

Supplementary Materials

Materials and Methods

DNA sequencing: Total genomic DNA of four individuals from the two sites was extracted using an EasyPure® Genomic DNA kit (TransGen Biotech, Beijing, China). Two mitochondrial fragments of the 12S ribosomal RNA gene (12S rRNA) and 16S ribosomal RNA gene (16S rRNA) from the four specimens were amplified using polymerase chain reaction (PCR) (Saiki et al., 1985). The 12S rRNA primers were L1091 (5'-AAACTGGGATTAGATAACCCACTAT-3') and H1478 (5'-GAGGGTGACGGGCGGTGTGT-3') (Kocher et al., 1989), and the 16S rRNA primers were L2206 (5'-GGCCTAAAAGCAGGCCACCTGTAAAGACAGCGT-3') and L2606 (5'-CTGACCGTGCAAAGGTAGCGTAATCACT-3'), and H3056 (5'-CTCCGGTCTGAACTCAGATCACGTAGG-3') (Hedges et al., 1993) and H2741 (5'-AAGCTCCACAGGGTCTTCTCGTCTTATG-3') (Honda et al., 2006). The PCR products were checked on a 0.8% agarose gel and purified using ethanol precipitation. Purified PCR products were directly sequenced in both direction with a BigDye terminator kit using an ABI 310 analyzer (Applied Biosystems, USA). New sequences were deposited in GenBank under accession Nos. MW413384–MW413387 and MW411357–MW411360 (Supplementary Table S1).

Phylogenetic reconstructions

Sequences of the genus *Tropidophorus* and the outgroup species (*Lygosoma koratense*) were downloaded from GenBank for phylogenetic relationship reconstruction (Supplementary Table S1). The 12S rRNA and 16S rRNA datasets were aligned using ClustalX v1.83 (Thompson et al., 1997). We applied Bayesian inference (BI) and maximum-likelihood (ML) methods to infer phylogenetic relationships. Analyses were conducted based on concatenated sequences (12S rRNA and 16S rRNA). BI analyses were performed using MrBayes v3.1.2 (Ronquist et al., 2012). The best model of evolution for the concatenated mtDNA sequences was determined using jModelTest v2 (Darriba et al., 2012), ranked by the Akaike Information Criterion (AIC). The best-fit model was GTR+I+G for concatenated mtDNA sequences. Two independent runs were carried out with four Monte Carlo Markov chains (MCMCs) for 10 million generations with parameters and topologies sampled every 100 generations. Bayesian posterior probability (BPP) was determined to test the confidence of tree topology; nodes in the trees were considered strongly supported when BPP \geq 0.95 (Rannala 2004).

Convergence was determined using Tracer v1.6 (Rambaut & Drummond, 2013), and the first 25% of trees were discarded as burn-in. The ML analyses were conducted in RAxML (Stamatakis, 2014) on the CIPRES Science Gateway v3.1 (Miller et al., 2010) <http://www.phylo.org>). The best-fit model of evolution was selected as GTR+Γ (GTRGAMMA). Tree searches were performed 100 times and bootstrap proportions (BSP) were assessed using the rapid-bootstrapping algorithm (1 000 non-parametric bootstrap replicates) to test node support, where nodes with $BSP \geq 70$ were significantly supported. Genetic distances among *Tropidophorus* taxa were calculated using MEGA v5.1 (Kumar et al., 2004) based on the uncorrected *p*-distances (Kimura, 1980) for the 16S rRNA gene.

Morphological terminology

Morphological measurements were taken with a digital caliper to the nearest 0.1 mm. The following abbreviations were used (Nguyen et al., 2010): snout-vent length (SVL); tail length (TaL), total length (TL); distance from posterior junction of forelimb and body wall to anterior junction of hindlimb and body wall when limbs held at right angles to body (AG); snout length (SL), distance between tip of snout and anterior corner of eye; snout-forelimb length (SFIL), measured from tip of snout to anterior junction of forelimb and body wall to tip of fourth finger when limb held at right angles to body; head length (HL), measured from tip of snout to posterior margin of parietal or interparietal, depending on longest distance; head width (HW), measured at widest portion of temporal region; head height (HH), measured at deepest portion of temporal region; length of head and neck (HNL); distance from snout to anterior border of tympanum (STL); distance from anterior corner of eye to posterior border of nostril (END); eye length (EL), distance between anterior and posterior corners of eyelid; distance from anterior border of tympanum to posterior corner of eye (ETL); maximum diameter of tympanum (TYD); forelimb length (FIL), measured from anterior junction of forelimb and body wall to tip of fourth finger when limb held at right angles to body; hindlimb length (HIL), measured from anterior junction of hindlimb and body wall to tip of fourth finger when limb held at right angles to body; internarial distance, distance between nostrils (IN); inter-eye distance (IO), distance between eyes; eye-nostril distance (E-N), distance between anterior-edge of eyes and posterior-edge of nostrils; eye-snout distance, distance between

anterior-edge of eyes and tip of snout (E-S); body width, greatest width of body (BW); nostril-snout distance, distance between anterior-edge of nostril and tip of snout (N-S). The following characteristics were counted (Nguyen et al., 2010): nuchals, enlarged scales behind parietals; paravertebral scales, number of scales in line from posterior edge of parietals to dorsal point opposite posterior margin of medial precloacals; ventral scales, scales from first gular to anterior margin of precloacals; midbody ventral scales, scales from posterior margin of fore limb to last scale before precloacals; number of tail scale rows at tenth subcaudal scale (including subcaudal). Bilateral scale counts are given as left/right. Other abbreviations: SD: Standard deviation; a.s.l.: above sea level; HNU: Hunan Normal University; GMC: Guangxi Medical University.

REFERENCES

- Darriba D, Taboada GL, Doallo R, Posada D. 2012. JModelTest 2: more models, new heuristics and parallel computing. *Nature Methods*, **9**(8): 772.
- Hedges SB, Nussbaum RA, Maxson LR. 1993. Caecilian phylogeny and biogeography inferred from mitochondrial DNA sequences of the 12S rRNA and 16S rRNA genes (Amphibia: Gymnophiona). *Herpetological Monographs*, **7**: 64–76.
- Honda M, Ota H, Murphy RW, Hikida T. 2006. Phylogeny and biogeography of water skinks of the genus *Tropidophorus* (Reptilia: Scincidae): a molecular approach. *Zoologica Scripta*, **35**(1): 85–95.
- Kimura M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution*, **16**(2): 111–120.
- Kocher TD, Thomas WK, Meyer A, Edwards SV, Pääbo S, Villablanca FX, et al. 1989. Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers. *Proceedings of the National Academy of Sciences of the United States of America*, **86**(16): 6196–6200.
- Kumar S, Tamura K, Nei M. 2004. MEGA3: integrated software for molecular evolutionary genetics analysis and sequence alignment. *Briefings in Bioinformatics*, **5**(2): 150–163.
- Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: Proceedings of the 2010 Gateway Computing Environments Workshop. New Orleans: IEEE, 1–8.
- Nguyen TQ, Nguyen TT, Schmitz A, Orlov NL, Ziegler T. 2010. A new species of the genus

tropidophorus duméril & bibron, 1839 (squamata: sauria: scincidae) from vietnam. *Zootaxa*, **2439**(1): 53–68.

