

First Morphological Description and Phylogenetic Analysis of *Zhangixalus omeimontis* (Anura: Rhacophoridae) from Chongqing, China

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ABSTRACT

Zhangixalus omeimontis (Stejneger, 1924) has been recorded widely in Sichuan, Chongqing, Yunnan (Zhaotong, Pingbian, and Lvchun), Guizhou, Hubei (Lichuan), Hunan (Yizhang and Changde), Guangxi (Jinxu and Longshen), and Guangdong (Nanling), China. Although *Z. omeimontis* was once recorded from Chongqing, no morphological description and phylogenetic analysis has been conducted on the Chongqing population. During recent field work in Wulong, Chongqing, China, we collected several specimens of *Z. omeimontis*, and we performed morphological description and phylogenetic analysis for them. Phylogenetic analysis indicates that *Z. omeimontis* is comprised of two major clades, one containing samples from Sichuan, Chongqing, and northeastern Yunnan, and one mainly containing samples from southern Yunnan, Guangdong, Guangxi, and Hunan. This study enriches morphological description of *Z. omeimontis* and sheds some light on the divergence pattern of this species.

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Key words

Zhangixalus omeimontis, Chongqing, China, Morphological description, Phylogenetic analysis

INTRODUCTION

The genus *Zhangixalus* is distributed widely in eastern Asia and northern Indochina and currently contains 46 species (Frost, 2024). In China, 32 species of *Zhangixalus* have been recorded to date (Pan *et al.*, 2025), five of which are distributed in Chongqing: *Z. chenfu* (Liu, 1945), *Z. dennysi* (Blanford, 1881), *Z. hongchibaensis* (Li, Liu, Chen, Wu, Murphy, Zhao, Wang, and Zhang, 2012), *Z. leucofasciatus* (Liu and Hu, 1962), and *Z. omeimontis* (Stejneger, 1924), *Amphibia China*, 2024; Luo *et al.*, 2012; Yang *et al.*, 2017).

Zhangixalus omeimontis was described based on specimens from Xinkaisi, Emei Mountain, Sichuan Province, China, and is distributed widely in China

(Chongqing, Yunnan, Guizhou, Guangxi, Sichuan, Hunan, Hubei Guangdong) and Vietnam (Lao Cai). It is characterized by narrow, elongated, and flattened body; fingers half-webbed; webbing between toes developed well, toes entire-webbed with the exception of toe IV; tibio-tarsal joint reaching posterior angle of eye; skin rough covered with small tubercles; dorsal surface typically green interweaved with brown (Stejneger, 1924; Fei *et al.*, 2012). Dufresnes and Litvinchuk (2022) considered that *Z. omeimontis* could be treated as a senior synonym of *Z. duboisi* (Ohler, Marquis, Swan, and Grosjean, 2000) given the weak divergence between them at 16S sequences. However, more recent studies showed that *Z. duboisi* is closer to *Z. puerensis* (He, 1999) (Shui *et al.*, 2023; Pan *et al.*, 2025) and *Z. omeimontis* is closer to *Z. franki* (Ninh, Nguyen, Orlov, Nguyen, and Ziegler, 2020) (Pan *et al.*, 2025), which implies that *Z. omeimontis* and *Z. duboisi* are two distinct species.

In May 2024, during our field survey in Wulong, Chongqing, we collected some adult specimens belonging to the genus *Zhangixalus*. Our morphological examination and molecular phylogenetic analysis confirmed that they were *Z. omeimontis* (Fig. 1). This species has been recorded in Chongqing, but no morphological description or phylogenetic analysis has been conducted. Therefore, this study fills the gaps in these aspects.

