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Goniurosaurus chengzheng sp. nov., a new species of Leopard Gecko from Guangxi, China (Squamata: Eublepharidae)

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Abstract

Six species of geckos in the genus *Goniurosaurus* have been recorded from Guangxi, China. Here we describe a new species, *Goniurosaurus chengzheng* **sp. nov.** The new species is similar to allied species from Guangxi, but unique in a combination of the following characters: (1) four body bands with three between limb insertions; (2) precloacal pores 20; (3) body color reddish- brown; (4) snout to eye distance: eye to ear distance < 1. We used the mitochondrial genes *16S* and *cytb* to confirm the distinctiveness of the species and place it within a molecular phylogeny of *Goniurosaurus*. The type specimens are deposited in the Museum of Biology, East China Normal University (ECNU).

Key words: gecko, taxonomy, molecular phylogeny, karst, Guangxi, China

Introduction

The genus *Goniurosaurus* currently comprises 23 described species (Mocquard 1897; Orlov & Darevsky 1999; Grismer *et al.* 1999, 2002; Orlov *et al.* 2008; Ziegler *et al.* 2008; Wang *et al.* 2010, 2013, 2014; Honda *et al.* 2014; Yang & Chan 2015; Honda & Ota 2017; Zhou *et al.* 2018; Zhu *et al.* 2020a, 2020b; Qi *et al.* 2020a, 2020b). Recent molecular phylogenetic analyses have indicated the existence of four major lineages of *Goniurosaurus* (Liang *et al.* 2018; Zhu *et al.* 2020a; Qi *et al.* 2020b), namely the *G. kuroiwae*, *G. lichtenfelderi*, *G. luii*, and *G. yingdeensis* groups. In 2020, one new species was described in the *G. lichtenfelderi* group (*G. kwanghua*, Zhu *et al.* 2020b), one in the *G. luii* group (*G. gezhi*, Zhu *et al.* 2020a), and two in the *G. yingdeensis* group (*G. gollum* and *G. varius*, Qi *et al.* 2020a, 2020b). The *G. luii* group is the most diverse group of *Goniurosaurus* and its species are primarily found in the karst environment of Guangxi and Guizhou provinces of China and adjacent Northern Vietnam (Zhu *et al.* 2020a). In 2017 an individual was photographed from a new locality in Guangxi during our herpetological surveys (Fig. 1A). The following year, two specimens of *Goniurosaurus* were collected from the same locality. Morphological and molecular analyses presented in this study support that these individuals belong to a currently undescribed species within the *G. luii* group.

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FIGURE 1. *Goniurosaurus chengzheng* **sp. nov.** from Guangxi, China. A. Adult female (photographed in 2017, but not collected); B. Scalation and coloration characters of the head of the holotype; C. Adult male, holotype. (photos by Zhu Xiao-Yu)

Methods

Sampling. We collected specimens of the new species by conducting visual survey encounters in karst areas along the ground at night. Two male individuals of the new species (ECNU-V0068 and ECNU-V0090) were collected. The Personalbio Saliva/Swab Genomic DNA Kit (Shanghai Personalbio Biotechnology Co., Ltd.) was used to collect DNA. We followed the protocol by swabbing the mouth of each individual for about 10 seconds. DNA samples were preserved at room temperature. We preserved the vouchers in 75% ethanol. Only the general collection locality for each of the examined specimens is provided in Table 1 in order to protect the species from illegal exploitation through the pet trade. All specimens were deposited in the Museum of Biology, East China Normal University (ECNU), which retains full locality data for the specimens.

TABLE 1. GenBank accession number for each sequence used in this study, * = type specimen. All localities in China unless otherwise indicated.

