

Description of a new karst-adapted species of the subgenus *Japonigekko* (Squamata: Gekkonidae: *Gekko*) from Guangxi, southern China

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Abstract

A new species of the genus *Gekko* Laurenti, 1768, *Gekko paucituberculatus* sp. nov., is described here, based on two specimens from Tianyang District, Baise City, Guangxi Zhuang Autonomous Region, China. It was placed in subgenus *Japonigekko* on the basis of morphological and molecular phylogenetic analysis and can be distinguished from all congeners in this subgenus by significant divergences in the mitochondrial 16S and ND2 genes and by a combination of the following morphological characters: Moderate body size, SVL 77.2 mm in the adult male and SVL 85.9 mm in the adult female; tubercles only present along dorsolateral trunk and absent on other regions; fingers and toes with weak webbing; continuous precloacal pores 12 in the male, absent in the female; a single postcloacal tubercle on each side; a light-coloured vertebral line from nape to tip of tail; dorsum greyish-brown, with 7–8 dirty-white bands between nape and sacrum. Meanwhile, the distribution of *G. palmatus* in China has been confirmed as occurring in Guangxi and Guangdong Provinces. This study brings the total species of the subgenus *Japonigekko* in China to 19.

Key words

Gekko paucituberculatus sp. nov., *Gekko palmatus*, karst, new national record, taxonomy

Introduction

The genus *Gekko* Laurenti, 1768, currently containing 88 recognised species assigned to seven subgenera, is a widely distributed group of nocturnal lizards (Wood et al. 2020; Uetz et al. 2023; Zhang et al. 2023). Amongst these subgenera, *G. (Japonigekko)* is the most diverse group with many karst-dwellers. At present, there are three described *G. (Japonigekko)* species-adapted karst ecosystems in China, namely *G. adleri* Nguyen et al., 2013 and *G. kwangsiensis* Yang, 2015 from Guangxi and *G. liboensis* Zhou & Li, 1982 from Guizhou and Guangxi

(Nguyen et al. 2013; Jono et al. 2015; Yang 2015). During the field survey in the karst forest of western Guangxi, southern China (Fig. 1), two gekkonid individuals were collected. Morphologically, the specimens possess the common characteristics of subgenus *G. (Japonigekko)*, but are apparently distinct from all known congeners by the following characters: Moderate body size, tubercles only present along dorsolateral trunk, continuous precloacal pores 12 in the male, a single postcloacal tubercle on each side and a light-coloured vertebral line from nape

to tip of tail. Phylogenetic studies reveal that these specimens belong to a separated taxon most closely related to *G. kwangsiensis*. Hence, we consider it as a new species and describe it below.

Materials and Methods

Specimens and morphology

Two specimens were collected from Tianyang District, Baise City, Guangxi Zhuang Autonomous Region, China on 3 August 2023. The specimens were euthanised and then fixed in 10% buffered formalin, later being transferred to 75% ethanol and deposited in the Museum of Biology, Sun Yat-sen University (SYS), Guangzhou, China. Liver tissue samples were preserved in 95% ethanol for molecular analysis.

Measurements were taken with digital callipers (Deli DL91200 Digital Vernier Caliper) to the nearest 0.1 mm on the right side of the body and scelation features were counted under a binocular scope (Leica EZ4 HD). Bilateral scale counts are given as left/right. External measurements, meristic traits and their abbreviations follow Lyu et al. (2021) and Grismer et al. (2022). They are snout–vent length (**SVL**, from tip of snout to anterior margin of cloaca); tail length (**TaL**, from posterior margin of cloaca

to tip of tail); axilla-groin length (**AG**, distance between axilla and groin); head length (**HL**, maximum head length from tip of snout to posterior margin of ear opening); head width (**HW**, measured at the angle of the jaws); head height (**HH**, from the top of the head posterior to the eyes to the bottom of the lower jaw); snout length (**SNT**, from snout tip to anterior corner of eye); maximum eye diameter (**ED**); maximum ear opening diameter (**EOD**); maximum rostral width (**RW**); maximum rostral height (**RH**); maximum mental width (**MW**); maximum mental length (**ML**); nasals (**N**, nasorostrals, supranasals and postnasals); intersupranasals (**I**, scales between supranasals, in contact with rostral); supralabials and infralabials (**SPL** and **IFL**, number of scales from commissure of jaw to the rostral /mental scale); interorbitals (**IO**, number of scales in a line between anterior corners of eyes); preorbitals (**PO**, number of scales in a line from nostril to anterior corner of the eye); postmentals (**PM**, scales bordering the mental); gulars bordering the postmentals (**GP**); dorsal tubercle rows at mid-body (**DTR**); granules surrounding dorsal tubercles (**GSDT**); scales in a line from mental to the front of cloacal slit (**SMC**); ventral scale rows at mid-body (**V**); scale rows at mid-body (**SR**, including ventral scales); subdigital lamellae under entire first finger (**LF1**); subdigital lamellae under entire fourth finger (**LF4**); subdigital lamellae under entire first toe (**LT1**); subdigital lamellae under entire fourth toe (**LT4**); precloacal pores (**PP**); postcloacal tubercles (**PAT**); dorsal scale rows in the middle of the third caudal whorl (**S3W**).