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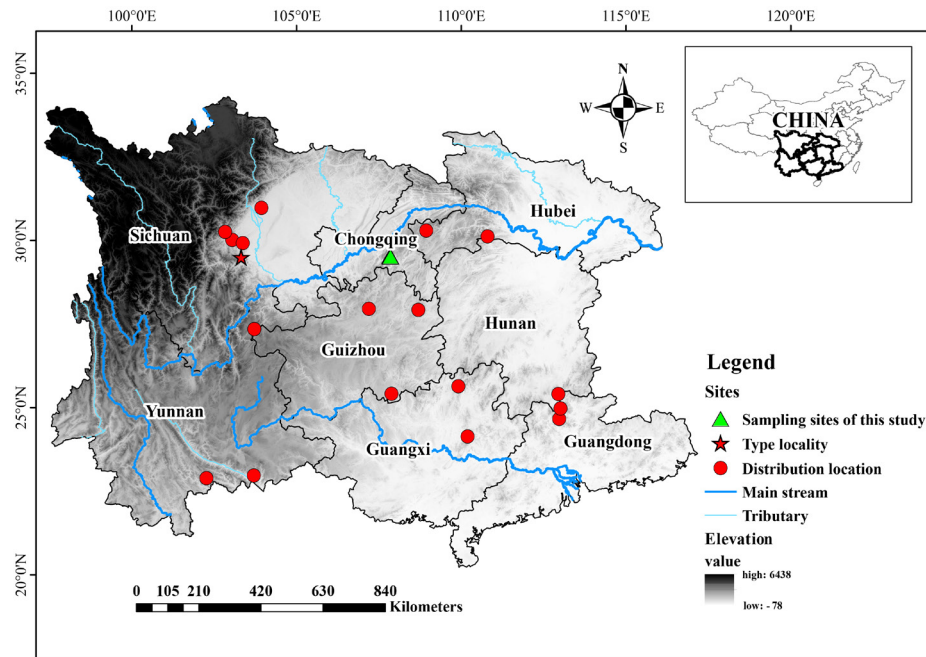


Fig. 1. Distribution and sampling sites of *Zhangixalus omeimontis*.

MATERIALS AND METHODS

This study was carried out in accordance with the ethical guidelines issued by the Ethics Committee of Guangxi Normal University. Specimens were collected during field surveys in 15-17 May 2024 at Fairy Mountain, Wulong, Chongqing, China, and a total of five treefrog specimens resembling *Z. omeimontis* were collected during the surveys. Sex was determined, based on whether the vocal sac opening presents on the floor of the mouth at each corner. Specimens were photographed, euthanised, fixed and then stored in 75% ethanol. Liver tissues were preserved in 99% ethanol. Specimens were deposited at Guangxi Normal University (GXNU).

Morphometric data were taken using electronic digital calipers to the nearest 0.1 mm. Morphological terminology followed Yu *et al.* (2019). Measurements included: Snout vent length (SVL, from tip of snout to vent); head length (HL, from tip of snout to rear of jaws); head width (HW, width of head at its widest point); snout length (SL, from tip of snout to anterior corner of eye); internarial distance (IND, distance between nares); interorbital distance (IOD, minimum distance between upper eyelids); upper eyelid width (UEW, maximum width of upper eyelid); eye diameter (ED, diameter of exposed portion of eyeball); distance between nostril and eye (DNE, from nostril to anterior border of eye); tympanum diameter (TD, the greater of tympanum vertical and horizontal diameters);

forearm and hand length (FHL, from elbow to tip of third finger); tibia length (TL, distance from knee to heel); foot length (FL, from proximal end of inner metatarsal tubercle to tip of fourth toe); and length of foot and tarsus (TFL, from tibiotarsal joint to tip of fourth toe). Webbing formula followed Myers and Duellman (1982).

Total genomic DNA was extracted from liver tissues stored in 99% ethanol. A fragment encoding mitochondrial 16S rRNA gene was amplified and sequenced using the primers L2188 (Matsui *et al.*, 2006)/16H1 (Hedges, 1994). The experiment protocols are the same as those described in Du *et al.* (2020). Sequences were aligned using MUSCLE with default parameters in MEGA v.XI (Tamura *et al.*, 2021) (Table I). Genetic distances between species were calculated in MEGA v.XI using Kimura 2-parameter model. The best substitution model was selected using the corrected Akaike Information Criterion (AICc) in jModelTest v.2.1.10 (Darriba *et al.*, 2012). Bayesian Inference was performed in MrBayes v.3.2.7 (Ronquist *et al.*, 2012) under the selected substitution model (GTR + I + G). Two runs were performed simultaneously with four Markov chains starting from a random tree. The chains were run for 5,000,000 generations and sampled every 100 generations. The first 25% of the sampled tree was discarded as burn-in after the standard deviation of split frequencies of the two runs was less than 0.01. The remaining trees were then used to create a consensus tree and to estimate Bayesian posterior probabilities (BPPs).