Species	Specimen ID	Locality	*16S*	*cytb*	References
G. araneus	ECNU-V0008	Chongzuo, Guangxi	MT533259	MW534119	Zhu *et al.*, 2020a/this study
G. bawanglingensis	BL-RBZ-021	Bawangling, Hainan Islandd.	MH247190	MH247201	Liang, B., *et al.* 2018
G. bawanglingensis	BL-RBZ-022	Bawangling, Hainan Island	MH247191	MH247202	Liang, B., *et al.* 2018
G. bawanglingensis	BL-RBZ-023	Bawangling, Hainan Island	MH247192	MH247203	Liang, B., *et al.* 2018
G. bawanglingensis	BL-RBZ-024	Bawangling, Hainan Island	MH247193	MH247204	Liang, B., *et al.* 2018
G. bawanglingensis	SYS r002162	Bawangling, Hainan Island	MT995758	MT995773	Qi *et al.* 2020a
G. gezhi	ECNU-V0038	Southwest , Guangxi	MT533260	MW534120	Zhu *et al.*, 2020a/this study
G. gezhi	ECNU-V0042	Southwest , Guangxi	MT533262	MW534121	Zhu *et al.*, 2020a/this study
G. gezhi	ECNU-V0046	Southwest , Guangxi	MT533263	MW534122	Zhu *et al.*, 2020a/this study
G. gezhi	ECNU-V0047	Southwest , Guangxi	MT533264	IMW534123	Zhu *et al.*, 2020a/this study
G. hainanensis	BL-RBZ-041	Shishan County, Haikou, Hainan Island	MH247194	MH247205	Liang, B., *et al.* 2018
G. hainanensis	BL-RBZ-042	Liulianling, Wanning, Hainan Island	MH247195	MH247206	Liang, B., *et al.* 2018
G. huuliensis	N/A	Vietnam	AB853453	AB853479	Honda *et al.*, 2014
G. kadoorieorum	ECNU-V0058	Southwest, Guangxi	MT533258	MW534124	Zhu *et al.*, 2020a/this study
G. kadoorieorum	ECNU-V0060	Southwest, Guangxi	MT533265	MW534125	Zhu *et al.*, 2020a/this study
G. kadoorieorum	ECNU-V0061	Southwest, Guangxi	MT533266	MW534126	Zhu *et al.*, 2020a/this study
G. kuroiwae	N/A	Northern Okinawajima Island, Japan	AB853448	AB853473	Honda *et al.*, 2014
G. kwanghua	ECNU-V0003	Western area, Hainan Island, China	MK782788	MK782782	Zhu *et al.*, 2002b
G. kwanghua	ECNU-V0004	Western area, Hainan Island, China	MK782789	MK782783	Zhu *et al.*, 2002b
G. kwanghua	ECNU-V0005	Western area, Hainan Island, China	MK782790	MK782784	Zhu *et al.*, 2002b
G. kwangsiensis	ECNU-V0009	Nanning, Guangxi	MK782786	MK782780	Zhu *et al.*, 2002b
G. lichtenfelderi	ECNU-V0007	Chongzuo, Guangxi, China	MK782785	MK782779	Zhu *et al.*, 2002b
G. luii	ECNU-V0012	Chongzuo, Guangxi, Chinai	MK782787	MK782781	Zhu *et al.*, 2002b
G. luii	GL511	Pingxiang, Guangxi	NC_026105	NC_026105	Li *et al.*, 2016
G. luii	N/A	Guangxi Province	AB853452	AB853478	Honda *et al.*, 2014
G. orientalis	N/A	Iejima Island, Japan	AB853446	AB853467	Honda *et al.*, 2014
G. chengzheng **sp. nov.**	ECNU-V0068	Central Guangxi	MW519616	MW534127	this study
G. chengzheng **sp. nov.**	ECNU-V0090	Central Guangxi	MW519617	MW534128	this study
G. splendens	N/A	Tokunoshima Island, Japan	AB853451	AB853477	Honda *et al.*, 2014

......continued on the next page

TABLE 1. (Continued)

Species	Specimen ID	Locality	*16S*	*cytb*	References
G. toyamai	N/A	Iheyajima Island, Japan	AB853447	AB853471	Honda *et al.*, 2014
G. varius	SYS r002330	Yangshan, Guangdong	MT995753	MT995768	Qi *et al.* 2020a
G. varius	SYS r002331	Yangshan, Guangdong	MT995754	MT995769	Qi *et al.* 2020a
G. varius	SYS r002333	Yangshan, Guangdong	MT995755	MT995770	Qi *et al.* 2020a
G. varius	SYS r002362	Yangshan, Guangdong	MT995756	MT995771	Qi *et al.* 2020a
G. varius	SYS r002363	Yangshan, Guangdong	MT995757	MT995772	Qi *et al.* 2020a
G. yamashinae	N/A	Kumejima Island, Japan	AB853442	AB853460	Honda *et al.*, 2014
G. yingdeensis	SYS r001271	Yingde, Guangdong	MT995759	MT995774	Qi *et al.* 2020a
G. yingdeensis	SYS r001272	Yingde, Guangdong	MT995760	MT995775	Qi *et al.* 2020a
G. yingdeensis	SYS r001493	Yingde, Guangdong	MT995761	MT995776	Qi *et al.* 2020a
G. yingdeensis	SYS r002115	Yingde, Guangdong	MT995762	MT995777	Qi *et al.* 2020a
G. zhelongi	SYS r000816	Yingde, Guangdong	KJ423105	MT995778	Wang *et al.* 2014, Qi *et al.* 2020a
G. zhelongi	SYS r001491	Yingde, Guangdong	MT995763	MT995779	Qi *et al.* 2020a
G. zhelongi	SYS r001492	Yingde, Guangdong	MT995764	MT995780	Qi *et al.* 2020a
G. zhelongi	SYS r002108	Yingde, Guangdong	MT995765	MT995781	Qi *et al.* 2020a
G. zhoui	BL-RBZ-001	Central area, Hainan Island	MH247196	MH247207	Liang, B., *et al.* 2018
G. zhoui	BL-RBZ-004	Central area, Hainan Island	MH247197	MH247208	Liang, B., *et al.* 2018
G. zhoui	BL-RBZ-006	Central area, Hainan Island	MH247198	MH247209	Liang, B., *et al.* 2018
G. zhoui	BL-RBZ-007	Central area, Hainan Island	MH247199	MH247210	Liang, B., *et al.* 2018
G. zhoui	BL-RBZ-008	Central area, Hainan Island	MH247200	MH247211	Liang, B., *et al.* 2018
G. zhoui	SYS r002213	Central area, Hainan Island	MT995766	MT995782	Qi *et al.* 2020a
G. zhoui	SYS r002214	Central area, Hainan Island	MT995767	MT995783	Qi *et al.* 2020a
G. gollum	SYS r002420	Huaiji, Guangdong	MT995784	MT995787	Qi *et al.* 2020b
G. gollum	SYS r002421	Huaiji, Guangdong	MT995785	MT995788	Qi *et al.* 2020b
G. gollum	SYS r002422	Huaiji, Guangdong	MT995786	MT995789	Qi *et al.* 2020b
Gekko chinensis	N/A	Quanzhou, Fujian	NC_027191	NC_027191	Hao *et al.*, 2016
Holodactylus africanus	KUZ 45192	East Africa	AB853456	AB853482	Honda *et al.*, 2014

