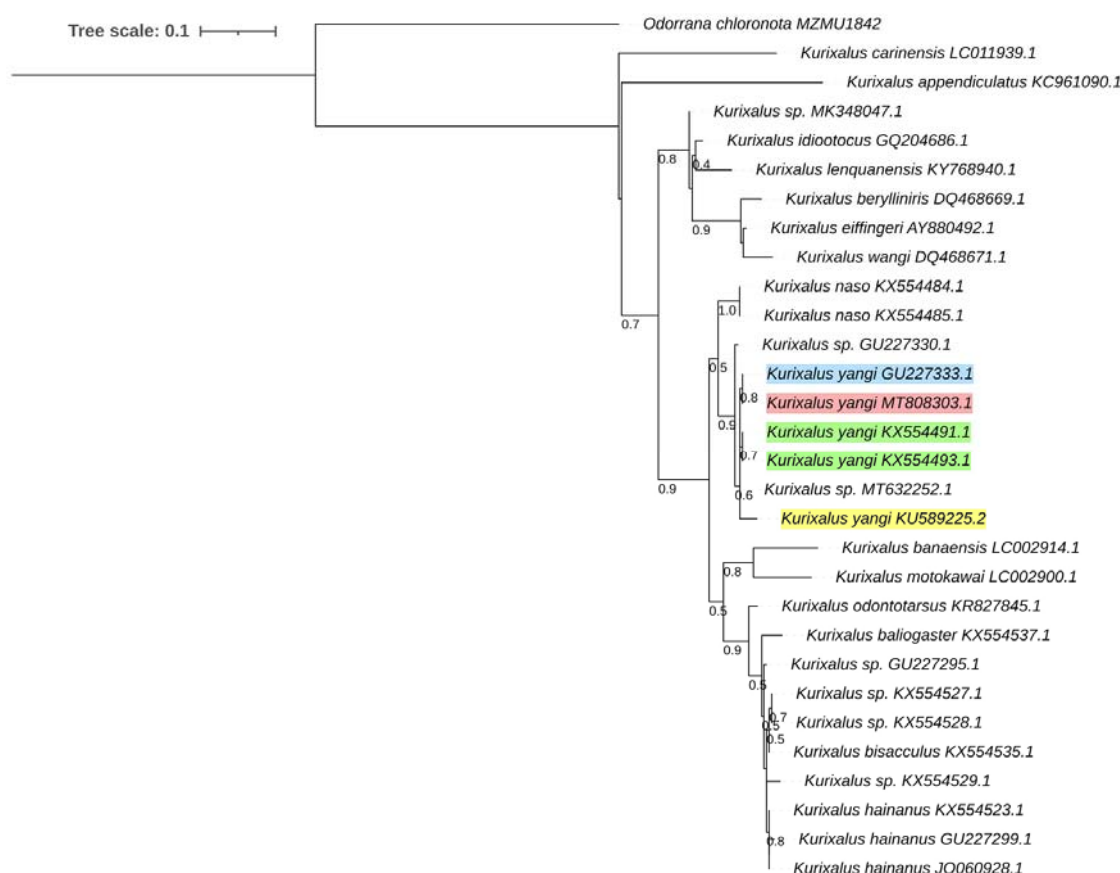


Figure 4: The Bayesian inference tree inferred from the combined dataset of partial 16S rRNA gene, with *Odorrana chloronota* as the outgroup. Taxon labels represent the species names and followed by GenBank accession numbers. The sequences of *Kurixalus yangi* from Mohynin, (Kachin State, Myanmar-in blue), this study (Mizoram State, India-in pink), Longdao, (Yunnan Province, China-in green), and Wokha (Nagaland State, India-in yellow). Posterior probabilities are given at each node.

Acknowledgements

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Conflict of interest

The authors declare that there are no conflicting issues related to this research article.

Table 2: Morphometric characteristics of the present specimens and Mathew and Sen (2008; 2010) of *Kurixalus yangi* based on different localities in Mizoram state, India.