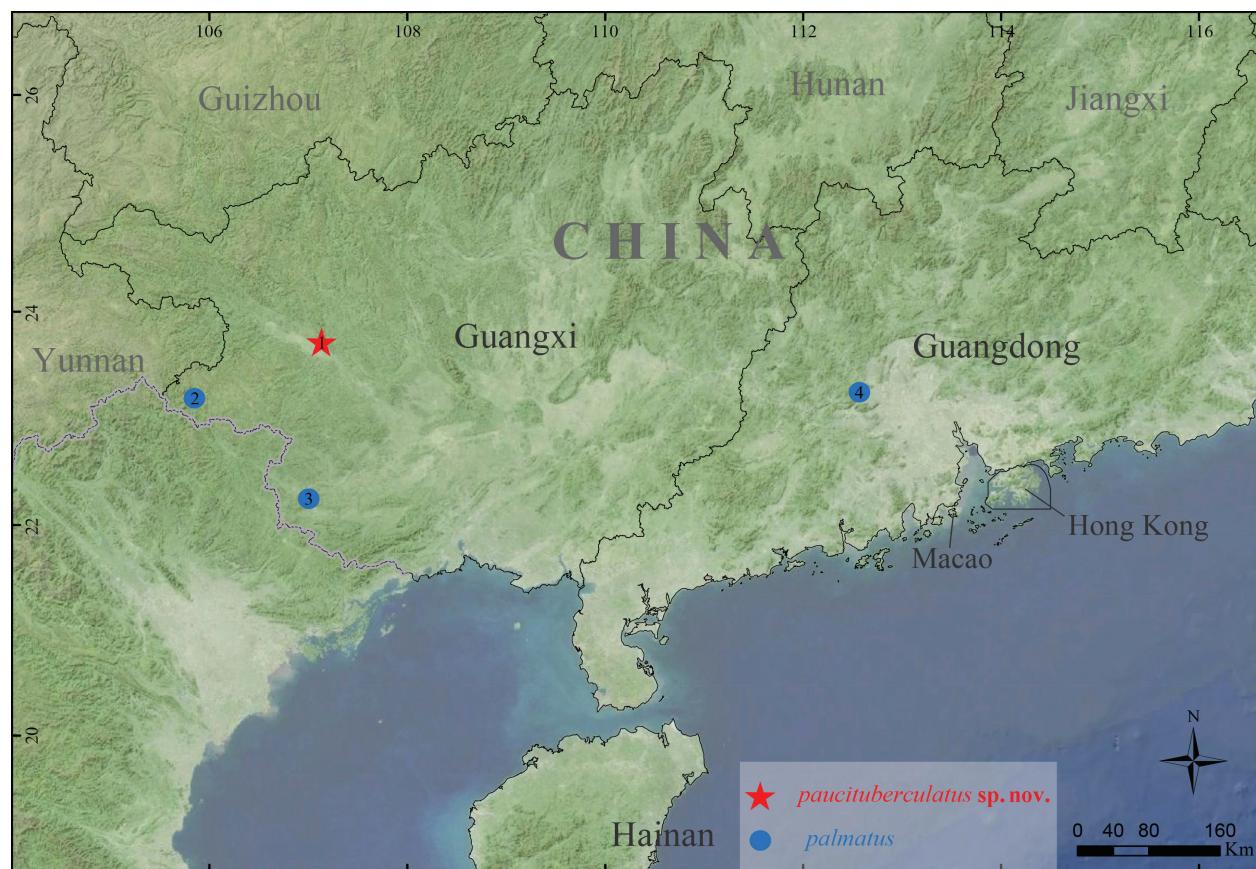


Figure 1. Localities of *Gekko paucituberculatus* sp. nov. and *G. palmatus*. 1 Tianyang District, Baise City, Guangxi; 2 Napo County, Baise City, Guangxi; 3 Nonggang Nature Reserve, Chongzuo City, Guangxi; 4 Mt. Dinghu, Zhaoqing City, Guangdong.

In addition, the specimens were compared with other *Gekko (Japonigekko)* congeners on the basis of descriptions in literature (Zhou et al. 1982; Song 1985; Ota et al. 1995; Toda et al. 2008; Phung and Ziegler 2011; Rösler et al. 2011; Nguyen et al. 2013; Luu et al. 2014, 2015, 2017; Jono et al. 2015; Ngo et al. 2015; Yang 2015; Lin and Yao 2016; Hou et al. 2021; Lyu et al. 2021; Sitthivong et al. 2021; Zhang et al. 2023).

Phylogenetic sampling and analyses

A total of 24 samples of subgenus *Gekko (Japonigekko)* were used for molecular analysis in this study. All samples were attained from euthanasia specimens and then

preserved in 95% ethanol and stored at -40°C. Furthermore, 22 sequences were obtained from GenBank and incorporated into our dataset for phylogenetic analysis. *G. gecko* and *G. reevesii*, belonging to subgenus *G. (Gekko)*, were used to root the tree, based on Rösler et al. (2011) and Lyu et al. (2021). Detailed information of these samples is given in Table 1.

Genomic DNA was extracted from liver tissue using a DNA extraction kit (Tiangen Biotech Co., Ltd, Beijing). Two fragments of the mitochondrial genes that encode the partial 16S ribosomal RNA gene (16S) and partial NADH dehydrogenase subunit 2 gene (ND2) were amplified. The primers used for two genes are listed in Table 2. PCR amplifications were processed with the following cycling conditions: Initial denaturing step at 95°C for

Table 1. Localities, voucher information and GenBank accession numbers for all samples used in this study.