DNA extraction and gene amplification. We sequenced *16S* and *cytb* mitochondrial gene regions of the new species, three *G. kadoorieorum* samples, three specimens of *G. gezhi*, and one *G. araneus* (Table 1). Total genomic DNA was extracted from the saliva DNA samples according to the manufacturer's instructions. Primers used for PCR amplification of *16S* are r16S-5L GGTMMYGCCTGCCCAGTG and 16Sbr-H CCGGTCTGAACTCAGATCACGT (Jonniaux & Kumazawa 2008) and those for *cytb* are Cytb-2019F CGAAAAACCAYYGTTGTTATTCAACT and Cytb-2019R AGRTTTGTGATTACGGTTGCGCCT (Zhu *et al.* 2020b). Amplification conditions for PCR were as follows: pre-denaturation for 2 min at 94°C, 35 cycles of 30 s at 94°C, 30 s at 55°C or 50°C for *16S* and *cytb*, respectively, 30 s at 72°C, and a final extension at 72°C for 7 min. All PCR products were sequenced directly with the same primers. GenBank accession numbers are provided in Table 1.

Phylogenetic analyses. Our analyses are mainly based on the published sequence alignment by Zhu *et al*. (2020b). The sequence alignment analyzed in the current study is equivalent to the one in Zhu *et al*. (2020b), but included sequences for two specimens of the new species and seven additional specimens of other *G. luii* group members. Sequence alignment was performed using MEGA version X (Stecher *et al*. 2020). The resulting alignment included 55 sequences from 21 *Goniurosaurus* species, two outgroup species (*Gekko chinensis* Gray and *Holodactylus africanus* Boettger), and had a total length of 862 bp. We inferred the phylogenetic relationships among all 21 *Goniurosaurus* species in our dataset using stochastic algorithms under maximum likelihood in IQ-TREE (Nguyen *et al*. 2015) along with a Bayesian approach implemented in MrBayes (Huelsenbeck & Ronquist, 2001). The best-fitting partitioning scheme across genes was selected using PartitionFinder v2 (Lanfear *et al*. 2017). Analyses in PartitionFinder were exhaustive (argument "search=all"), assumed branch lengths to be linked across partitions, compared using AIC values, and examined models that were implemented in MrBayes. PartitionFinder identified two independent gene-based partitions in our dataset. Partitioning analyses also assigned a GTR+G model to *16S* and GTR+I+G to *cytb*. Maximum-likelihood analyses were conducted in IQ-TREE based on the partitions identified before using PartitionFinder. Support values were estimated based on a total of 1,000 bootstrap pseudoreplicates. Bayesian phylogenies were inferred in MrBayes. For these analyses, we conducted two independent MCMC runs, each with 10 million generations. The maximum clade credibility tree under MrBayes was constructed based on the 90% of posterior samples (i.e., 10% burn-in). We confirmed convergence under MrBayes 3.2.4 (Ronquist *et al.* 2012) in Tracer (Fig. 2). Finally, we estimated uncorrected pairwise *p*-distances between all the samples in our dataset using Mega version X (Stecher *et al*. 2020). These estimates of genetic distances were used to examine whether the median distances between the new species and all other *Goniurosaurus* were comparable to those estimates for other species in the dataset. We used the base R package version 4.0.3 (R Core Team 2020) to estimate median *p*-distance and range of values per species based on sequence-specific pairwise distance per species. We repeated the same procedure for *16S* and *cytb* gene regions.

Morphology. The following measurements were recorded using digital calipers (± 0.01 mm) following Zhou *et al.* (2018): snout vent length (SVL) from tip of snout to vent; tail length (TaL) from vent to tip of tail; distance between axilla and groin (AG) from posterior edge of forelimb insertion to anterior edge of hindlimb insertion; snout to eye distance (SE) measured from tip of snout to anterior-most point of eye; eye to ear distance (EE) from posterior margin of eye to posterior margin of ear; maximum head width (HW); head length (HL) from tip of snout to posterior margin of ear. Scalation characters recorded are as follows: supralabials (SPL); sublabials/infralabials (SBL); nasal scales surrounding naris (N); internasals (IN); granular scales bordering the internasals (PostIN); postmentals (PM); gular scales bordering the postmentals (GP); eyelid fringe scales or ciliaria (CIL); preorbital scales (PO); granular scales surrounding dorsal tubercles (GST); dorsal longitudinal tubercle rows at midbody (DTR); paravertebral tubercles between limb insertions (TL); scales around midbody (MB); subdigital lamellae under the first finger (LD1) and the fourth finger (LD4); subdigital lamellae under the first toe (LT1) and the fourth toe (LT4); precloacal pores (PP); postcloacal tubercles (PAT). Bilateral scale counts are given as left/right.