Museum No. (MZMU)	243	615	1014	1022	1016	1018	1815	1816	1924	2048	618	621	1013	1017	617	VA/ERS/ZSI/769	VA/ERS/ZSI/728
SEX	Male	Male	Male	Female	Sub- adult	Male	Male	Female	Female	Male	Male	Female	Male	Male	Female	Male	Female
SVL	30.90	30.3	30.00	32.40	29.40	32.50	35.30	43.60	44.10	31.10	30.70	33.11	31.90	33.50	31.30	30.00	43.00
HW	12.10	11.90	11.10	12.00	11.60	12.30	12.84	15.40	16.34	12.41	11.80	12.20	12.20	12.10	11.10	11.00	16.00
HL	10.70	11.50	10.80	11.50	10.10	10.50	11.20	14.80	15.06	11.48	10.40	10.10	9.90	12.00	9.96	10.00	14.00
MN	8.85	8.56	9.53	9.12	8.18	7.89	9.70	13.50	15.80	9.16	8.08	7.93	8.14	10.00	8.12	8.50	8.50
MFE	6.31	5.12	6.79	7.41	5.90	5.34	7.38	10.40	10.30	7.23	6.11	5.05	5.19	8.48	6.25	6.50	8.00
MBE	2.43	2.43	3.85	3.13	2.48	2.82	4.20	6.19	6.66	3.50	3.63	3.01	3.16	3.86	3.36	2.50	4.50
IFE	6.04	6.21	6.21	7.33	6.09	6.39	6.34	7.90	7.84	3.54	6.28	6.13	6.28	7.09	6.88	5.00	7.50
IBE	11.10	9.03	9.48	10.7	9.23	9.26	11.80	12.10	12.80	10.10	9.33	9.68	9.57	10.10	10.50	9.00	13.00
IN	3.41	2.96	3.05	3.49	3.15	3.67	3.37	3.74	4.50	3.14	3.66	3.37	3.79	3.40	3.69	2.80	4.00
EN	2.84	2.80	2.84	2.99	3.94	3.31	3.60	4.96	4.60	3.18	3.29	3.18	3.12	3.40	3.09	2.00	4.5
EL	4.20	4.00	3.65	3.92	4.22	3.99	3.96	3.72	4.90	3.28	3.83	4.14	4.22	3.74	3.99	3.60	5.5
SN	2.19	1.83	1.93	2.84	2.16	2.36	2.58	2.22	2.12	2.48	2.17	2.39	2.51	2.45	2.30	2.00	3.5
SL	5.17	4.72	5.19	5.56	5.23	5.75	6.80	5.62	7.78	5.18	5.22	5.22	5.34	5.86	4.71	4.50	8.00
TYD	2.11	2.38	2.16	3.02	2.22	2.38	2.32	2.84	3.48	2.27	1.90	2.30	2.38	2.16	2.48	1.80	3.20
TYE	1.06	1.85	0.83	1.82	1.08	1.23	1.55	1.62	1.55	1.44	1.06	1.32	1.35	0.67	1.23	0.70	1.00
IO	5.37	3.68	4.93	3.60	4.80	3.71	5.96	6.53	6.25	4.45	3.82	4.18	4.29	4.20	3.96	3.00	5.00
UEW	3.23	3.27	3.75	2.78	3.06	3.23	3.67	4.77	4.48	2.03	2.86	2.80	2.92	3.67	3.12		
FLL	5.82	5.69	6.39	6.40	6.36	7.11	6.63	7.38	10.8	6.59	6.45	6.49	7.51	6.47	7.25	5.50	7.00
HAL	8.03	8.74	7.95	9.24	7.52	7.01	7.64	10.4	10.1	6.77	8.04	8.54	7.41	7.65	8.01	9.50	13.00
F I	4.85	5.44	4.84	4.69	5.09	5.01	5.80	6.86	6.57	4.45	5.03	5.72	5.12	5.04	5.52	-	-
F II	6.74	7.26	5.99	5.91	6.22	7.28	5.13	9.49	9.27	5.76	6.91	7.13	6.16	6.24	7.34	-	-
F III	9.30	10.30	9.33	9.34	8.94	10.4	9.62	13.1	13.4	8.09	9.75	8.70	8.08	10.10	10.90	-	-
F IV	7.71	8.53	7.77	8.51	7.35	8.84	8.60	11.00	12.8	7.49	8.10	8.46	6.50	8.56	9.17	-	-
FL	15.60	15.00	15.10	13.90	13.40	17.00	17.80	20.60	20.10	15.60	15.90	16.20	14.90	14.70	16.60	15.00	23.00
TL	11.10	12.00	13.00	12.30	8.66	12.20	13.60	19.80	18.20	13.20	11.00	11.40	12.10	12.30	12.50	16.00	23.50
TFOL	20.50	21.80	20.20	20.60	17.70	19.05	23.20	29.10	31.40	19.70	17.00	21.90	20.80	21.00	22.80	-	-
FOL	13.90	13.70	12.20	14.10	13.40	13.10	14.00	17.60	21.90	12.70	11.20	15.60	12.90	13.20	14.50	14.00	19.00
FTL	10.80	10.80	9.79	9.59	10.20	9.10	12.10	11.00	12.00	11.10	8.92	12.70	11.30	9.13	10.80	-	-
T I	6.25	5.12	3.94	4.77	4.46	4.92	5.32	7.48	8.30	4.15	4.43	5.97	5.85	4.27	6.25	-	-
T II	7.41	7.41	5.36	6.39	7.61	8.18	7.65	10.60	11.20	6.56	7.00	7.77	8.85	6.61	8.69	-	-
T III	10.30	10.10	8.74	8.17	8.81	11.20	10.10	15.20	17.00	9.69	8.71	11.50	11.00	10.50	11.80	-	-
T IV	12.30	12.20	12.30	10.80	12.40	13.40	14.10	20.90	19.40	12.70	9.96	14.00	13.20	12.60	13.90	-	-
T V	11.00	8.62	9.24	9.73	11.00	11.80	13.30	16.90	16.60	11.00	9.28	12.50	12.90	11.00	12.90	-	-