ID	Species	Localities	Voucher ID	GenBank accession numbers		References
				16S	ND2	
Ingroups						
1	<i>Gekko paucituberculatus</i> sp. nov.	China: Guangxi: Baise, Tianyang	SYS r002806	OR903154	OR902163	This study
2	<i>Gekko paucituberculatus</i> sp. nov.	China: Guangxi: Baise, Tianyang	SYS r002807	OR903155	OR902164	This study
3	<i>G. cib</i>	China: Sichuan: Hejiang	SYS r001489	MW451655	OR902165	Lyu et al. (2021), this study
4	<i>G. cib</i>	China: Sichuan: Mt. Emei	SYS r000708	MW451629	OR902166	Lyu et al. (2021), this study
5	<i>G. subpalmatus</i>	China: Zhejiang: Fenghua	SYS r001762	MW451662	OR902167	Lyu et al. (2021), this study
6	<i>G. subpalmatus</i>	China: Zhejiang: Fenghua	SYS r001767	MW451663	OR902168	Lyu et al. (2021), this study
7	<i>G. melli</i>	China: Guangdong: Dongyuan	SYS r001742	MW451661	OR902169	Lyu et al. (2021), this study
8	<i>G. melli</i>	China: Guangdong: Puning	SYS r001702	MW451660	OR902170	Lyu et al. (2021), this study
9	<i>G. swinhonis</i>	China: Hebei: Zunhua	SYS r001814	MW451666	OR902171	Lyu et al. (2021), this study
10	<i>G. hokouensis</i>	China: Jiangxi: Mt. Meiling	SYS r001311	MW451648	OR902172	Lyu et al. (2021), this study
11	<i>G. hokouensis</i>	China: Fujian: Mt. Wuyi	SYS r001290	MW451647	OR902173	Lyu et al. (2021) this study
12	<i>G. kwangsiensis</i>	China: Guangxi: Wuming	SYS r001194	MW451641	OR902174	Lyu et al. (2021), this study
13	<i>G. kwangsiensis</i>	China: Guangxi: Wuming	SYS r001195	MW451642	OR902175	Lyu et al. (2021) this study
14	<i>G. japonicus</i>	China: Fujian: Mt. Wuyi	SYS r000672	MW451628	OR902176	Lyu et al. (2021), this study
15	<i>G. japonicus</i>	China: Jiangxi: Lushan	SYS r001317	MW451649	OR902177	Lyu et al. (2021), this study
16	<i>G. adleri</i>	Vietnam: Cao Bang	IEBR A.2012.24	KC700623	—	Nguyen et al. (2013)
17	<i>G. adleri</i>	China: Guangxi: Jingxi	SYS r001400	MW451654	OR902178	Lyu et al. (2021), this study
18	<i>G. palmatus</i>	China: Guangdong: Mt.Dinghu	SYS r002797	OR903156	OR902179	This study
19	<i>G. palmatus</i>	China: Guangdong: Mt.Dinghu	SYS r002804	OR903157	OR902180	This study
20	<i>G. palmatus</i>	Vietnam: Lang Son	IEBR 2474	KC710234	—	Nguyen et al. (2013)
21	<i>G. palmatus</i>	Vietnam: Lang Son	IEBR 3620	KC710238	—	Nguyen et al. (2013)
22	<i>G. palmatus</i>	Vietnam: Bac Giang	IEBR A.0807	KC710233	—	Nguyen et al. (2013)
23	<i>G. palmatus</i>	China: Guangxi: Nonggang Nature Reserve	SYS r001192	MW451639	OR902181	Lyu et al. (2021), this study
24	<i>G. palmatus</i>	China: Guangxi: Napo	SYS r001185	MW451637	OR902182	Lyu et al. (2021), this study
25	<i>G. chinensis</i>	China: Hong Kong	SYS r001211	MW451644	OR902183	Lyu et al. (2021), this study
26	<i>G. chinensis</i>	China: Guangdong: Shenzhen	SYS r001085	MW451632	OR902184	Lyu et al. (2021), this study
27	<i>G. similignum</i>	China: Hainan: Mt. Wuzhi	SYS r001597	MW451658	OR902185	Lyu et al. (2021), this study
28	<i>G. similignum</i>	China: Hainan: Mt. Wuzhi	SYS r001598	MW451659	OR902186	Lyu et al. (2021), this study
29	<i>G. auriverrucosus</i>	China: Shanxi: Yuncheng	NNU Z 20050716.004	—	JN019062	Rösler et al. (2011)
30	<i>G. bonkowskii</i>	Laos: Khammouane	VFU R.2014.10	—	KT266818	Luu et al. (2015)
31	<i>G. khunkhamensis</i>	Laos: Khammouane	VNUF R.2021.23	—	OL416111	Sitthivong et al. (2021)
32	<i>G. khunkhamensis</i>	Laos: Khammouane	VNUF R.2021.02	—	OL416109	Sitthivong et al. (2021)
33	<i>G. jinjiangensis</i>	China: Yunnan: Deqin	CIB5334220115	—	MT449431	Hou et al. (2021)

ID	Species	Localities	Voucher ID	GenBank accession numbers		References
				16S	ND2	
34	<i>G. jinjiangensis</i>	China: Sichuan: Derong	CIB5133380017	—	MT449437	Hou et al. (2021)
35	<i>G. scabridus</i>	China: Sichuan: Yanbian	CIB-YN201909199	—	MT449429	Hou et al. (2021)
36	<i>G. scabridus</i>	China: Sichuan: Yanbian	CIB-YN201909200	—	MT449430	Hou et al. (2021)
37	<i>G. scientiadventura</i>	Vietnam: Quang Binh	IEBR A.2014.7	—	KP205392	Luu et al. (2014)
38	<i>G. scientiadventura</i>	Laos: Khammouane	VFU2014.2	—	KP205394	Luu et al. (2014)
39	<i>G. sengchanthavongi</i>	Laos: Khammouane	VFU R2014.14	—	KT266816	Luu et al. (2015)
40	<i>G. sengchanthavongi</i>	Laos: Khammouane	IEBR A.2015.33	—	KT266817	Luu et al. (2015)
41	<i>G. thakhekensis</i>	Laos: Khammouane: Thakhek	IEBR A.2014.6	—	KP205396	Luu et al. (2014)
42	<i>G. thakhekensis</i>	Laos: Khammouane: Thakhek	VFU R.2014.9	—	KP205397	Luu et al. (2014)
43	<i>G. truongi</i>	Vietnam: Khanh Hoa	IEBR A.2011.1	—	KP205398	Luu et al. (2014)
44	<i>G. nadenensis</i>	Laos: Khammouane	ZFMK 98741	—	KY421618	Luu et al. (2017)
Outgroups						
45	<i>G. gecko</i>	China: Guangxi: Nanning	N/A	AY282753	AY282753	Zhou et al. (2006)
46	<i>G. reevesii</i>	China: Guangdong: Mt. Yiping	SYS r000796	MW451630	OR902187	Lyu et al. (2021), this study

Table 2. Primers used in this study.

Gene	Primer	Sequence	Reference
16S	L3975	5'-CGCCTGTTACCAAAAAACAT-3'	Simon et al. (1994)
	H4551	5'-CCGGTCTGAACTCAGATCACGT-3'	
ND2	rMet-3L	5'- ATACCCCCGACAATGTTGG-3'	Jonniaux and Kumazawa (2008)
	rAla-1H	5'- GCCTTAGCTTAATTAAAGTG-3'	

4 min and 5 min (16S and ND2, respectively), 35 cycles of denaturing at 95°C for 40 s, annealing at 53°C for 34 s (16S) and 55°C for 40 s (ND2), extending at 72°C for 60 s and a final extending step at 72°C for 10 min. PCR products were purified with spin columns and then sequenced with a forward primer using BigDye Terminator Cycle Sequencing Kit (Applied Biosystems, Waltham, MA, USA). Sequencing was performed on an ABI Prism 3730 automated DNA sequencer by Wuhan Tianyi Huiyuan Bioscience and Technology Inc.

DNA sequences were aligned by the MUSCLE algorithm with default parameters (Edgar 2004). PartitionFinder2 was used to determine the best partitioning scheme (Lanfear et al. 2017) and jModelTest v.2.1.2 was used to determine the best fitting nucleotide substitution models (Darriba et al. 2012), resulting in the partitions by gene. ND2 was further partitioned by codon position and the best fit models for all partitions was GTR+I+G. Sequenced data were analysed using Bayesian Inference (BI) in MrBayes 3.2.4 (Ronquist et al. 2012) and Maximum Likelihood (ML) in raxmlGUI 1.3 (Silvestro and Michalak 2012). Two independent runs were conducted in the BI analysis with 2,000,000 generations each and sampled every 1000 generations with the first 25% of samples discarded as burn-in, resulting in a potential scale reduction factor (PSRF) of < 0.005. In the ML analysis, a bootstrap consensus tree inferred from 1000 replicates was generated. MEGA11 was used to calculate uncorrected pairwise sequence divergence for 16S and ND2 amongst and with-

in species using the complete deletion option which removes missing data and gaps (Tamura et al. 2021).