Results

Phylogenetic relationships. Phylogenetic inference under Maximum Likelihood and Bayesian Inference recovered congruent evolutionary relationships among the 21 *Goniurosaurus* species analyzed in this study (Fig. 1). Overall, our results are in agreement with those in Zhu *et al.* (2020a), with the major groups in *Goniurosaurus* being similar to those in previous studies (e.g., Liang *et al.* 2018). The two samples assigned to *G. chengzheng* **sp. nov.** based

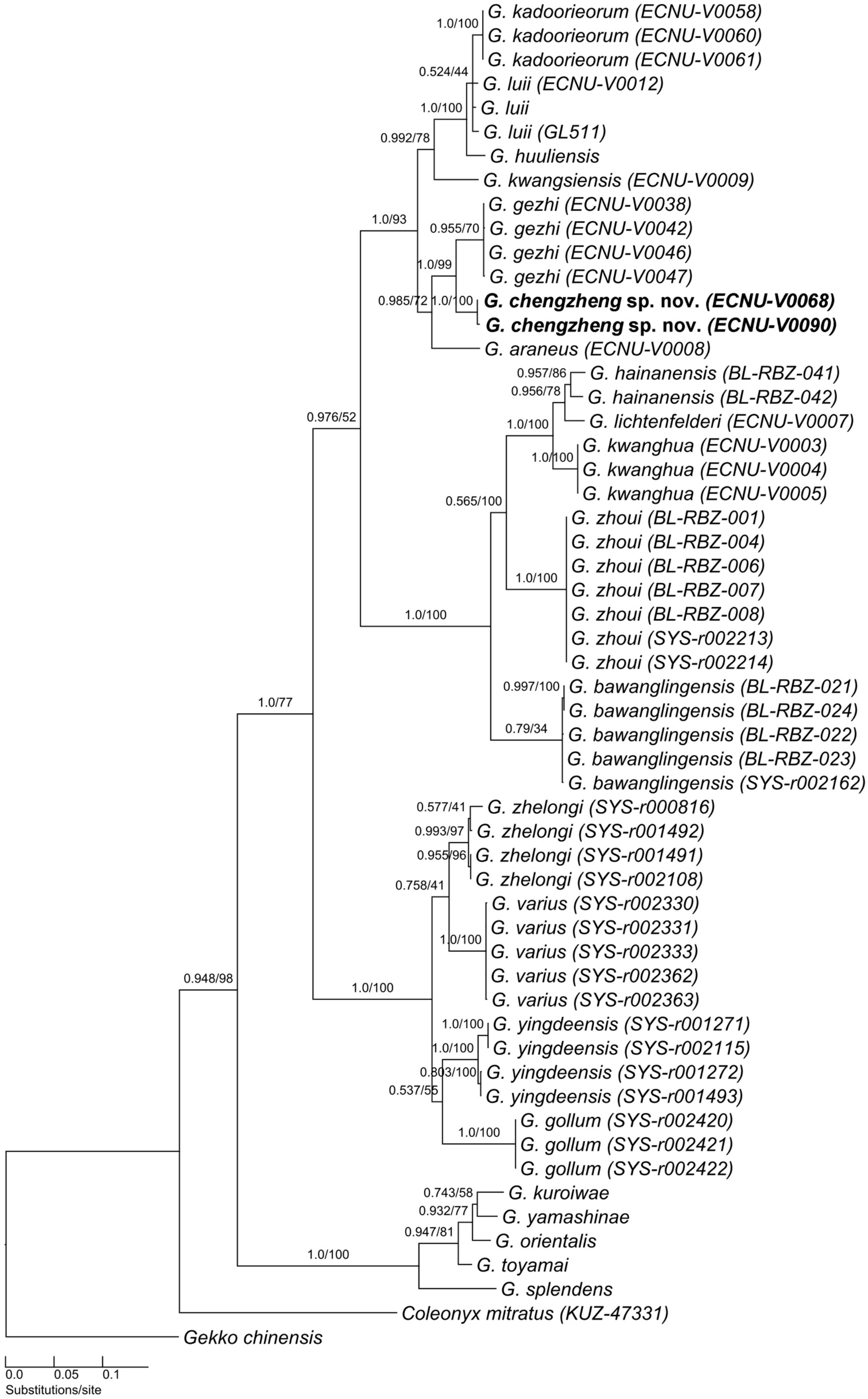

FIGURE 2. Bayesian Inference phylogram showing relationships among 21 *Goniurosaurus* species and two outgroup taxa. Support values in the form posterior probabilities (Bayesian Inference)/ bootstrap values (maximum likelihood) are shown above branches. The tree is a Bayesian topology. The position of *G. chengzheng* **sp. nov.** is highlighted in the tree.

on morphology formed a strongly supported monophyletic group in our phylogenies (bootstrap=100%, posterior probability=1). Our phylogenetic analyses suggest that *G. chengzheng* **sp. nov.** is nested within the *G. luii* clade, with its closest relative being *G. gezhi* (bootstrap=99%, posterior probability=1; Fig. 2).