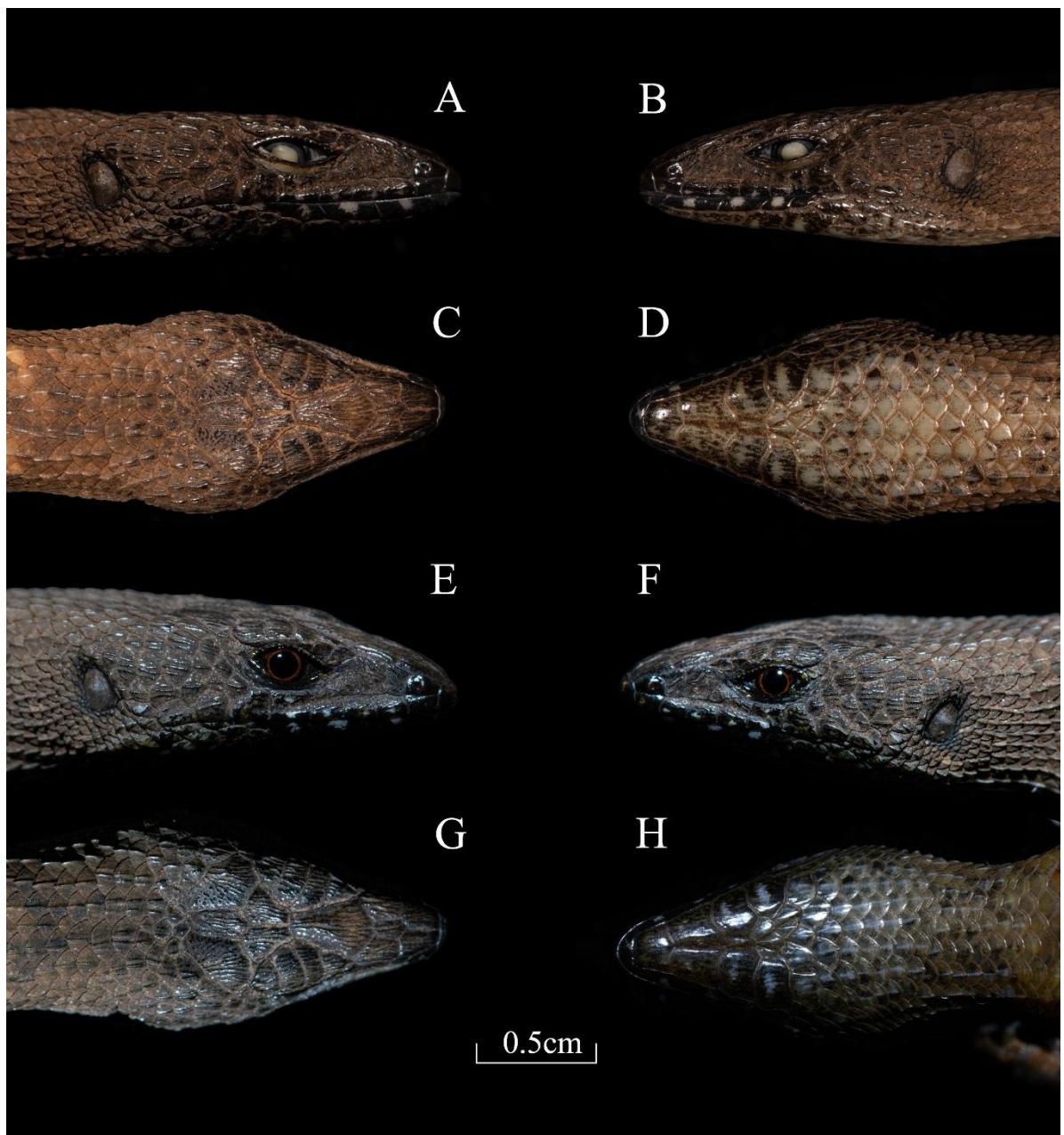
Rambaut A, Drummond A. 2013. Tracer 1.6. University of Edinburgh, Edinburgh, UK.

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, et al. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology*, **61**(3): 539–542.

Saiki RK, Scharf S, Faloona F, Mullis KB, Horn GT, Erlich HA, et al. 1985. Enzymatic amplification of β-genomic sequences and restriction site analysis for diagnosis of sickle cell anemia. *Science*, **230**(4732): 1350–1354.

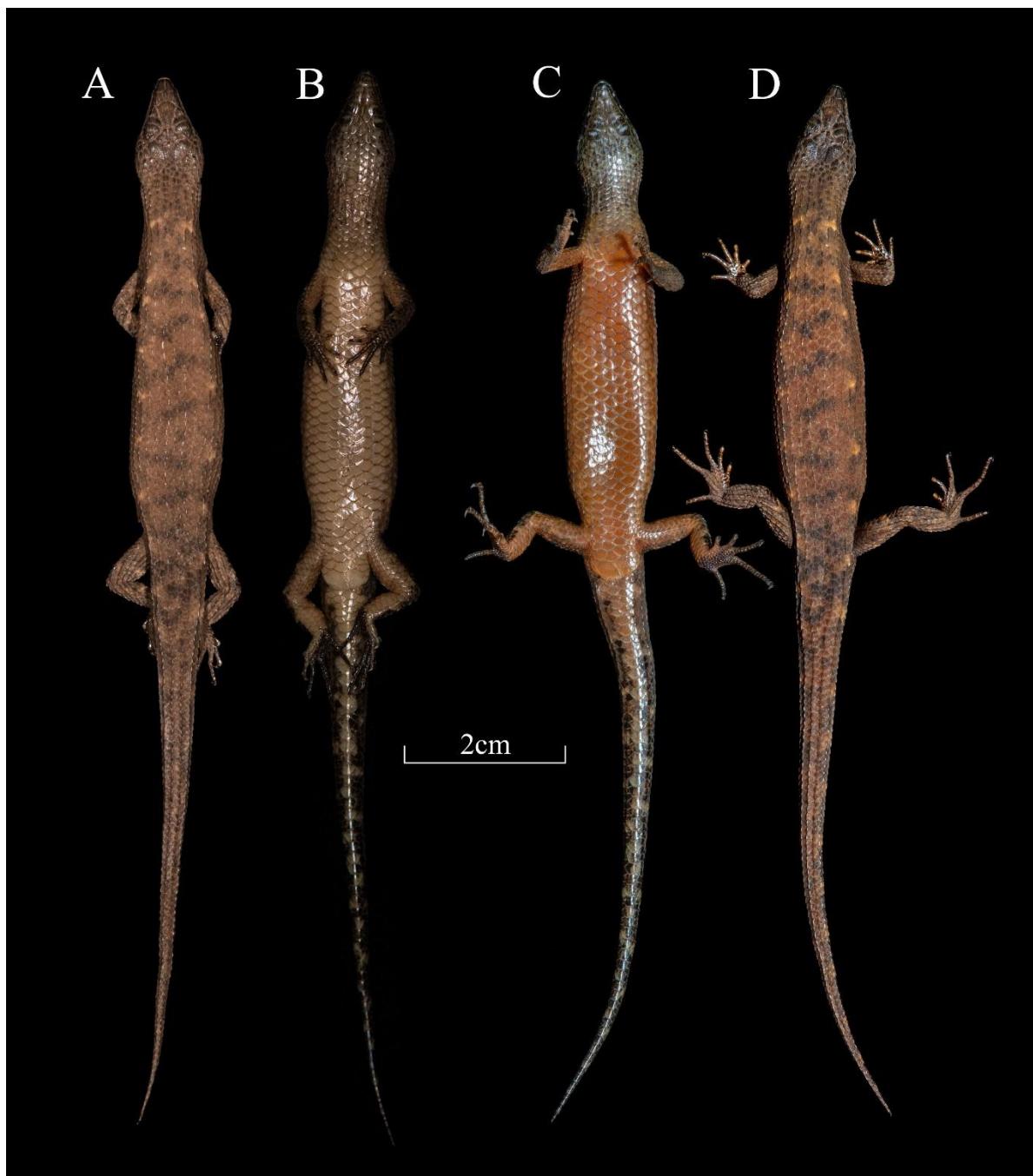
Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*, **30**(9): 1312–1313.