Table I. Samples and gene sequences used in this study.

Species	Locality	Voucher ID	GenBank accession number
<i>Theloderma albopunctatum</i>	Vietnam	ROM 30246	AF458148
<i>Leptomantis gauni</i>	Sarawak, Malaysia	FMNH273928	JX219456
<i>Rhacophorus rhodopus</i>	Mengyang, Yunnan, China	SCUM 060692L	EU215531
<i>Zhangixalus burmanus</i>	Mt. Gaoligong, Yunnan, China	SCUM 060614L	EU215537
<i>Z. chenfui</i>	Mt. Omei, Sichuan, China	SCUM 060404L	EU215534
<i>Z. daweshanensis</i>	Pingbian, Yunnan, China	GXNU YU000392	PQ998508
<i>Z. daweshanensis</i>	Pingbian, Yunnan, China	GXNU YU000392	PV010195
<i>Z. dennysi</i>	Vietnam	ROM 30249	AF458139
<i>Z. dorsoviridis</i>	Sa Pa, Lao Cai, Vietnam	ROM 38015	JX219423
<i>Z. dorsoviridis</i>	Jinping, Yunnan, China	Rao060821200	JX219424
<i>Z. dorsoviridis</i>	Pingbian, Yunnan, China	YN080446	JX219425
<i>Z. dorsoviridis</i>	Jinping, Yunnan, China	KIZ060821287	EF564563
<i>Z. duboisi</i>	Lao Cai, Vietnam	VNMN:4103	LC010581
<i>Z. duboisi</i>	Lao Cai, Vietnam	VNMN:4104	LC010582
<i>Z. dugritei</i>	Baoxing, Sichuan, China	SCUM 051001L	EU215541
<i>Z. dultensis</i>	Borneo, Malaysia	BORNEENSIS09087	AB847123
<i>Z. feae</i>	Hekou, Yunnan, China	SCUM 050642W	EU215544
<i>Z. franki</i>	Ha Giang, Vietnam	VNMN 011687	LC548746
<i>Z. hongchibaensis</i>	Wuxi, Chongqing, China	CIB 097687	JN688883
<i>Z. hui</i>	Zhaojue, Sichuan, China	Li01	JN688878
<i>Z. hungfuensis</i>	Wenchuan, Sichuan, China	SCUM 060425L	EU215538
<i>Z. jodiae</i>	Vietnam	VNMN 07122	LC545595
<i>Z. lishuiensis</i>	Lishui, Zhejiang, China	YPX47792	KY653720
<i>Z. melanoleucus</i>	Phou Samsoum Mt., Xiengkhoang, Laos	ZMMU A7781	OQ305234
<i>Z. melanoleucus</i>	Phou Samsoum Mt., Xiengkhoang, Laos	BEI 01010	OQ305233
<i>Z. minimus</i>	Mt. Dayao, Guangxi, China	KIZ 061214YP	EU215539
<i>Z. moltrechti</i>	Lianhuachi, Taiwan, China	SCUM 061106L	EU215543
<i>Z. nanshanensis</i>	Chengbu, Hunan, China	GXNU YU000773	PV010200
<i>Z. nanshanensis</i>	Chengbu, Hunan, China	GXNU YU000774	PV010201
<i>Z. nigropunctatus</i>	Weining, Guizhou, China	GZ070658	JX219430
<i>Z. omeimontis</i>	Pingbian, Yunnan, China	SCUM 061104L	EU215566
<i>Z. omeimontis</i>	Mt.huanglian, Honghe, Yunnan, China	SYS a007762	PQ069748
<i>Z. omeimontis</i>	Mt.huanglian, Honghe, Yunnan, China	SYS a007761	PQ069749
<i>Z. omeimontis</i>	Mt.tianjing, Nanling, Guangdong, China	SYS a008609	PQ069753
<i>Z. omeimontis</i>	Mt.babao, Nanling, Guangdong, China	SYS a008611	PQ069751
<i>Z. omeimontis</i>	Mt.babao, Nanling, Guangdong, China	SYS a008610	PQ069752
<i>Z. omeimontis</i>	Changde, Hunan, China	SYS a008387	PQ069750
<i>Z. omeimontis</i>	Huaping, longsheng, Guangxi, China	SYS a005121	PQ069747
<i>Z. omeimontis</i>	Yaan, Sichuan, China	Li02	JX219420