We also examined the distribution of genetic distances across *Goniurosaurus* species based on uncorrected genetic distances for both the *16S* and *cytb* gene regions. Overall, median pairwise genetic distances in *G. chengzheng* **sp. nov.** were comparable to those in other species sampled in our dataset (Table 2). Specifically, *G. chengzheng* **sp. nov.** has similar values of genetic distances relative to those for *G. araneus* (*16S*), *G. huuliensis* (*16S*), *G. bawanglingensis* (*cytb*), and *G. zhelongi* (*cytb*) and even larger than those in *G. kwanghua* (*16S*) and *G. kwangsiensis* (*16S* and *cytb*). Thus, estimates of median pairwise genetic distances across species in our dataset suggest that the new species, *G. chengzheng* **sp. nov.**, genetically differs from other species on a scale that is largely congruent with previously erected species within *Goniurosaurus*.

TABLE 2. Summary uncorrected *p*-distances for the species of *Goniurosaurus* analyzed in this study. The median and range (minimum and maximum across pairwise distances across all samples within each species) of genetic distances relative to all other congeners are provided.

Species	***16S*** **(median, range)**	***cytb*** **(median, range)**
G. araneus	0.150 (0.060–0.221)	–
G. bawanglingensis	0.155 (0.055–0.223)	0.219 (0.158–0.318)
G. chengzheng **sp. nov.**	0.150 (0.060–0.232)	0.216 (0.098–0.245)
G. gollum	0.174 (0.057–0.224)	0.242 (0.123–0.274)
G. hainanensis	0.155 (0.023–0.231)	0.237 (0.057–0.322)
G. huuliensis	0.150 (0.013–0.219)	0.235 (0.036–0.264)
G. kadoorieorum	0.153 (0.011–0.215)	–
G. kuroiwae	0.207 (0.016–0.255)	0.255 (0.063–0.284)
G. kwanghua	0.148 (0.028–0.205)	0.242 (0.065–0.284)
G. kwangsiensis	0.146 (0.046–0.224)	0.213 (0.095–0.251)
G. lichtenfelderi	0.155 (0.023–0.211)	0.238 (0.057–0.308)
G. luii	0.153 (0.011–0.224)	0.229 (0.036–0.261)
G. orientalis	0.202 (0.016–0.235)	0.264 (0.063–0.281)
G. splendens	0.209 (0.063–0.249)	0.294 (0.147–0.322)
G. toyamai	0.200 (0.023–0.240)	0.264 (0.063–0.288)
G. varius	0.165 (0.036–0.211)	0.248 (0.076–0.318)
G. yamashinae	0.202 (0.016–0.237)	0.268 (0.063–0.294)
G. yingdeensis	0.170 (0.048–0.206)	0.242 (0.082–0.305)
G. zhelongi	0.181 (0.036–0.255)	0.219 (0.076–0.288)
G. zhoui	0.164 (0.055–0.207)	0.229 (0.144–0.294)

Systematics

Goniurosaurus chengzheng **Zhu, Li & He sp. nov.**

(Figs. 1, 3)

Holotype. Adult male (ECNU-V0090), from central Guangxi, China, 100-250 m in altitude. Exact locality withheld because of conservation concerns, available to qualified researchers upon request. Collected during July 2018 by Zhu Xiao-Yu.

Paratypes. Subadult male (ECNU-V0068), same data as holotype.

Diagnosis. *Goniurosaurus chengzheng* **sp. nov.** differs from other congeners by a combination of the following characters: SE shorter than EE (Table 3); one nuchal loop, four body bands; number of precloacal pores 20; body color reddish brown in life (Table 4).

TABLE 3. Comparisons of morphometric characters (in mm) and scale counts for nine *Goniurosaurus* species within the *luii* group. Character abbreviations are explained in material and methods (data for *G. gezhi* from Zhu *et al.* 2020; *G. kadoorieorum* and *G. kwangsiensis* from Yang & Chan 2015, *G. araneus* and *G. luii* from Grismer *et al.* 1999, *G. liboensis* from Wang *et al.* 2013, *G huuliensis* from Orlov *et al.* 2008; *G. catbaensis* from Orlov & Darevsky 1999). Subadults are not included. Data are lacking for some values as they were not reported in the original literature.