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. 1997. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research*, **25**(24): 4876–4882.



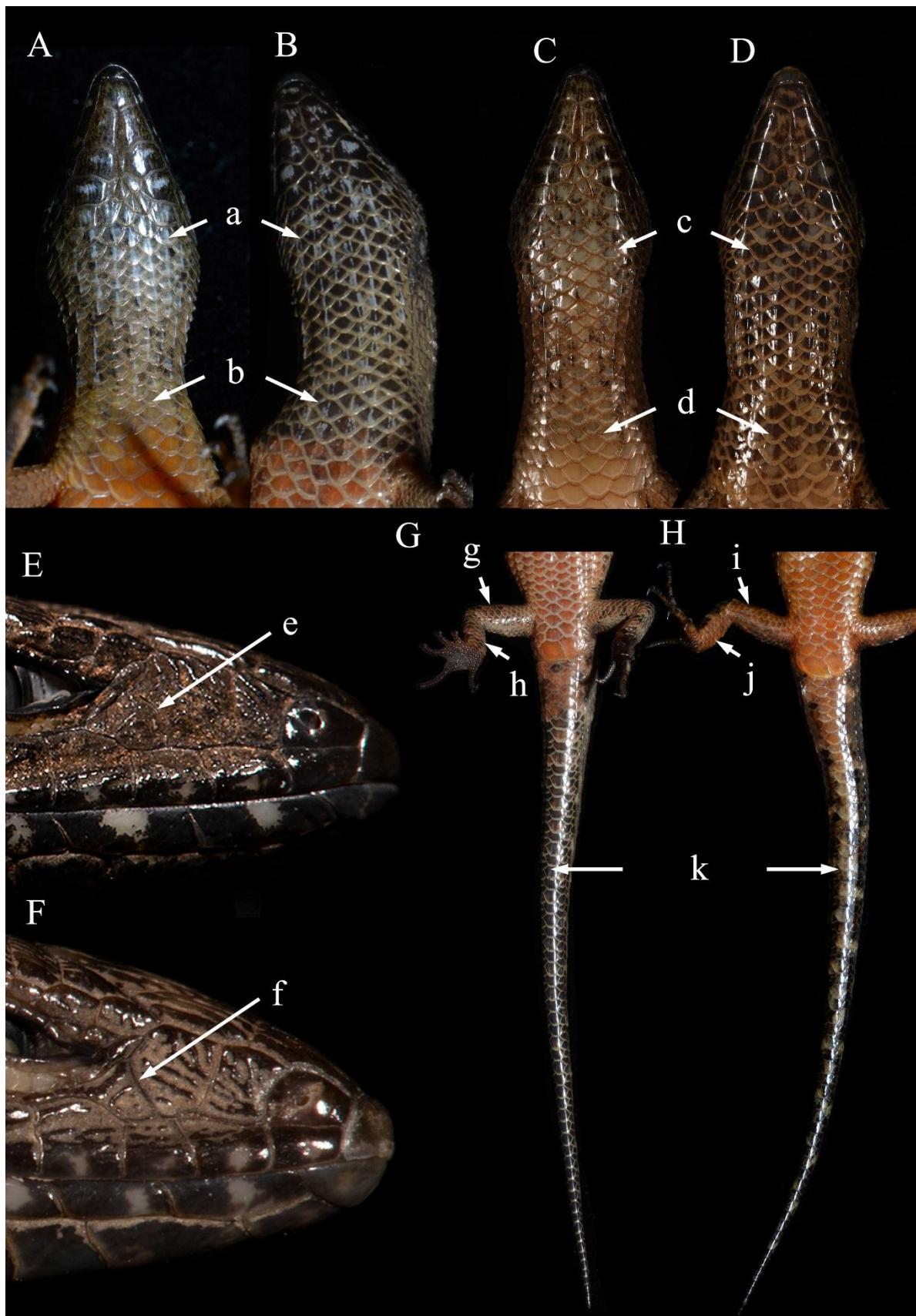
Supplementary Figure S1. Head feature photographs of *Tropidophorus guangxiensis guangxiensis* neotype.

HNU GKJ-2019007, Adult female; A, B, C, D: Photos in preservative; E, F, G, H: Photos in life; A, B, E, F: Lateral view of head; C, G: Dorsal view of head; D, H: Ventral view of head. Photos by Ke-Ji Guo.