Table 3: The estimates of evolutionary divergence based on uncorrected K2P distance among *Kurixalus* species using 16S rRNA partial gene sequence.

Species	K2P distance																												
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29
1 <i>Kurixalus yangi</i> (MT808303) This study																													
2 <i>Kurixalus yangi</i> (KU589225)	0.024																												
3 <i>Kurixalus yangi</i> (KX554491)	0.007	0.024																											
4 <i>Kurixalus yang</i> (KX554493)	0.007	0.024	0.000																										
5 <i>Kurixalus yangi</i> (GU227333)	0.000	0.024	0.007	0.007																									
6 <i>Kurixalus appendiculatus</i> (KC961090)	0.232	0.260	0.237	0.237	0.232																								
7 <i>Kurixalus baliogaster</i> KX554537)	0.089	0.108	0.081	0.081	0.089	0.261																							
8 <i>Kurixalus banaensis</i> (LC002914)	0.128	0.144	0.120	0.120	0.128	0.235	0.120																						
9 <i>Kurixalus berylliniris</i> (DQ468669)	0.149	0.166	0.149	0.149	0.149	0.215	0.162	0.156																					
10 <i>Kurixalus bisacculus</i> (KX554535)	0.089	0.116	0.089	0.089	0.089	0.261	0.028	0.128	0.162																				
11 <i>Kurixalus carinensis</i> (LC011939)	0.190	0.216	0.194	0.194	0.190	0.222	0.217	0.220	0.170	0.212																			
12 <i>Kurixalus eiffingeri</i> (AY880492)	0.132	0.148	0.124	0.124	0.132	0.211	0.136	0.143	0.032	0.145	0.184																		
13 <i>Kurixalus hainanus</i> (KX554523)	0.105	0.133	0.105	0.105	0.105	0.261	0.043	0.141	0.171	0.014	0.222	0.162																	
14 <i>Kurixalus hainanus</i> (JQ060928)	0.097	0.125	0.097	0.097	0.097	0.261	0.035	0.132	0.162	0.007	0.212	0.153	0.007																
15 <i>Kurixalus hainanus</i> (GU227299)	0.097	0.125	0.097	0.097	0.097	0.261	0.035	0.132	0.162	0.007	0.212	0.153	0.007	0.000															
16 <i>Kurixalus idiootocus</i> (GQ204686)	0.116	0.132	0.108	0.108	0.116	0.213	0.141	0.153	0.080	0.150	0.184	0.065	0.150	0.141	0.141														
17 <i>Kurixalus lenquanensis</i> (KY768940)	0.138	0.154	0.129	0.129	0.138	0.228	0.154	0.175	0.088	0.163	0.193	0.089	0.163	0.154	0.154	0.054													
18 <i>Kurixalus motokawai</i> (LC002900)	0.137	0.150	0.129	0.129	0.137	0.220	0.112	0.111	0.152	0.116	0.245	0.135	0.116	0.116	0.116	0.136	0.157												