Table continues on next page.....

Species	Locality	Voucher ID	GenBank accession number
<i>Z. omeimontis</i>	Mt. Omei, Sichuan, China	SC080505	JX219421
<i>Z. omeimontis</i>	Zhaotong, Yunnan, China	RaoZT0806010	JX219419
<i>Z. omeimontis</i>	Pengxian, Sichuan, China	SCUM 0606137L	EU215535
<i>Z. omeimontis</i>	Sichuan, China	CIB20060104	LC010595
<i>Z. omeimontis</i>	Mt. Omei, Sichuan, China	EM1906001	NC_046387.1
<i>Z. omeimontis</i>	Zhaotong, Yunnan, China	KIZ2006025	EF564565
<i>Z. omeimontis</i>	Hongya, Sichuan, China	KIZ060821282	EF564564
<i>Z. omeimontis</i>	Baoxing, Sichuan, China	SYS a005373	PQ069745
<i>Z. omeimontis</i>	Baoxing, Sichuan, China	SYS a005369	PQ069746
<i>Z. omeimontis</i>	Mt. Fairy, Chongqing, China	GXNU YU000804	PV400350
<i>Z. omeimontis</i>	Mt. Fairy, Chongqing, China	GXNU YU000805	PV400351
<i>Z. omeimontis</i>	Mt. Fairy, Chongqing, China	GXNU YU000806	PV400367
<i>Z. omeimontis</i>	Mt. Fairy, Chongqing, China	GXNU YU000807	PV400368
<i>Z. omeimontis</i>	Mt. Fairy, Chongqing, China	GXNU YU000808	PV400370
<i>Z. pachyproctus</i>	Puer, Yunnan, China	KIZ090148	MN613222
<i>Z. pinglongensis</i>	Shiwandashan, Guangxi, China	NHMG201002011	KU170684
<i>Z. puerensis</i>	Puer, Yunnan, China	SCUM 060649L	EU215542
<i>Z. schlegelii</i>	Hiroshima, Japan	-	AB202078
<i>Z. smaragdinus</i>	Yingjiang, Yunnan, China	KIZ 20160298	MN613219
<i>Zhangixalus</i> sp.	Ta Xua, Son La, Vietnam	VNMN:4099	LC010577
<i>Z. thaoae</i>	Sa Pa, Lao Cai, Vietnam	ROM 38011	JX219427
<i>Z. thaoae</i>	Lao Cai, Vietnam	IEBR:A5138	LC762094
<i>Z. yaoshanensis</i>	Jinxiu, Guangxi, China	NHMG150408	MG322122
<i>Z. yunnanensis</i>	Xinping, Yunnan, China	YU20160267	PP187270
<i>Z. yunnanensis</i>	Longling, Yunnan, China	Rao3494	JX219429
<i>Z. zhoukaiyae</i>	Jinzhai, Anhui, China	AHU-RhaDb-150428	KU601502