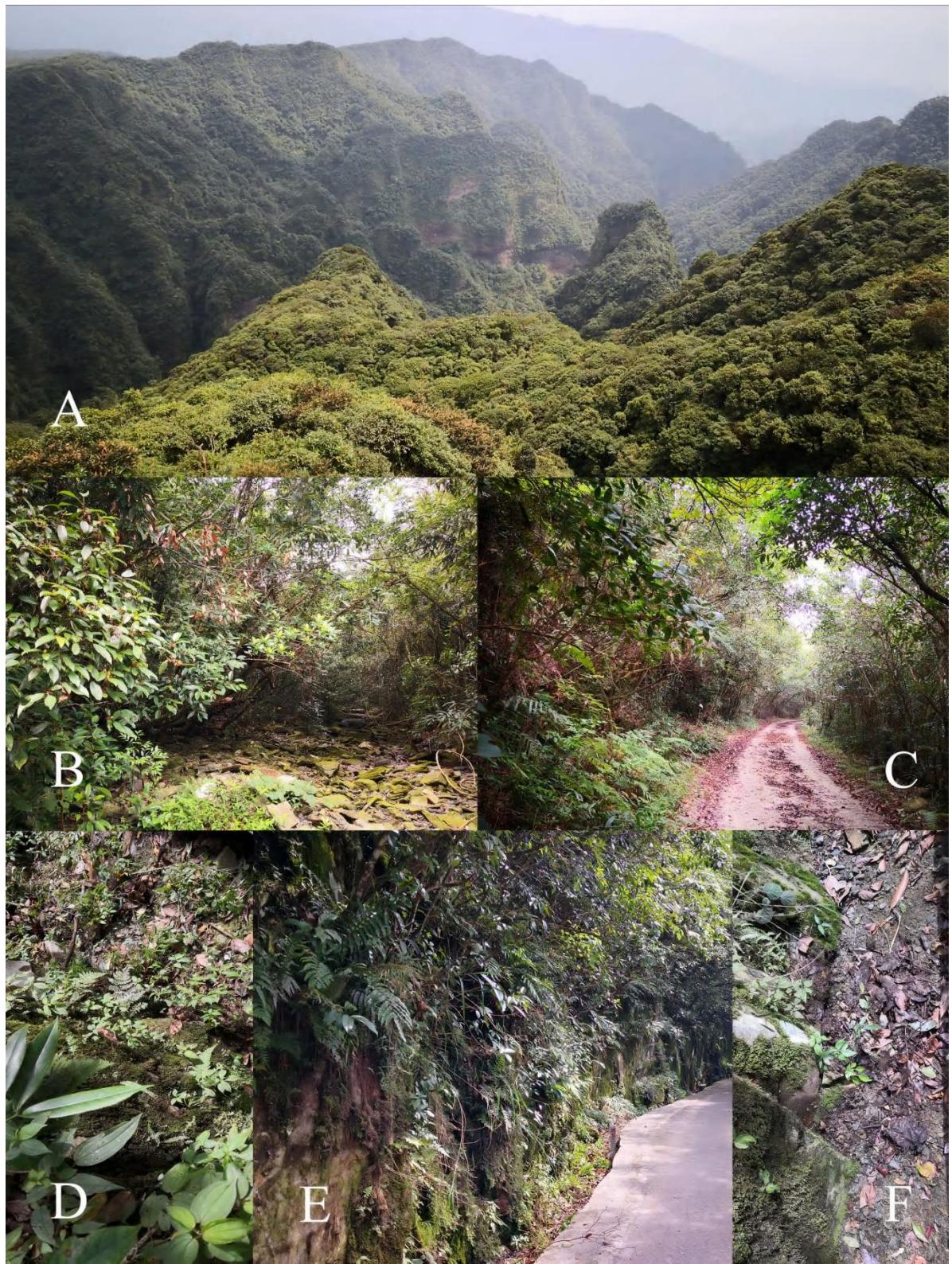
Supplementary Figure S2. Body feature photographs of *Tropidophorus guangxiensis guangxiensis* neotype.

HNU GKJ-2019007, Adult female; A, B: Photos in preservative; C, D: Photos in life; A, D: Dorsal view; B, C: Ventral view. Photos by Ke-Ji Guo.



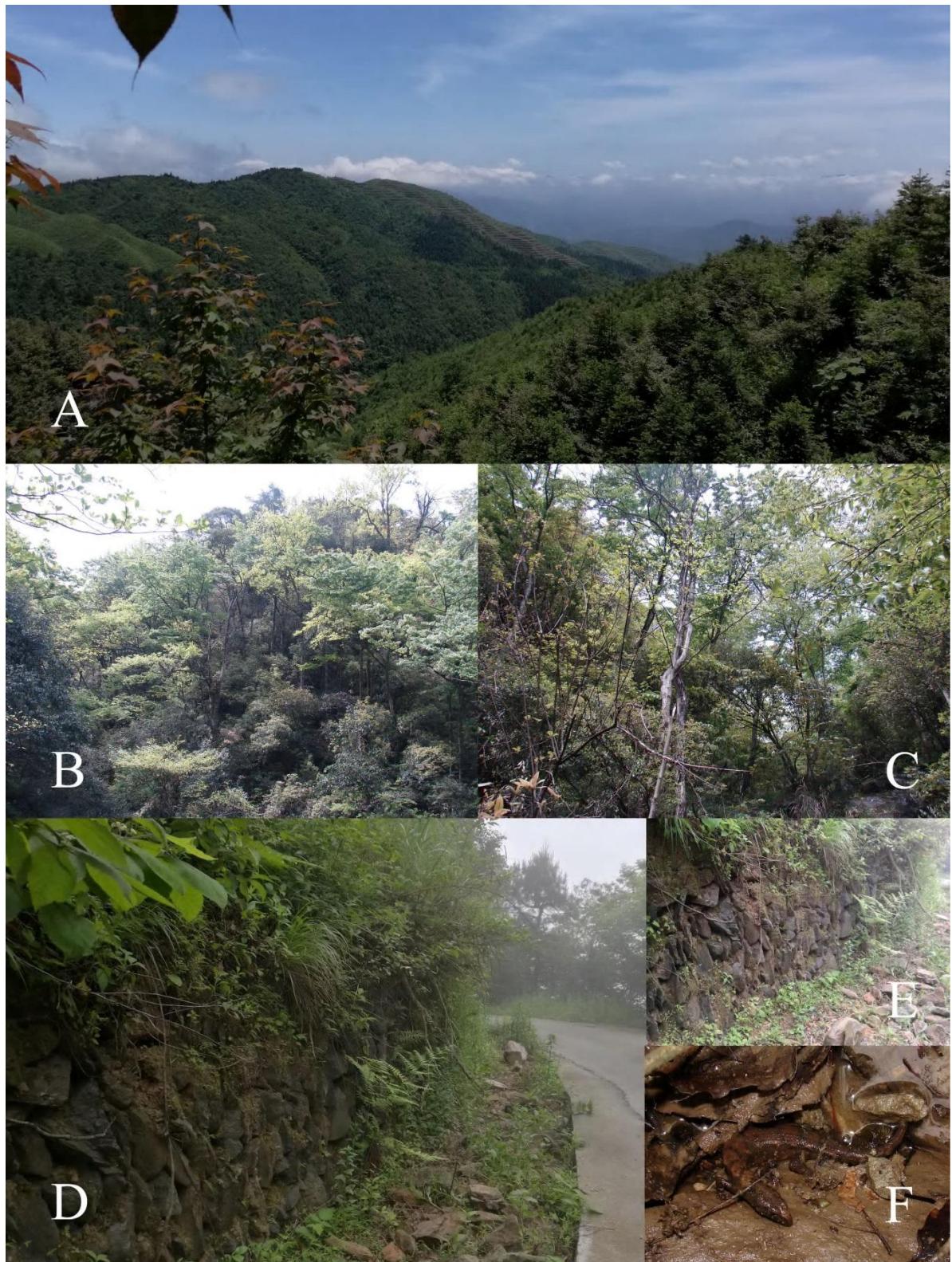
Supplementary Figure S3. Comparison of scales and patterns between *Tropidophorus guangxiensis hongjiangensis* ssp. nov. and *Tropidophorus guangxiensis guangxiensis*.