Species		SVL	SPL	SBL	PO	CIL	PM	GST	TL	MB	LT4	PP	SE:EE
G. chengzheng	Mean	107	8.50	9.5	14	54.5	3.00	11.75	29.00	128.00	23.00	20.00	0.99
	SD	—	0.70	0.70	0	2.12	0	1.41	0	12.73	0	0	0
	Range	107	8–9	9–10	14	53–56	3.00	11–13	29.00	119–137	23.00	20.00	0.99
G. gezhi	Mean	77	9.33	9.00	17.17	48.33	4.00	11.33	34.67	136.83	23.50	19.33	1.17
	SD	6.64	0.52	0.63	1.47	3.26	1.41	0.82	3.78	10.03	1.52	1.15	0.07
	Range	71–84	9–10	8–10	15–19	44–52	3–5	10–12	32–39	123–151	21–25	18–20	1.09–1.21
G. araneus	Mean	—	8.80	8.70	16.70	64.00	5.30	9.80	35.80	135.70	23.50	19.80	—
	SD	—	0.98	0.52	1.86	2.19	0.82	4.33	2.71	7.26	0.55	1.71	—
	Range	115–124	8–10	8–9	13–18	61–67	4–6	10–14	32–38	129–147	23–24	18–22	—
G. luii	Mean	—	9.50	10.00	15.80	59.50	3.00	12.20	33.80	134.50	23.50	26.00	—
	SD	—	0.55	0.63	1.17	1.87	0.89	1.34	0.75	12.00	1.38	2.58	—
	Range	107–116	9–12	9–11	14–17	57–61	2–4	9–14	33–34	119–144	21–24	23–29	—
G. kadoorieorum	Mean	116	10.33	9.00	16.17	50.83	5.00	12.00	32.00	128.67	22.00	26.75	1.24
	SD	2.78	0.52	0	0.75	2.77	0	1.10	2.00	4.16	0.89	0.96	0.07
	Range	112–118	10–11	9	15–17	47–54	5	11–13	30–34	124–132	21–23	26–28	1.14–1.34
G. huuliensis	Mean	115	10.40	9.80	—	43.50	2.40	12.20	34.60	123.60	17.40	26.75	1.28
	SD	3.69	0.52	0.63	—	0.95	0.55	0.44	0.89	3.91	0.70	1.26	0
	Range	109–117	10–11	9–11	—	41–44	2–3	12–13	34–36	118–129	17–19	25–28	1.28
G. kwangsiensis	Mean	104	9.38	8.38	17.00	54.50	4.00	11.50	30.25	125.25	24.12	32.00	1.31
	SD	4.77	0.84	0.82	1.63	1.17	1.41	1.21	2.36	2.75	0.82	1.41	0.03
	Range	98–109	8–10	7–9	15–19	52–58	3–6	10–13	27–32	122–128	22–27	31–33	1.28–1.34
G. catbaensis	Mean	—	8.80	7.70	—	53.70	2.70	9.70	33.30	119.30	23.30	18.70	1.12
	SD	—	0.40	0.80	—	1.00	0.60	1.50	0.60	7.50	0.80	2.50	0.07
	Range	85–112	8–9	6–8	—	52–55	2–3	8–11	33–34	112–127	22–24	16–21	1.03–1.15
G. liboensis	Mean	106	10.38	10.38	16.83	55.83	4	12.00	27.67	128	24.33	23	1.23
	SD	3.10	0.92	0.92	0.75	2.64	1.15	1.12	0.58	1.15	1.21	0	0.05
	Range	103–110	9–12	9–12	16–18	52–59	3–5	10–13	27–28	127–129	23–26	23	1.20–1.30

TABLE 4. Diagnostic characters of color pattern distinguishing *Goniurosaurus chengzheng* from congeners.

Taxon	**dorsal color of body and limbs**	**color of iris**	**color of nuchal loops**
G. chengzheng	reddish brown	yellow	reddish brown
G. luii	grey-brown to dull-white	brilliant orange	dull yellow
G. araneus	dull yellow-grey	dark brown	yellowish
G. huuliensis	brown with dark	red-brown	pink or orange
G. liboensis	gray-brown	gray	white
G. catbaensis	grey-brown to pale brown	orange-brown	dull yellow
G. gezhi	grey	brown	pale yellow
G. kwangsiensis	yellowish brown	light orange yellow	yellow
G. kadoorieorum	greyish lilac	olive green	greyish

Description. Holotype. ECNU-V0090, adult male; SVL: 107.08 mm; TaL (regenerated): 62.15 mm; AG: 46.95 mm; SE 11.53 mm; EE: 11.70 mm; HW: 20.57 mm; HL: 29.12 mm; SVL: AG 2.28; SVL: HL: 3.68; HL: HW 1.42; SE: EE: 0.99; head triangular, wider than neck, covered with uniform granular scales interspersed with tubercles on top of head; conspicuous row of enlarged supraorbital tubercles; external nares bordered by 8/8 nasals, anteriorly by prenasal, dorsolaterally by supranasal and two granular scales, dorsally by one internasal, posteriorly by four smaller granular scales; prenasals with long recurved ventral portion; supranasals in contact at the midline; separated by one internasal (Fig. 3B); supralabials 9/8, rectangular; eyes relatively large, pupils vertical; eyelid fringe scales 53/56; a fold of skin originating in suborbital region extends posteroventrally across angle of jaw; external auditory meatus elliptical with long axis directed dorsoventrally; tympanum deeply recessed, bordered anteriorly by two spinose scales; mental triangular, bordered laterally by first infralabial and posteriorly by three postmentals; postmentals collectively bordered by six gular scales (Fig. 3C); infralabials rectangular 10/9. Neck narrower than body, covered with uniform granular scales interspersed with conical tubercles on nape; dorsal body tubercles surrounded by 11–13 smooth granular scales; 21 longitudinal rows of dorsal tubercles at midbody; 29 paravertebral tubercles between limb insertions, distinct vertebral row of scales absent. Body relatively thin, covered with granular scales grading ventrally into larger flattened subimbricate ventral scales; 119–137 scales around midbody; larger ventral scales grade abruptly into smaller granular scales immediately anterior to vent; 20 pore-bearing precloacal scales in a continuous transverse series extending onto proximal regions of thighs (Fig. 3D); one enlarged postcloacal tubercle laterally on each side at level of vent. Limbs covered dorsally with granular scales interspersed with closely spaced tubercles and ventrally with flat, subimbricate scales; hind limbs more robust and longer than forelimbs; deep axillary pockets present; subdigital lamellae wide, 8/8 on first finger, 17/16 on fourth finger, 11/11 on first toe, 23/23 on fourth toe. Tail regenerated and gradually narrowing to the tip.