RESULTS

Phylogenetic relationship

The obtained sequence alignment was 897 bp. Phylogenetic analyses revealed that *Z. omeimontis* is consisted of two clades (Clades 1 and 2) and the *Zhangixalus* specimens newly collected from Mt. Fairy, Chongqing, China (GXUN YU000804–YU000808) clustered together with topotypes of *Z. omeimontis* from Mt. Emei, Sichuan, China and other populations of *Z. omeimontis* from Sichuan and northeastern Yunnan (Zhaotong) with high support (BPP 100%) in Clade 2 (Fig. 2). The genetic distances between *Zhangixalus* species range from 0.6% [*Z. hui* (Liu, 1945) vs. *Z. dugritei* (David, 1872)] to 18.4% [*Z. jodiae* (Nguyen, Ninh, Orlov, Nguyen, and Ziegler, 2020) vs. *Z. dulitensis* (Boulenger, 1892)], and the genetic distance between the two clades of *Z. omeimontis* (Clades 1 and 2) is 2.1% (Supplementary Table S1).

Therefore, on the basis of the above molecular evidence, we considered that the *Zhangixalus* specimens newly collected from Mt. Fairy, Chongqing, China, belonged to *Z. omeimontis*.

Description of *Z. omeimontis*

Morphometric data are summarized in Tables II and III. Adult male SVL 52.9–57.9 mm, adult female SVL 64.6 mm; head length (HL) shorter than head width (HW); pupil horizontal; snout rounded, sloping in profile, protruding beyond the edge of the lower jaw in ventral view; canthus rostralis distinct; nostrils oval, closer to snout tip; IND slightly shorter than IOD; cheeks slightly slanted; IOD equal to IND and wider than UEW; tympanum distinct, rounded, shorter than eye diameter (ED); vomerine teeth distinct; tongue attached anteriorly and distinct notched posteriorly; temporal fold straight and smooth, extending posteriorly to the dorsal base of the forelimb.