Results

The aligned dataset contained a total of 1578 nucleotide base pairs (bp), with 566 bp for 16S and 1012 bp for ND2. The BI and ML analyses resulted in essentially identical topologies (Fig. 2). The mean uncorrected p distances, based on 16S and ND2 used in this study, are given in Tables 3 and 4.

All *Gekko* (*Japonigekko*) samples used in this study formed a strongly-supported monophyletic lineage (BPP = 1.00; BS = 100). However, intrageneric relationships within this lineage remained unclear due to low intrageneric nodal supports. Two samples from Baise City, Guangxi were placed in subgenus *G. (Japonigekko)*, which clustered together with strong support (BPP = 1.00; BS = 100) and exhibited low intra-lineage genetic differentiation (0%). This unnamed lineage is the sister taxon to *G. kwangsiensis* from Wuming County, Guangxi and these together formed the sister group to *G. hokouensis* Pope, 1928. The lowest genetic distance between the unnamed lineage and a known *Gekko* species were, on average, 8.96% in 16S and 15.54% in ND2, as compared to *G. kwangsiensis*, although we did not use genetic divergences to make species delimi-

tation, as it served as a reference only. The newly-collected specimens showed recognisable morphological differences from all known congeners (see **Taxonomic account** below). Hence, the unnamed population from Baise City is considered as an undefined species.

In addition, two samples from Mt. Dinghu, Guangdong grouped together with other *G. palmatus* Boulenger, 1907 samples from Vietnam and Guangxi, China and exhibit a robust monophyletic lineage with strong support (BPP = 1.00; BS = 100) and low intrapopulational genetic differentiation (0.34% in 16S and 0.82% in ND2). Morphologically, the characters of the specimens from Guangdong mostly agree with the original description and re-description of *G. palmatus* Boulenger, 1907 (Ota et al. 1995).

Combined with results of Lyu et al. (2021), we regard *G. palmatus* as representing a new national record from China, occurring in Guangdong and Guangxi.

Taxonomic account

Gekko paucituberculatus sp. nov.

<https://zoobank.org/C2814152-01A1-4558-892B-9D538ED-1FE9D>

Figures 3, 4 and 5

Table 3. Uncorrected p distances (%) of the 16S gene amongst species of *Gekko* (*Japonigekko*) used in this study.

	Species	1	2	3	4	5	6	7	8	9	10	11	12
1	<i>G. paucituberculatus</i> sp. nov.	0.00											
2	<i>G. cib</i>	9.76	0.00										
3	<i>G. subpalmatus</i>	13.15	6.37	0.00									
4	<i>G. melli</i>	10.96	4.68	6.87	0.60								
5	<i>G. swinhonis</i>	13.94	10.16	12.15	10.76	—							
6	<i>G. hokouensis</i>	9.56	10.46	12.35	10.56	12.85	0.40						
7	<i>G. kwangsiensis</i>	8.96	11.45	12.25	11.45	14.44	10.66	0.40					
8	<i>G. japonicus</i>	12.35	11.55	11.95	11.75	14.14	10.76	11.85	0.00				
9	<i>G. adleri</i>	11.75	11.55	12.75	10.76	14.14	12.15	12.35	13.35	0.40			
10	<i>G. palmatus</i>	10.70	10.90	12.29	10.70	14.17	11.60	11.81	12.89	2.59	0.34		
11	<i>G. chinensis</i>	10.26	10.26	11.65	10.46	13.84	11.25	10.96	11.45	3.49	3.09	0.20	
12	<i>G. similignum</i>	10.96	10.96	11.75	10.96	14.14	11.16	11.85	11.16	3.78	3.39	1.29	0.00