Coloration. Dorsal ground color of head, body, and limbs reddish brown, bearing irregularly shaped small black blotches, black blotches on head; iris yellow; nuchal loop reddish brown, posterior margin rounded, not pointed; longitudinal black lines between nuchal loop and the first body band; three body bands between limb insertions, one postsacral band on tail base; all bands are reddish brown; ventral surfaces of head, body, and limbs dull white.

Variation. Measurements and scalation data of the type series are provided in Table 5. The paratype (a subadult) largely matches the overall scalation and coloration characters of the holotype, however, it has two internasals and three PostIn.

Comparisons. *Goniurosaurus chengzheng* **sp. nov.** is most similar to *G. gezhi*, but has a proportionally smaller snout (SE:EE; see Table 3), and differs in having reddish-brown body color (*versus* orange or yellow). It also differs from *G. lichtenfelderi* by having three body bands (*versus* four body bands). It differs from *G. luii*, *G. huuliensis*, *G. kadoorieorum*, *G. kwangsiensis*, and *G. liboensis* by having 20 precloacal pores as opposed to 23-33 (Table 3). It differs from *G. araneus* by having no blotches on the body (versus black blotches).

Distribution and Life History. *Goniurosaurus chengzheng* **sp. nov.** is only known from central Guangxi, China at 100-250 m elevation. The known distributions of *G. chengzheng* **sp. nov.** and *G. gezhi* are not overlapping and are separated by the Zuo River. Specimens of the new species were found on limestone and soil slopes near a swallet at night. *Goniurosaurus chengzheng* **sp. nov.** was found to co-occur with Moellendorf's Rat Snake (*Elaphe moellendorffi* Boettger) and a terrestrial crab (*Tiwaripotamon* sp.) in the limestone area.

Etymology. The specific epithet *chengzheng* is from the Chinese phonetic alphabet 诚正, which was noted in the ancient work of Chinese literature *Daxue* around 2000 years ago. It means having true ideas to put one's mind in a proper and well-ordered condition. The word chengzheng is often used in parallel with gezhi. Given this new species is sister to *G. gezhi* in our molecular phylogeny, we use chengzheng for the specific epithet. For the common name, we suggest "Chengzheng Cave Gecko, 诚正睑虎".