A, C, E, H: *Tropidophorus guangxiensis guangxiensis* (HNU GKJ-2019007); B, D, F, G: *Tropidophorus guangxiensis hongjiangensis* ssp. nov. (HNU GKJ-2016009); A, B: Ventral front of body of in life; C, D: Ventral front of body in preservative; E, F: Lateral view of head in preservative; G, H: Ventral view of hindlimb and tail; a, c: Color of throat; b, d: Color of ventral neck; e, f: Scales below eyes; g, i: Color of ventral thighs; H, j: Color of ventral shanks; k: Color of ventral tail. Photos by Ke-Ji Guo & Fu Shu.



Supplementary Figure S4. Habitat of *Tropidophorus guangxiensis guangxiensis*.

A, B, C: Macrohabitat of *Tropidophorus guangxiensis guangxiensis* at type locality; D, E, F: Microhabitat of *Tropidophorus guangxiensis guangxiensis* at type locality. Photos by Ke-Ji Guo.



Supplementary Figure S5. Habitat of *Tropidophorus guangxiensis hongjiangensis* ssp. nov.

A: Macrohabitat of *Tropidophorus guangxiensis hongjiangensis* ssp. nov. at type locality; B, C: Vegetation of type locality; D, E: Microhabitat of *Tropidophorus guangxiensis hongjiangensis* ssp. nov. at type locality; F: Ecological photos of *Tropidophorus guangxiensis hongjiangensis* ssp. nov. in life. Photos by Ke-Ji Guo.

Supplementary Tables

Supplementary Table S1. Samples used in this study with locality data and GenBank

Accession numbers

Species	Voucher ID	12S rRNA	16S rRNA	Sample localities	Refrence
<i>Tropidophorus apulus</i>		AY308	AY308	/	Schmitz, 2003
	<i>GenBank</i>	473	322		
<i>Tropidophorus baconi</i>		AB222	AB222	Sulawesi	Honda, et al., 2006
	<i>GenBank</i>	937	953		
<i>Tropidophorus baviensis</i>		AB222	AB222	Ha Tay, Vietnam	Honda, et al., 2006
	<i>GenBank</i>	942	958		
<i>Tropidophorus beccarii</i>		AB222	AB222	Sarawak, Borneo,	Honda, et al., 2006
	<i>GenBank</i>	935	951		
<i>Tropidophorus berdmorei</i>		AB028	AB028	Phu Luang, Thailand,	Honda, et al., 2000
	<i>GenBank</i>	811	823		
<i>Tropidophorus boehmei</i>			GU550	Mt. Hoang Lien, Lao Cai, northern	Nguyen, et al., 2000
	<i>GenBank</i>	-	104	Vietnam	
<i>Tropidophorus boehmei</i>			GU550	Mt. Hoang Lien, Lao Cai, northern	Nguyen, et al., 2000
	<i>GenBank</i>	-	105	Vietnam.	
<i>Tropidophorus brookei</i>		AB222	AB222	Sarawak, Borneo	Honda, et al., 2006
	<i>GenBank</i>	933	949		
<i>Tropidophorus cocincinensis</i>		AB222	AB222	Gia Lai, Vietnam	Honda, et al., 2006
	<i>GenBank</i>	943	959		
<i>Tropidophorus cocincinensis</i>		AY308	AY308	/	Schmitz, 2003
	<i>GenBank</i>	474	323		
<i>Tropidophorus grayi</i>		AB222	-	Philippines	Honda, et al., 2006
	<i>GenBank</i>	941	-		
<i>Tropidophorus hainanus</i>		AB222	AB222	Philippines	Honda, et al., 2006
	<i>GenBank</i>	944	960		
<i>Tropidophorus laticutatus</i>		AB222	AB222	Phu Wua, Thailand	Honda, et al., 2006
	<i>GenBank</i>	934	950		
<i>Tropidophorus matsuii</i>		AB222	AB222	Phu Pa Namtip, Thailand	Honda, et al., 2006
	<i>GenBank</i>	936	952		
<i>Tropidophorus microlepis</i>		AB222	AB222	Indochina	Honda, et al. 2006
	<i>GenBank</i>	947	963		
<i>Tropidophorus micropus</i>		KY488	KY488	Putai, upper Sungei Baleh, Kapit	Pui, et al., 2017
	<i>GenBank</i>	452	456	District, Sarawak, Malaysia	
<i>Tropidophorus micropus</i>		KY488	KY488	Putai, upper Sungei Baleh, Kapit	Pui, et al., 2017
	<i>GenBank</i>	453	457	District, Sarawak, Malaysia	

Species	Voucher ID	12S rRNA	16S rRNA	Sample localities	Reference
<i>Tropidophorus misaminius</i>		AB222 948	AB222 964	Mindanao, Philippines	Honda, et al., 2006
<i>Tropidophorus murphyi</i>	<i>GenBank</i>	AB222 945	AB222 961	Cao Bang, Vietnam	Honda, et al., 2006
<i>Tropidophorus noggei</i>	<i>GenBank</i>	-	EF611 186	/	Ziegler, et al., 2007
<i>Tropidophorus partelloi</i>	<i>GenBank</i>	AB222 946	AB222 962	Mindanao, Philippines	Honda, et al., 2006
<i>Tropidophorus robinsoni</i>	<i>GenBank</i>	AB222 939	AB222 955	Phang-Nga, Thailand	Honda, et al., 2006
<i>Tropidophorus sebi</i>	<i>GenBank</i>	KY488 450	KY488 454	Putai, upper Baleh, Kapit district, Sarawak, East Malaysia	Pui, et al., 2017
<i>Tropidophorus sebi</i>	<i>GenBank</i>	KY488 451	KY488 455	Putai, upper Baleh, Kapit district, Sarawak, East Malaysia	Pui, et al., 2017
<i>Tropidophorus sinicus</i>	<i>GenBank</i>	AB222 938	AB222 954	Hong Kong, China	Honda, et al., 2006
<i>Tropidophorus thai</i>	<i>GenBank</i>	AB222 940	AB222 956	Doi Suthep, Thailand	Honda, et al., 2006
<i>Tropidophorus guangxiensis</i> ssp. <i>guangxiensis</i>	HNU GKJ-201600 9	MW41 3387	MW41 1357	Huaihua, Hunan, China	This study
<i>Tropidophorus guangxiensis</i> ssp. <i>guangxiensis</i>	HNU GKJ-201602 2	MW41 3384	MW41 1358	Huaihua, Hunan, China	This study
<i>Tropidophorus guangxiensis</i> <i>guangxiensis</i>	HNU GKJ-201900 7	MW41 3386	MW41 1359	Mt. Daming, Zhejiang, China	This study
<i>Tropidophorus guangxiensis</i> <i>guangxiensis</i>	HNU GKJ-201900 9	MW41 3385	MW41 1360	Mt. Daming, Zhejiang, China	This study
<i>Lygosoma koratense</i>		AY308 421	AY308 269	/	Schmitz, 2003
<i>Lygosoma koratense</i>	<i>GenBank</i>	AB028 805	AB028 817	Thailand	Honda, et al., 2000