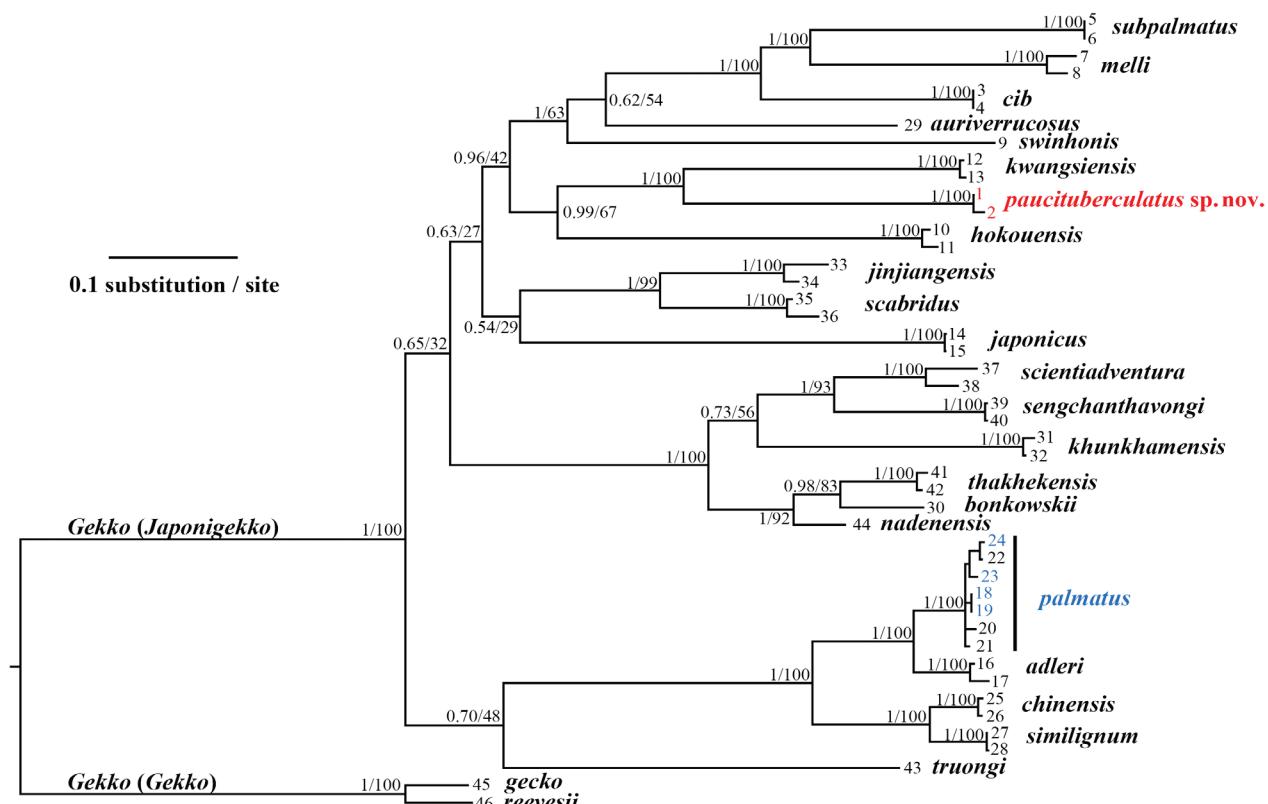


Figure 2. Bayesian Inference tree inferred from 16S and ND2 genes. Numbers before slashes indicate Bayesian posterior probabilities (BPP) and numbers after slashes are bootstrap support (BS).

Table 4. Uncorrected p distances (%) of the ND2 gene amongst species of *Gekko* (*Japonigekko*) used in this study.

Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1 <i>G. paucituberculatus</i> sp. nov.	0.00																					
2 <i>G. cib</i>	19.02	0.00																				
3 <i>G. subpalmatus</i>	20.45	17.38	0.00																			
4 <i>G. melli</i>	21.06	17.59	14.52	2.66																		
5 <i>G. swinhonis</i>	21.47	21.27	20.25	20.45	—																	
6 <i>G. hokouensis</i>	18.92	22.09	20.76	20.86	19.94	1.84																
7 <i>G. kwangsiensis</i>	15.54	18.61	22.09	21.68	19.84	20.86	0.41															
8 <i>G. japonicus</i>	19.84	23.11	21.68	21.27	20.86	21.06	22.29	0.00														
9 <i>G. adleri</i>	22.09	23.72	23.72	20.14	22.70	21.88	21.06	23.52	—													
10 <i>G. palmatus</i>	21.32	24.18	25.10	23.16	22.75	21.37	21.47	22.96	6.44	0.82												
11 <i>G. chinensis</i>	22.70	23.62	23.21	21.88	23.01	22.29	21.68	22.60	14.72	15.39	0.82											
12 <i>G. similignum</i>	22.39	24.64	23.82	22.49	22.39	22.80	21.68	23.01	14.83	15.18	4.19	0.20										
13 <i>G. auriverrucosus</i>	18.61	19.22	20.04	21.57	18.81	20.14	21.68	19.02	24.13	23.57	25.36	26.69	—									
14 <i>G. bonkowskii</i>	18.81	19.22	20.86	21.78	21.68	19.63	21.37	20.45	24.54	23.01	20.96	22.39	21.88	—								
15 <i>G. khunkhamensis</i>	21.47	20.86	22.49	23.52	23.52	23.93	21.47	22.49	25.77	25.66	24.23	24.44	24.13	15.24	0.41							
16 <i>G. jinjiangensis</i>	17.79	21.37	20.55	20.04	20.76	19.43	19.33	17.89	20.86	20.86	22.09	21.68	20.65	18.61	21.37	2.45						
17 <i>G. scabridius</i>	17.79	21.57	20.86	19.94	20.35	17.48	20.25	18.00	19.02	19.73	20.76	19.53	20.04	22.09	10.53	1.23						
18 <i>G. scientiadventura</i>	19.02	21.17	21.37	21.78	22.80	21.47	20.55	21.98	24.34	23.62	22.24	22.60	20.86	12.99	14.42	18.40	18.71	3.68				
19 <i>G. sengchanthavongi</i>	19.22	21.68	21.27	22.09	21.88	22.90	20.86	21.68	23.93	23.57	21.98	22.60	20.65	13.91	15.54	19.53	19.02	9.92	0.00			
20 <i>G. thakhokensis</i>	17.79	20.45	20.65	20.76	23.52	21.06	20.65	20.14	21.78	22.44	20.25	20.65	21.17	6.95	15.95	19.02	19.33	12.37	12.88	0.61		
21 <i>G. truongi</i>	20.86	21.68	21.47	20.45	23.72	21.98	22.29	19.84	21.32	20.04	20.35	24.54	22.09	22.09	20.35	18.40	21.88	21.88	20.76	—		
22 <i>G. madenensis</i>	18.61	20.86	19.43	20.76	21.68	22.29	20.55	21.27	23.52	22.96	21.57	22.39	21.06	6.95	13.70	18.00	19.63	13.39	12.07	6.95	22.29	—

Holotype. SYS r002806 (Figs 3A and 4), adult male, from Tianyang District (23°42'55"N, 106°59'14"E; 120 m a.s.l.), Baise City, Guangxi Zhuang Autonomous Region, China, collected on 3 August 2023 by Dan-Yang Zhou.

Paratype. SYS r002807 (Figs 3B and 5), adult female, data identical to the holotype.

Diagnosis. *Gekko paucituberculatus* sp. nov. is distinguished from all congeners in the subgenus *G. (Japonigekko)* by a combination of the following morphological characters: (1) moderate body size, SVL 77.2 mm in the adult male and SVL 85.9 mm in the adult female; (2) nares in contact with rostral, internasal absent; (3) two enlarged postmentals; (4) tubercles flattened, only present along dorsolateral trunk and absent on other regions; (5) ventral scales between mental and cloacal slit 189–192; (6) mid-body scale rows 136–140; (7) ventral scale rows 42–44; (8) subdigital lamellae on first fingers 10–11, on fourth fingers 12–13, on first toes 11, on fourth toes 11–13 and fingers and toes webbing weakly developed; (9) continuous precloacal pores 12 in the male, absent in the female; (10) a single postcloacal tubercle on each side; (11) a light-coloured vertebral line from nape to tip of tail; (12) dorsum greyish-brown, with 7–8 dirty-white bands between nape and sacrum.

Etymology. The specific name *paucituberculatus* means few tubercles in Latin and refers to its tubercles being fewer than other congeners. According to its type locality, we suggest the common name as “Baise gecko” in English and Chinese formal name as “bǎi sè bì hǔ” (百色壁虎).