19 <i>Kurixalus naso</i> (KX554485)	0.054	0.072	0.054	0.054	0.054	0.221	0.081	0.124	0.127	0.089	0.194	0.111	0.097	0.089	0.089	0.104	0.124	0.116											
20 <i>Kurixalus naso</i> (KX554484)	0.054	0.072	0.054	0.054	0.054	0.221	0.081	0.124	0.127	0.089	0.194	0.111	0.097	0.089	0.089	0.104	0.124	0.116	0.000										
21 <i>Kurixalus odontotarsus</i> (KR827845)	0.073	0.100	0.073	0.073	0.073	0.241	0.046	0.108	0.144	0.035	0.213	0.136	0.043	0.035	0.035	0.128	0.146	0.111	0.081	0.081									
22 <i>Kurixalus wangi</i> (DQ468671)	0.124	0.140	0.124	0.124	0.124	0.236	0.136	0.170	0.058	0.145	0.184	0.039	0.162	0.153	0.153	0.085	0.093	0.161	0.111	0.111	0.145								
23 <i>Kurixalus</i> sp. (MT632252)	0.003	0.021	0.003	0.003	0.003	0.232	0.085	0.124	0.154	0.093	0.194	0.128	0.110	0.101	0.101	0.112	0.133	0.133	0.050	0.050	0.077	0.120							
24 <i>Kurixalus</i> sp. (GU227330)	0.014	0.031	0.014	0.014	0.014	0.232	0.089	0.124	0.149	0.097	0.190	0.132	0.105	0.097	0.097	0.108	0.138	0.142	0.046	0.046	0.073	0.124	0.010						
25 <i>Kurixalus</i> sp. (GU227295)	0.093	0.121	0.093	0.093	0.093	0.250	0.032	0.132	0.148	0.010	0.207	0.140	0.017	0.010	0.010	0.137	0.159	0.120	0.085	0.085	0.032	0.149	0.097	0.093					
26 <i>Kurixalus</i> sp. (KX554527)	0.093	0.112	0.085	0.085	0.093	0.261	0.025	0.124	0.166	0.003	0.217	0.140	0.017	0.010	0.010	0.145	0.159	0.112	0.085	0.085	0.039	0.140	0.089	0.093	0.014				
27 <i>Kurixalus</i> sp. (KX554528)	0.093	0.112	0.085	0.085	0.093	0.261	0.025	0.124	0.166	0.003	0.217	0.140	0.017	0.010	0.010	0.145	0.159	0.112	0.085	0.085	0.039	0.140	0.089	0.093	0.014	0.000			
28 <i>Kurixalus</i> sp. (KX554529)	0.089	0.116	0.089	0.089	0.089	0.266	0.043	0.141	0.166	0.021	0.203	0.158	0.028	0.021	0.021	0.154	0.168	0.124	0.081	0.081	0.043	0.149	0.093	0.089	0.025	0.025	0.025		
29 <i>Kurixalus</i> sp. (MK348047)	0.116	0.132	0.108	0.108	0.116	0.208	0.132	0.153	0.073	0.141	0.175	0.065	0.141	0.132	0.132	0.017	0.050	0.136	0.096	0.096	0.128	0.085	0.112	0.108	0.128	0.137	0.137	0.145	
30 <i>Odorrana chloronota</i> (MZMU1842)	0.339	0.367	0.345	0.345	0.339	0.370	0.375	0.390	0.350	0.369	0.340	0.343	0.388	0.375	0.375	0.337	0.368	0.363	0.350	0.350	0.387	0.349	0.345	0.351	0.388	0.375	0.375	0.375	0.349

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