Supplementary Table S2 Uncorrected *p*-distances based on 16S rRNA among species and subspecies of *Tropidophorus* included in this study

	<i>T. apulus</i>	<i>T. bavie</i>	<i>T. bacensis</i>	<i>T. g. hongjiang</i>	<i>T. g. guangxi</i>	<i>T. berdmensis</i>	<i>T. beccarii</i>	<i>T. boehmei</i>	<i>T. brookei</i>	<i>T. cocincinensis</i>	<i>T. grayi</i>	<i>T. hainanus</i>	<i>T. laticutatus</i>	<i>T. matsuii</i>	<i>T. misaminius</i>	<i>T. microlepis</i>	<i>T. micropus</i>	<i>T. murphyi</i>	<i>T. noggei</i>	<i>T. partelloi</i>	<i>T. sebi</i>	<i>T. sinicus</i>	<i>T. thai</i>	<i>T. robinsoni</i>	<i>T. ssp. nov.</i>	<i>T. g. sini</i>	<i>T. sebi</i>	<i>T. thai</i>	<i>T. oni</i>
<i>T. apulus</i>																													
<i>T. bavie</i>	0.0																												
<i>bavie</i>	69																												
<i>bacensis</i>	0.0	0.07																											
<i>T. baconi</i>	03	2																											
<i>T. g. hongjiang</i>	0.0	0.06	0.0																										
<i>hongjiang</i>	72	6	72	0.000																									
<i>ensis</i>																													
<i>ssp. nov.</i>																													
<i>T. g. guangxie</i>	0.0	0.06	0.0																										
<i>guangxie</i>	84	9	84	0.027	0.000																								
<i>nsis</i>																													
<i>T. berdmorei</i>	0.0	0.06	0.0																										
<i>berdmorei</i>	66	3	66	0.069	0.060																								
<i>i</i>																													
<i>T. beccarii</i>	0.0	0.07	0.0																										
<i>beccarii</i>	66	5	69	0.090	0.093	0.075																							
<i>T. boehmei</i>	0.0	0.04	0.0																										
<i>boehmei</i>	69	2	72	0.078	0.081	0.066	0.06																						
<i>T. brookei</i>	0.0	0.08	0.0																										
<i>brookei</i>	75	1	78	0.099	0.090	0.075	0.03	0.06																					
<i>T. cocincinensis</i>	0.0	0.08	0.0																										
<i>cocincinensis</i>	54	5	57	0.084	0.087	0.079	0.08	0.07	0.09																				
<i>nsis</i>																													
<i>T. grayi</i>	0.0	0.08	0.0																										
<i>grayi</i>	48	4	48	0.069	0.072	0.075	0.08	0.07	0.09																				
<i>T. hainanus</i>	0.0	0.02	0.0																										
<i>hainanus</i>	57	1	60	0.066	0.072	0.048	0.07	0.05	0.07																				
<i>T. laticutatus</i>	0.0	0.06	0.0																										
<i>laticutatus</i>	69	3	72	0.084	0.081	0.063	0.07	0.05	0.07																				
<i>T. matsuii</i>	0.0	0.06	0.0																										
<i>matsuii</i>	66	3	69	0.087	0.072	0.060	0.08	0.05	0.08																				
<i>T. misaminius</i>	0.0	0.07	0.0																										
<i>misaminius</i>	78	8	81	0.107	0.101	0.081	0.03	0.07	0.03																				
<i>T. microlepi</i>	0.0	0.08	0.0																										
<i>microlepi</i>	63	1	66	0.090	0.081	0.069	0.07	0.06	0.07																				
<i>s</i>																													
<i>T. micropus</i>	0.0	0.08	0.0																										
<i>micropus</i>	58	8	61	0.073	0.073	0.076	0.07	0.07	0.07																				
<i>T. murphyi</i>	0.0	0.02	0.0																										
<i>murphyi</i>	66	4	69	0.063	0.066	0.048	0.08	0.04	0.08																				
<i>T. noggei</i>	0.0	0.05	0.0																										
<i>noggei</i>	60	1	63	0.072	0.069	0.063	0.07	0.04	0.07																				
<i>T. partelloi</i>	0.0	0.07	0.0																										
<i>partelloi</i>	75	8	72	0.104	0.099	0.078	0.03	0.07	0.03																				
<i>T. sebi</i>	0.0	0.08	0.0																										
<i>sebi</i>	84	4	87	0.104	0.104	0.084	0.02	0.07	0.05																				
<i>T. sinicus</i>	0.0	0.05	0.0																										
<i>sinicus</i>	78	7	78	0.039	0.024	0.054	0.09	0.06	0.09																				
<i>T. thai</i>	0.0	0.06	0.0																										
<i>thai</i>	69	9	72	0.084	0.084	0.057	0.08	0.05	0.07																				
<i>T. robinsoni</i>	0.0	0.05	0.0																										
<i>robinsoni</i>	57	1	60	0.066	0.069	0.057	0.08	0.05	0.07																				

Supplementary Table S3 Measurements (in mm) of *Tropidophorus guangxiensis* *guangxiensis* and *Tropidophorus guangxiensis hongjiangensis* ssp. nov. (abbreviations in Supplementary Materials and Methods, * = regenerated tail)