Description of holotype. Adult male, moderate size, SVL 77.2 mm; head depressed (HH/HL 0.38), length longer than width (HL/HW 1.24), distinct from neck; snout rounded at tip, elongate (SNT/HL 0.44), larger than eye (SNT/ED 1.69); rostral regular rectangular, nearly twice as wide as high (RW/RH 1.94) and wider than mental (RW/MW 1.22), with mid-dorsal notch approximately one third; nares oval, rounded by rostral, first supralabial, supranasal and two enlarged nasals posteriorly; internasals absent; preorbital 18/18,

preorbital region deeply concave; eye large (ED/HL 0.26), pupil vertical, margins crenulated; interorbital scales between anterior corners of eyes 37; ear opening elliptical, obliquely orientated, moderate in size (EOD/ED 0.40); mental pentagonal, wider than long (MW/ML 1.42); postmentals two, hexagonal and enlarged, twice as long as wide, touching mental and first infralabial on both sides and six gular scales posteriorly; supralabials 11/11; infralabials 10/10; tubercles absent on dorsal head, granulars on anteriodorsal head larger than those on posterior.

Body slender, elongate (AG/SVL 0.41); dorsals smooth, round or oval, granular and juxtaposed; tubercles flattened, only present on dorsal lateral surface, two rows on each side, surrounded by eight dorsal scales, absent on other regions; lateral fold present, without tubercles; ventrals distinctly larger than dorsal scales, smooth, imbricate and largest in middle of belly; ventral scale rows at mid-body 42; scale rows around mid-body 140; ventral scales in a row between mental and cloacal slit 189; precloacal scales enlarged, but no enlarged scales on

thighs; precloacal pores 12, in a continuous row; postcloacal tubercle 1/1, large.

Fore- and hind-limbs well-developed; tubercles absent on dorsal limbs; digits moderately dilated; II–IV fingers and toes clawed; claws depressed laterally, extending beyond terminal lamellae; webbing on fingers and toes weakly developed; subdigital lamellae undivided, under manus 11-11-12-13-10 (left) and 11-11-12-13-11 (right), under pes 11-12-12-13-13 (left) and 11-11-12-13-12 (right); relative length fingers and toes I < II < V < III < IV.

Original tail (broken when capturing), longer than body (TaL 89.3 mm, TaL/SVL 1.16); distinctly swollen at base, oval in section; dorsal scales small, flat, smooth; caudal whorl distinct, 10 dorsal scale rows in the middle of the third one; subcaudals enlarged, arranged in a longitudinal row.

Colouration of holotype. In life, the dorsal regions of head and body are greyish-brown in colour, with scattered white spots on the anterior of head. An inverted U-shaped



Figure 3. Type specimens of *Gekko paucituberculatus* sp. nov. in life. **A** Holotype SYSr002806, adult male; **B** paratype SYSr002807, adult female. Photos by Dan-Yang Zhou.

marking is present on the occipital region and there are seven regularly arranged, dirty-white bands between the nape and sacrum. The first band, located at the nape, extends forwards and backwards to the posterior corners of eye and the second band, respectively. A light-coloured vertebral line is present from the nape to the tail terminal. Some light spots are visible on the lateral sides. Limbs are light brown with many indistinct pale marks. Dorsal tail is black with seven bands, from dirty white to pure white in colour towards terminal. The ventral surface of the holotype is light flesh-coloured. The body colour becomes darker after capture.

In preservative, the dorsal ground colour of head, body and limbs is greyish-black; ventral surface fading to greyish-white.

Morphological variation. Measurements and scale counts of two individuals are shown in Tables 5 and 6 and the female paratype is shown in Figure 5.

Precloacal pores are absent in the female. In the male, the postcloacal tubercle is significantly larger than in the female. The paratype specimen exhibits eight light bands between the nape and sacrum.

Comparisons. *Gekko paucituberculatus* sp. nov. is compared with all 32 recognised species within the subgenus *G. (Japonigekko)*.

The new species can be easily distinguished from the following 13 congeners by the presence of tubercles on the dorsolateral trunk: Absence of tubercles in *G. aaronbaueri* Tri et al., 2015, *G. bonkowskii* Luu et al., 2015,