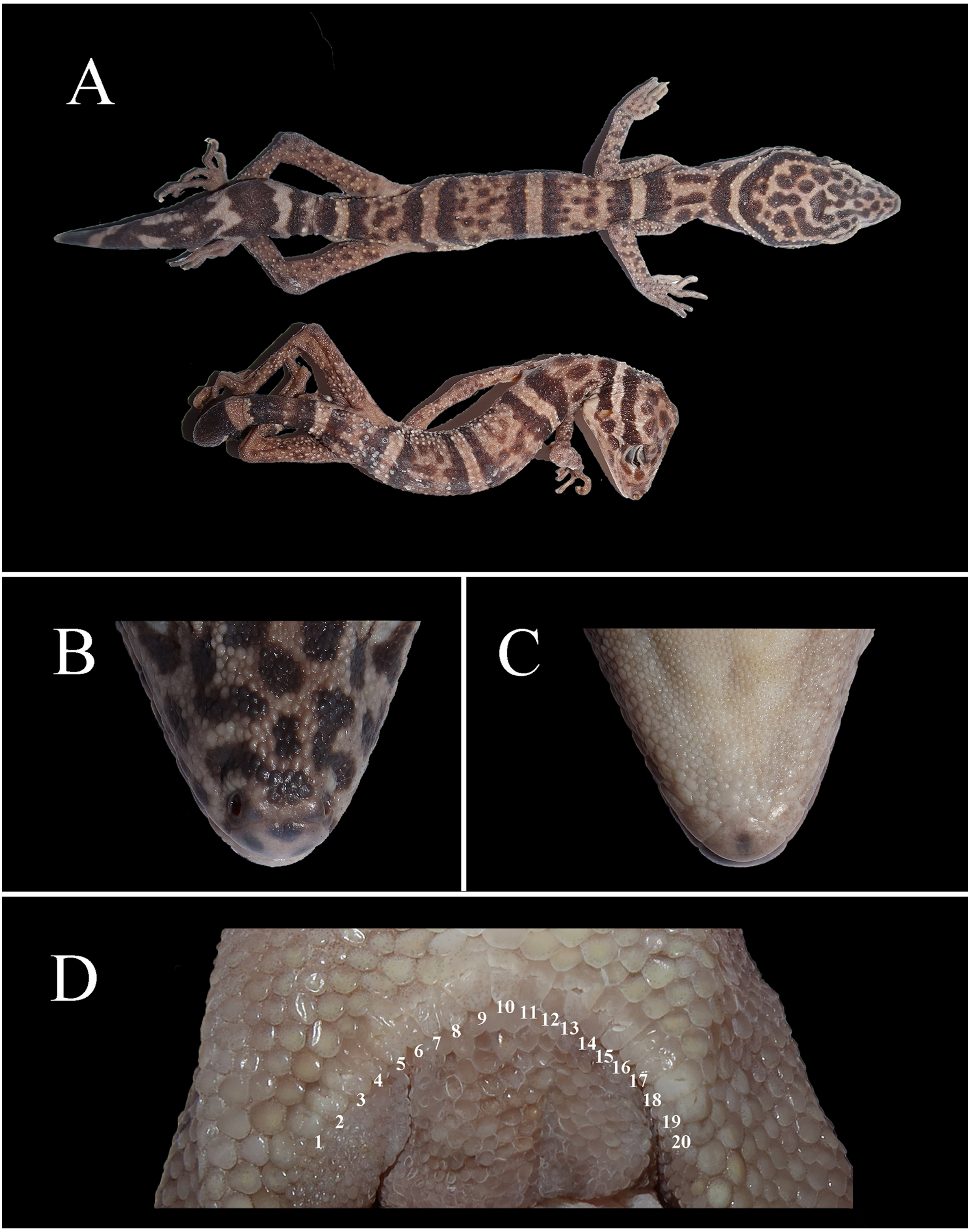

FIGURE 3. *Goniurosaurus chengzheng* **sp. nov.** A. Dorsal view of holotype, ECNU-V0090 (left) and paratype, ECNU-V0068 (right); B. Ventral view of the chin, holotype; C. Dorsal view of the snout tip, holotype; D. Precloacal region, with the precloacal pores numbered.

TABLE 5. Morphological measurements (in mm) and scalation characters of the type specimens of *Goniurosaurus chengzheng* **sp. nov.** Abbreviations are defined in the Materials and Methods. * = regenerated tail.

	HOLOTYPE ECNU-V0090	PARATYPE ECNU-V0068
sex	adult male	subadult male
SVL	107.08	77.35
TaL	62.15*	47.82*
AG	46.95	40.50
HL	29.12	26.57
HW	20.57	19.85
SE	11.53	11.08
EE	11.70	11.69
SVL:HL	3.68	2.91
SVL:AG	2.28	1.91
HL:HW	1.42	1.34
SE:EE	0.99	0.95
SPL	9/8	10/10
SBL	10/9	8/10
N	8/8	8/9
IN	1	2
PostIN	2	3
PM	3	3
GP	6	7
PO	14/14	18/17
CIL	53/56	54/59
MB	119–137	133–141
GST	11–13	11–12
TL	29	29
DTR	21	19
LD1	8/8	8/8
LD4	17/16	20/21
LT1	11/11	12/9
LT4	23/23	22/24
PP	21	–
PAT	1	1

Discussion

In this study, we added *16S* and *cytb* sequence data for four species of *Goniurosaurus* (*G. chengzheng* **sp. nov.**, *G. gezhi*, *G. kadoorieorum***,** *G. araneus*), and presented an updated phylogeny for 91% of the known *Goniurosaurus* species including new species that were published in 2020 (Zhu *et al.* 2020b). The topology is similar to that inferred in previous studies (e.g., Liang *et al.* 2018).

Our molecular analyses suggest *G. chengzheng* **sp. nov.** belongs to the *G. luii* group and is distinct from other congeners. *Goniurosaurus chengzheng* **sp. nov.** is morphologically most similar to *G. gezhi* and our molecular analyses also retrieve these two taxa as sister species. Genetic distances between *G. chengzheng* **sp. nov.** and congeners are comparable to those for other species within the same genus (Table 2), and also similar to uncorrected distances between species in other gekkotan genera (Bauer and Lamb 2002; Gamble *et al*. 2012; Metallinou *et al*. 2012). The geographical ranges of *G. gezhi* and *G. chengzheng* **sp. nov.** are separated by the Zuo River, which may serve as a barrier to gene flow between these two species.

This new species is only found in karst habitat in Guangxi province of China. Together with four *Goniurosaurus* species recently discovered in China (Zhu *et al.* 2020a, 2020b; Qi *et al.* 2020a, 2020b), this suggests potential unknown *Goniurosaurus* species remain to be discovered in the karst landscapes of China and northern Vietnam. This karst area is known for the high degree of endemism (Luo *et al*. 2016; Wang *et al*. 2017). The discovery of *G. chengzheng* **sp. nov.** and other species that have recently been found in the limestone area in Guangxi (e.g., Xu *et al*. 2021, Meng *et al*. 2020) highlights that the conservation efforts need to be improved to protect many endemic species living in this region. *Goniurosaurus* is known to be illegally collected for pet trade (Grismer *et al.* 1999; Stuart *et al.* 2006; Lindenmayer & Scheele 2017). To protect this new species, we follow the current community standard to withhold detailed type locality information (Yang & Chan 2015; Zhu *et al.* 2020a, 2020b).

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