Species	<i>Tropidophorus guangxiensis</i> <i>guangxiensis</i>		<i>Tropidophorus guangxiensis hongjiangensis</i> ssp. nov.								
	HNU GKJ-201900 7	HNU GKJ-20190 09	HNU GKJ-201600 9	HNU GKJ-200704 001	HNU GKJ-200704 003	HNU GKJ-200704 004	HNU GKJ-200704 002	HNU GKJ-201602 2	HNU GKJ-201602 3	Average	±SD
Type	Neotype	Paraneotype	Holotyp e	Paratyp e	Paratyp e	Paratyp e	Paratyp e	Paratyp e	Paratyp e	N=6	N=6
Sex	F	M(sub-adult)	F	F	F	F	M	F(sub-adult)	Juvenile	with out juvenile	witho ut juven ile
SVL	62.5	48.1	58.5	62.1	64.3	69.7	55.9	49.4	30.4	60	7.1
TaL	68.8	56.7	69.1	65.9	69.5	66.2*	57.2*	53.3	31.9	63.5	6.7
TL	131.4	104.8	127.5	128	133.9	135.9	113.1	102.8	62.4	123. 5	12.9
AG	29.7	24.4	30.6	31.5	32.3	37.8	29.3	25.4	16.3	31.1	4.1
SL	4.8	3.9	4.1	4	4.6	4.6	4.4	3.8	2.9	4.3	0.3
SFIL	41.2	33.1	34.8	36.6	36.5	36.6	35.3	31.5	20.4	35.2	2
HL	11	9.3	9.8	9.5	10.6	10.1	10.3	8.9	6.8	9.9	0.6
HW	8.5	7.2	7.8	8.5	8.7	8.7	8.6	7.3	4.9	8.3	0.6
HH	5.5	4.7	5.8	5.9	6.3	6.4	5.9	6	3.9	6.1	0.3
HNL	24.4	18.5	20.3	21.6	22	21.3	21.2	18.7	12	20.8	1.2
STL	10.5	10.3	10.7	11	11.8	11.6	11.6	9.7	6.9	11	0.8
END	3	2.4	2.4	2.6	3	2.7	2.6	2.3	1.6	2.6	0.2
EL	3.1	2.5	2.7	3.1	3.2	3	3.2	2.5	1.9	2.9	0.3
ETL	4.6	4	4.2	4.3	4.5	4.5	4.4	3.7	2.5	4.3	0.3
TYD	1.9	1.6	1.6	1.8	2.1	1.9	1.8	1.5	1.2	1.8	0.2
FIL	16.8	43.1	14.4	14.5	14.2	15.7	13.4	11.7	8	14	1.3
HIL	22.4	19.3	21.4	21.9	22.4	22.7	21.1	19	10.7	21.4	1.3

Supplementary Table S4 Scalation and Coloration of *Tropidophorus guangxiensis* *guangxiensis* and *Tropidophorus guangxiensis hongjiangensis* ssp. nov. (abbreviations in Supplementary Materials and Methods)

No.	<i>Tropidophorus guangxiensis</i> <i>guangxiensis</i>		<i>Tropidophorus guangxiensis hongjiangensis</i> ssp. nov.					
	HNU GKJ-2019007	HNU GKJ-2019009	HNU GKJ-2016009	HNU GKJ-2007040 01	HNU GKJ-2007040 03	HNU GKJ-2007040 04	HNU GKJ-2007040 02	HNU GKJ-2016022

Type	Neotype	Paraneotyp e M(sub-adu lt)	Holoty pe F	Paraty pe F	Paraty pe F	Paratyp e F	Paraty pe M	Paraty pe F(sub- adult)
Sex	F							
Scalation								
Upper head scales (sm=smooth, kl=keeled)	KL	KL	KL	KL	KL	KL	KL	KL
A shallow groove from posterior corner of nasal to the end of sixth upralabial	Y	Y	Y	Y	Y	Y	Y	Y
Frontonasal	1	0	1	1	1	0	0	1
Prefrontals widely separated	Y	N	Y	Y	Y	Y	N	Y
Interparietal with a small transparent spot	N	N	N	N	N	N	N	N
Number of scales bordering postero-lateral parietals	5	6	7	6	6	6	6	6
Parietals in contact posteriorly	N	N	N	N	N	N	N	N
Nuchals	N	N	N	N	N	N	N	N
Supraoculars	4	4	4	4	4	4	4	4
Loreals	2	2	2	2	2	2	2	2
Loreals separated from supralabials by small scales	N	N	N	N	N	N	N	N
Lower eyelid	scaly	scaly	scaly	scaly	scaly	scaly	scaly	scaly
Supraciliaries	8/8	8/8	7/7	8/8	7/6	7/8	7/8	7/7
Supraciliary row interrupted by fourth supraocular	N	N	N	N	N	N	N	N
Supralabials	8	7/8	8	8	8	8	8	8
Infralabials	7/6	7/6	6/6	6/6	6/6	7/7	6/6	6/6
Primary temporal	3/3	4/4	3/3	4/4	4/4	4/3	4/4	3/3
Secondary temporal	4/4	4/5	5/5	4/4	4/4	6/4	4/4	4/4
Midbody scale rows	29	28	33	31	30	31	31	32
Dorsal scale rows across the back	8	8	8	8	8	8	8	8
Paravertebral scales	50	49	47	47	47	47	45	47
Paravertebral scales widened	N	N	N	N	N	N	N	N
Ventral scales(number of scales from first gular to anterior margin of precloacals)	50	44	50	53	50	51	50	52
Midbody ventral scales(counted from posterior margin of fore limb to last scale before precloacals)	29	27	31	33	32	32	30	32
Ventral scales(sm=smooth, kl=keeled)	SM	SM	SM	SM	SM	SM	SM	SM
Ventral scales of neck (sm=smooth, kl=keeled)	KL	KL	KL	KL	KL	KL	KL	KL
Precloacals	4	4	4	4	4	4	4	4
Right precloacal overlapped by left one	N	Y	N	Y	N	N	Y	Y

No.	<i>Tropidophorus guangxiensis</i>		<i>Tropidophorus guangxiensis hongjiangensis</i> ssp. nov.					
	HNU GKJ-2019007	HNU GKJ-2019009	HNU GKJ-2016009	HNU GKJ-200704001	HNU GKJ-200704003	HNU GKJ-200704004	HNU GKJ-200704002	HNU GKJ-2016022
Type	Neotype	Paraneotype	Holotype	Paratype	Paratype	Paratype	Paratype	Paratype
Sex	F	M(sub-adult)	F	F	F	F	M	F(sub-adult)
Medial precloacal enlarged, overlaps outer scales	Y	Y	Y	Y	Y	Y	Y	Y
Supracaudals(sm=smooth, kl=keeled)	KL	KL	KL	KL	KL	KL	KL	KL
Subcaudals	5+53+1	5+50+1	6+52+1	6+51+1	4+51+1	5+44+1 *(tip lost)	5+47+1 *	5+48+1
Tail scale rows at position of tenth subcaudal	13	11	14	14	13	13	13	14
Lamellae under fourth finger	11/11	13/14	12/12	12/12	12/12	11/12	12/11	11/12
Lamellae under fourth toe	17/17	18/17	19/18	18/18	16/17	18/17	17/18	17/16
Ventralfront scales of hindlimbs(sm=smooth, kl=keeled)	SM	SM	SM	SM	SM	SM	SM	SM
Adpressed limbs touching	Y	Y	Y	N	N	N	Y	Y
Coloration in preservative								
Background of head and dorsum	dark	dark	dark	dark	dark	dark	dark	dark
Dorsum with light bands	indistinct	indistinct	indistinct	indistinct	indistinct	indistinct	indistinct	indistinct
Longitudinal rows of white spots on neck dorsum	2	2	2	2	2	2	2	2
Lateral side with white spots	Y	Y	Y	Y	Y	Y	Y	Y
Upper labial with white spots	Y	Y	Y	Y	Y	Y	Y	Y
Chin and throat with dark marbling	Y	Y	Y	Y	Y	Y	Y	Y
Ventral of neck dark brown with white pinstripe	Y	Y	Y	Y	Y	Y	Y	Y
Venter brownish-cream	Y	Y	Y	Y	Y	Y	Y	Y
Underside of tail tip dark grey	N	N	Y	Y	Y	Y	Y	Y

Y= Yes; N=No.