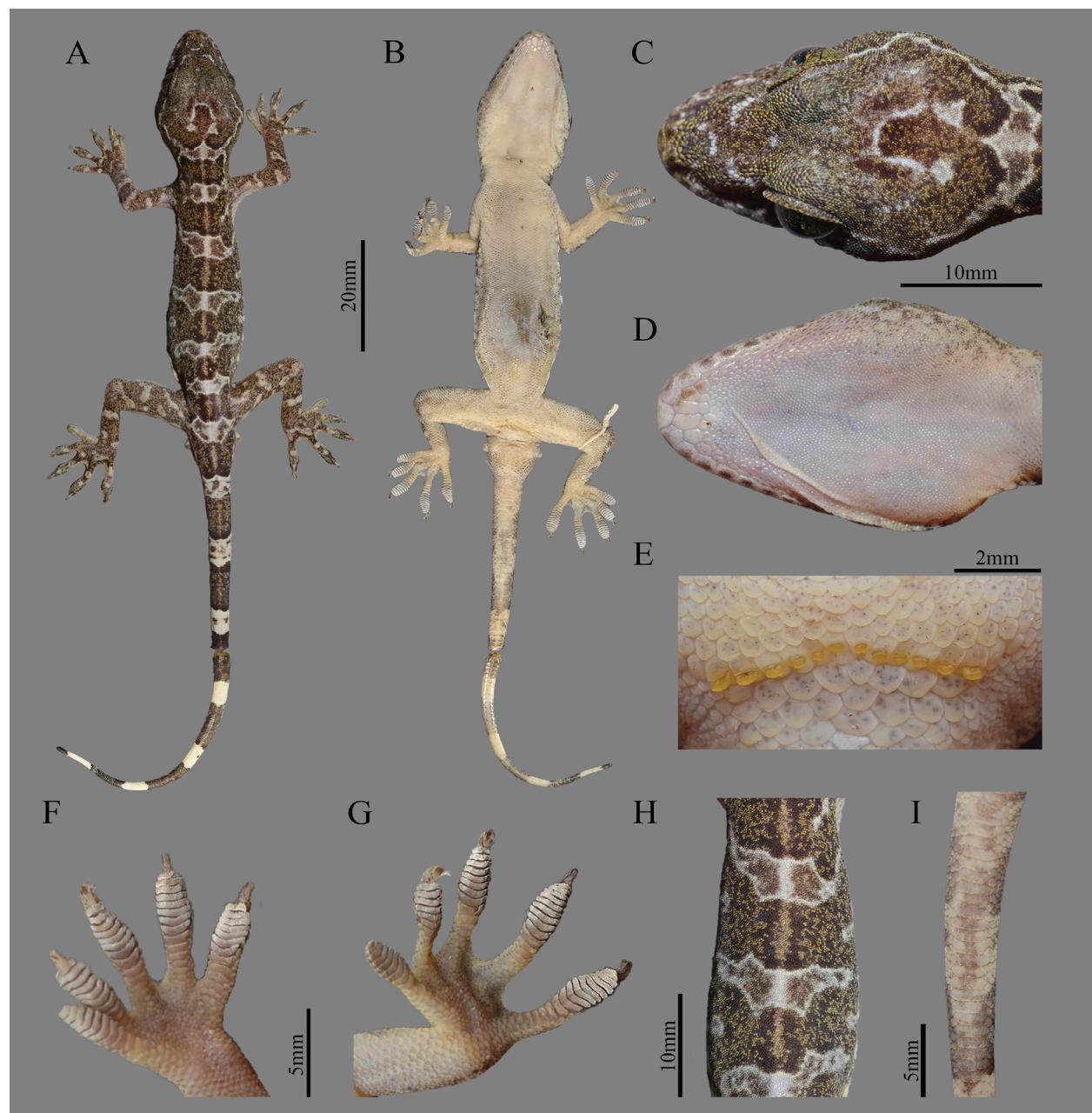


Figure 4. Morphological features of the adult male holotype SYS r002806 of *Gekko paucituberculatus* sp. nov. **A** Dorsal view of body; **B** ventral view of body; **C** dorsal head; **D** ventral head; **E** precloacal pores; **F** left hand; **G** left foot; **H** dorsal scalation at mid-body; **I** ventral tail. Photos by Hao-Tian Wang and Han-Ming Song.

G. cib Lyu et al., 2021, *G. guishanicus* Lin & Yao, 2016, *G. khunkhamensis* Sitthivong et al., 2021, *G. melli* Vogt, 1922, *G. nadenensis* Luu et al., 2017, *G. scientiadventura* Rösler et al., 2004, *G. sengchanthavongi* Luu et al., 2015, *G. subpalmatus* Günther, 1864, *G. tawaensis* Okada, 1956, *G. thakhekensis* Luu et al., 2014, and *G. truongi* Phung & Ziegler, 2011.

The new species can be easily distinguished from the following 12 congeners by having 12 precloacal pores in the male: *Gekko adleri* (17–21), *G. canhi* Rösler et al., 2010 (5), *G. chinensis* Gray, 1842 (17–27), *G. jinjiangensis* Hou et al., 2021 (4–5), *G. palmatus* (23–30), *G. shibatai* Toda, Sengoku, Hikida & Ota, 2008 (0), *G. similenum* Smith, 1923 (17), *G. taibaiensis* Song, 1985 (4–6), *G. vertebralis* Toda, Sengoku, Hikida & Ota, 2008 (0),

G. vietnamensis Sang, 2010 (0), *G. wenxianensis* Zhou & Wang, 2008 (6–8) and *G. yakuensi* Matsui & Okada, 1968 (6–8).

The new species can be easily distinguished from the following three congeners by having four dorsal tubercle rows: *Gekko auriverrucosus* Zhou & Liu, 1982 (16–20), *G. hokouensis* (12–18), *G. kaiya* Zhang et al., 2023 (11–18), *G. scabridus* Liu & Zhou, 1982 (17–21).

For the remaining congeners, by having a single post-cloacal tubercles, the new species differs from *G. japonicus* (Schlegel, 1836) (2–4) and *G. swinhonis* Günther, 1864 (2–3).

The new species is most similar to *G. kwangsiensis* and *G. liboensis*, which are also from karst areas in Guangxi, but it differs from the former by the following characters:

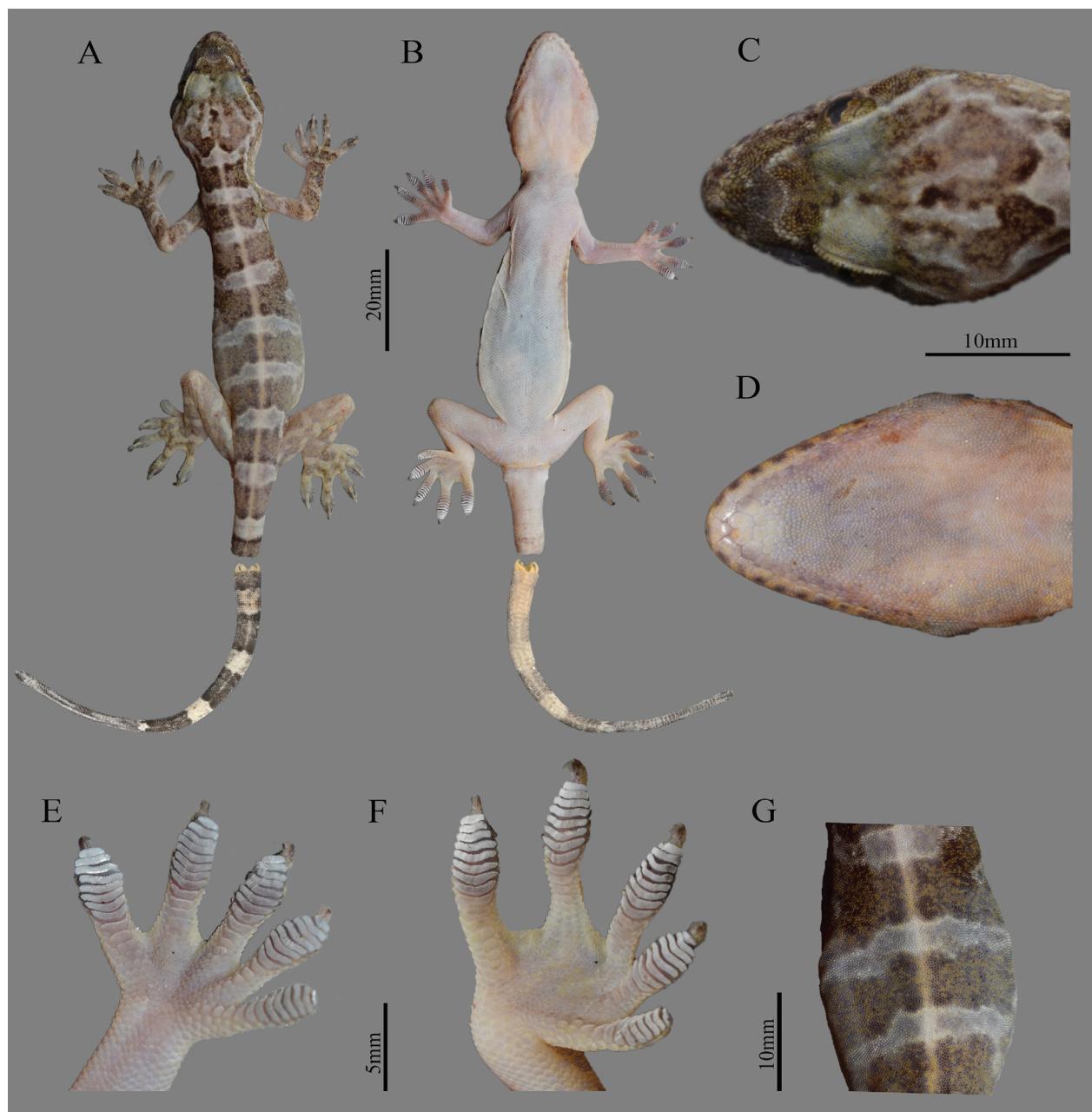


Figure 5. Morphological features of the adult female paratype SYS r002807 of *Gekko paucituberculatus* sp. nov. **A** Dorsal view of body; **B** ventral view of body; **C** dorsal head; **D** ventral head; **E** right hand; **F** right foot; **G** dorsal scalation at mid-body. Photos by Hao-Tian Wang and Han-Ming Song.

Table 5. Measurements (in mm) and body proportions of the type series of *Gekko paucituberculatus* sp. nov. See Materials and Methods section for abbreviations. “**” regenerated tail.

	Holotype SYS r002806	Paratype SYS r002807
Sex	♂	♀
SVL	77.2	85.9
TaL	89.3	83.9*
AG	31.9	38.8
HL	20.0	21.2
HW	16.1	17.4
HH	7.6	8.4
SNT	8.8	9.8
ED	5.2	5.7
EOD	2.1	2.3
RH	1.7	2.0
RW	3.3	3.6
MW	2.7	2.8
ML	1.9	2.2
TaL/SVL	1.16	0.98
AG/SVL	0.41	0.45
HL/SVL	0.26	0.25
HL/HW	1.24	1.22
HH/HL	0.38	0.40
SNT/HL	0.44	0.46
SNT/ED	1.69	1.72
ED/HL	0.26	0.27
EOD/ED	0.40	0.40
RW/RH	1.94	1.80
RW/MW	1.22	1.29
MW/ML	1.42	1.27

Less dorsal tubercle rows (4 vs. 9–11); more interorbital scales (37 vs. 29–31); more precloacal pores in male (12 vs. 9–10); fewer subdigital lamellae on fourth toes (11–13 vs. 13–18); fewer, but broader bands between nape and sacrum (7–8 vs. 9–10).

Furthermore, the new species differs from *G. liboensis* by tubercles only present along the dorsolateral surface not on other regions (vs. present from occipital region to tail base) and having regular and broad bands between nape and sacrum (vs. irregular and thin bands with many scattered round-shaped spots).

Distribution and ecology. Currently, *Gekko paucituberculatus* sp. nov. is limited to Tianyang District, Baise City, in Guangxi Zhuang Autonomous Region of China. The new gecko species is a rock-dwelling specialist. Both of the two individuals were discovered on rocks near the entrance to a limestone karst cave at night.

Discussion

Gekko palmatus was initially described by G. A. Boulenger in 1907 (as *Gecko palmatus*), based on a single female specimen from the mountains of Man Son, Vietnam

Table 6. Scalation features of the type series of *Gekko paucituberculatus* sp. nov. Bilateral scale counts are given as left/right.

	Holotype SYS r002806	Paratype SYS r002807
N	3/3	3/3
I	0	0
SPL	11/11	11/11
IFL	10/10	9/10
IO	37	37
PO	18/18	15/14
PM	2	2
GP	6	4
DTR	4	4
GSDT	8	8
SMC	189	192
SR	140	136
V	42	44
LF1	11/11	10/10
LF4	13/13	12/12
LT1	11/11	11/11
LT4	13/13	12/11
PP	12	—
PAT	1/1	1/1
S3W	10	9

(Boulenger 1907). Poyarkov et al. (2023) cited Nguyen et al. (2009) who argued that *G. palmatus* occurs in China, but it was not recognised due to lack of evidence (Wang et al. 2020; Cai et al. 2022). Both this study and Lyu et al. (2021) confirmed distributions of *G. palmatus* in Napo County and Nonggang Natural Reserve in Guangxi and Mt. Dinghu in Guangdong of China. Regarding morphology, the specimens from Guangdong share the diagnoses with *G. palmatus*: nostril in contact with rostral; internasals 0–2, much smaller than supranasal when present; tubercles present on dorsum of body, lacking on forelimb and thigh; webs well developed; male preanal pores 24–27; cloacal spur single; one pair of dark, roundish or somewhat elongated spots in occipital region; smaller, but more distinct dark spot in nuchal region; light broken mid-dorsal stripe evident on body (Ota et al. 1995).

The discoveries of *Gekko paucituberculatus* sp. nov. and *G. palmatus* bring the number of known species in the subgenus *G. (Japonigekko)* in China to 19, with seven in Guangxi, the provincial district with the highest diversity. Four of them are karst dwellers: *Gekko adleri*, *G. kwangsiensis*, *G. liboensis* and *G. paucituberculatus*.

The multiple landforms (e.g. peak cluster, depression, cave and peak forest) in the karst region have led to the formation of fragmented and unique microhabitats, resulting in a comparatively significant biodiversity and the presence of numerous endemic species (Clements et al. 2006; Grismer et al. 2021). The globally-concentrated karst is primarily found in south-central Europe, eastern North America and southern China (Li and Xiong 2021). Karstic landscapes from southern China are considered one of the most representative regions of tropical-subtropical karst formation (Xiong et al. 2008). In the last decade, researchers have discovered several narrow-ranged

species of amphibian and reptile that are specifically adapted to the karst ecosystems in this region (Mo et al. 2015; Qi et al. 2020; Luo et al. 2021; Agung et al. 2022; Lin et al. 2022). However, these studies have been limited to only very recent and unconnected survey areas, leaving much of the region unexplored. Additionally, the slow soil formation rate of limestone in karst creates a thin soil layer that is prone to soil erosion and rocky desertification (Yang 1990). These features render the karst ecosystem highly vulnerable and challenging to restore after damage. Consequently, conducting a thorough and comprehensive survey of amphibians and reptiles in this expansive karst region is imperative to assess their diversity and the hazards they encounter. This will enable the development of effective conservation strategies to prevent further loss of unidentified species.

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