Supplementary Table S5 Comparisons of diagnostic characters in *Tropidophorus* from China (* = data obtained from literature)

Characters	<i>T. berdmorei</i>	<i>T.</i>	<i>T.</i>	<i>T. guangxiensis</i>	
		<i>hainanus</i>	<i>sinicus</i>	<i>guangxiensis</i>	<i>hongjiangensis</i>
					ssp. nov.
Upper head scales smooth (sm) or keeled (kl)	sm	kl	kl	kl	kl
Frontonasal	2	2	2	1/0	1/0
Frontonasal divided (2) or undivided (1)	1	1	2	-	-
Prefrontals in contact (1) or separated (0)	0/1	0, rarely 1	1	1/0	1/0
Parietals in contact (1) or separated (0) posteriorly	1,rarely 0	1	-	0	0
Loreals	2	4	2/1	2	2
Anterior loreal divided	Y /N	-	-	N	N
Supraciliaries	8	5	6	8	6-8
Supraciliary row interrupted by fourth supraocular	Y	Y		N	N
Supralabials	6	6	6	7-8	8
Infralabials	5-7	5-7	5	6-7	6
Midbody scale rows	32-40	30-34	29-3 0	28-29	30-33
Paravertebral scales	64	-	-	45-50	45-47
Paravertebral scales widened (1) or not (0)	-	-	-	0	0
Dorsal body scales smooth (sm) or keeled (kl)	sm(kl in juveniles)	kl	kl	kl	kl
Ventral scales	53	-	-	44-50	50-53
Midbody ventral scales	-	-	-	27-29	30-33
Ventral scales smooth (sm) or keeled (kl)	sm	sm	kl	sm	sm
Scale rows at position of tenth subcaudal	-	-	-	11-13	13-14
Subcaudals divided on anterior part of tail (1) or on whole tail (2)	1	-	-	1	1
Lamellae under fourth toe	22	13-16	13-1 4	17-18	16-19
White spots on dorsum	present	present	prese nt	present	present
Sample size (n)	n=10*	n=5*	n=7*	n=5*	n=6

Supplementary Table S6 Distribution information of samples from China used in this study

Sit e	Detail Sample localities	Longitu de	Latitu de	Species and Subspecies	Source
1	Husa, Yunnan, China	97.9087 00	24.465 275	<i>T. berdmorei</i>	Zhao EM et al., 1999
2	Daming Moutain National Nature Reserve, Guangxi, China	108.365 346	23.525 552	<i>T. g. guangxiensis</i>	This study; Zhao EM et al., 1999
3	Mt. Jiulian, Jiangxi, China	114.552 264	24.632 778	<i>T. hainanus</i>	Zhao EM et al., 1999
4	Mt. Qiyun, Jiangxi, China	114.331 558	25.565 663	<i>T. hainanus</i>	Yang DD et al., 2008
5	Mt. Wuzhi, Hainan, China	109.587 792	18.830 943	<i>T. hainanus</i>	Zhao EM et al., 1999
6	Mt. Diaolu, Hainan, China	109.868 154	18.702 561	<i>T. hainanus</i>	Zhao EM et al., 1999
7	Mt. Jianfengling, Hainan, China	108.895 500	18.718 302	<i>T. hainanus</i>	Lv SQ et al., 2005
8	Mt. Bawangling, Hainan, China	109.260 438	19.136 068	<i>T. hainanus</i>	Lv SQ et al., 2005
9	Mt. Limu, Hainan, China	109.766 802	19.204 772	<i>T. hainanus</i>	Lv SQ et al., 2005
10	Mt. Dayao, Guangxi, China	110.107 577	23.939 175	<i>T. hainanus</i>	Zhao EM et al., 1999
11	Mt. Chebaling, Guangdong, China	114.258 143	24.731 912	<i>T. hainanus</i>	Rao JT et al., 2011
12	Mt. Mang, Hainan, China	112.925 401	24.928 465	<i>T. hainanus</i>	Fei DB et al., 2010
13	Mt. Raoren, Guizhou, China	107.961 229	25.952 088	<i>T. hainanus</i>	Zhang YH et al., 2012
14	Mt. Dinghu, Guangdong, China	112.537 245	23.168 927	<i>T. sinicus</i>	Zhao EM et al., 1999
15	Mt. Baiyun, Guangdong, China	111.333 164	23.485 651	<i>T. sinicus</i>	Luo ZH, 2018
16	Mt. Luofu, Guangdong, China	114.040 293	23.267 053	<i>T. sinicus</i>	Zhao EM et al., 1999
17	Mt. Xiangtou, Guangdong, China	114.403 827	23.337 080	<i>T. sinicus</i>	Yang DD et al., 2001
18	Dapeng Peninsula Nature Reserve, Guangdong, China	114.550 159	22.519 795	<i>T. sinicus</i>	Zhang J et al., 2019

Sit e	Detail Sample localities	Longitu de	Latitu de	Species and Subspecies	Source
19	Mt. Wutong, Guangdong, China	114.218 955	22.577 534	<i>T. sinicus</i>	Tang YL et al., 2015
20	Hongkong, China	114.027 786	22.394 206	<i>T. sinicus</i>	Zhao EM et al., 1999
21	Mt. Dayao, Guangxi, China	110.335 234	24.292 401	<i>T. sinicus</i>	Zhao EM et al., 1999
22	Nonggang National Nature Reserve, Guangxi, China	106.960 510	22.466 298	<i>T. sinicus</i>	Zhao EM et al., 1999
23	Dizhou Nature Reserve, Guangxi, China	106.387 440	23.006 121	<i>T. sinicus</i>	Zeng XB & Su SL, 2008
24	Diding Nature Reserve, Guangxi, China	105.991 578	23.094 119	<i>T. sinicus</i>	Mo YM, et al., 2007
25	Laohutiao Nature Reserve, Guangxi, China	105.717 503	23.098 433	<i>T. sinicus</i>	Zeng XB et al., 2015
26	Mulun National Nature Reserve, Guangxi, China	108.272 357	24.830 213	<i>T. g. guangxiensis</i>	Wang QQ, 2014
27	Xuefeng Mountain National Forest Park, Hunan, China	110.398 461	27.307 747	<i>T. g. hongjiangensis</i> ssp. nov.	This study; Guo KJ et al., 2010