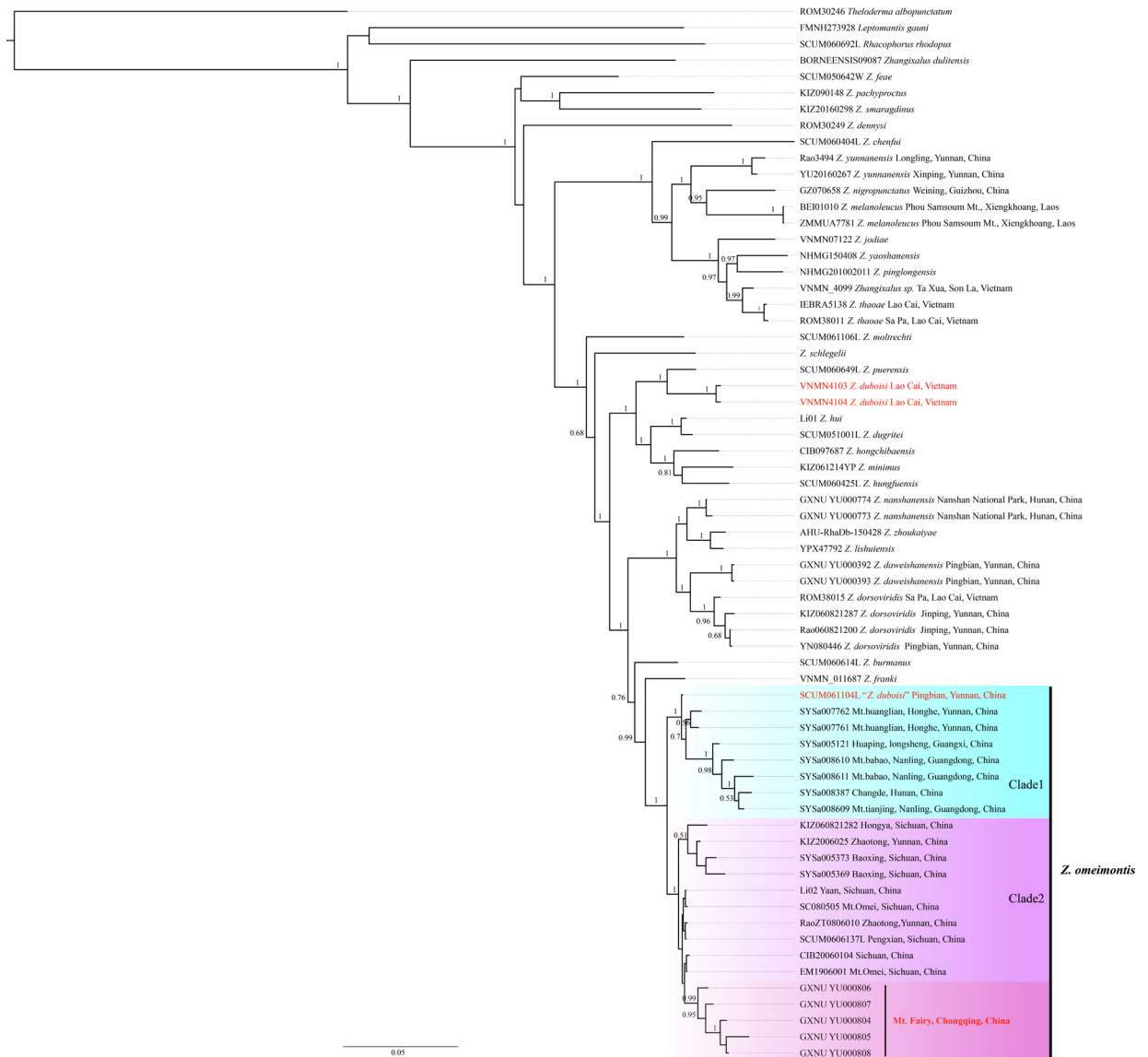


Fig. 2. Bayesian phylogenetic tree of *Zhangixalus* based on 16S rRNA sequence (only values above 50% are shown).

Forelimbs elongated; forearm and hand length (FHL) 60% of body size; relative length of fingers I < II < IV < III; tips of all fingers expanded into discs with circum-marginal grooves; disc of the first finger is significantly smaller than the other fingers discs; discs on the outer three fingers approximately equal to the width of the toe discs; subarticular tubercles well-developed; supernumerary tubercles small or undeveloped; an inner metacarpal tubercle, large, ovoid; two outer metacarpal tubercles; fingers half webbed; fringe along outer edge of fingers present.

Relative length of toes I < II < III = V < IV; nuptial pad on base of finger I in males; tips of all toes expanded

into discs with circum-marginal grooves; subarticular tubercles well developed and rounded, larger than supernumerary tubercles; inner metatarsal tubercle oval and undeveloped; outer metatarsal tubercle absent; toes entire webbed, only the fourth toe with fringe extended to toe tip, the rest toes with webbing connected to toes discs; fringe along outer edge of toes present, the free fringe of the fifth toes extended to the base of tibiotarsal articulation with small projections; tibiotarsal articulation reaching anterior margin of eye; heels overlap when legs positioned at right angle to body; tibia approximately half of body size, longer than foot.

Table II. Morphometric measurements of adult *Z. omeimontis* from Wulong, Chongqing (Unit: mm).

Character	Male (n=4)		Female (n=1)
	Range	Mean±SD	
SVL	52.8-57.9	54.71±2.28	64.6
HL	18.6-18.9	18.74±0.12	21.0
HW	18.8-20.9	19.65±0.87	24.4
SL	8.2-8.7	8.56±0.21	9.9
IND	5.2-5.9	5.68±0.30	6.8
IOD	5.9-6.7	6.17±0.34	6.6
UEW	4.2-5.1	4.63±0.38	5.1
ED	6.4-7.6	6.82±0.55	7.8
TD	4.2-4.7	4.49±0.22	4.7
DNE	4.0-4.7	4.39±0.39	5.0
FHL	33.5-36.0	34.27±1.16	42.8
TL	28.6-32.22	30.24±1.83	37.4
TFL	41.2-44.9	42.55±1.76	51.6
FL	26.7-28.1	27.57±0.64	34.8

SVL, snout vent length; HL, head length; HW, head width; SL, snout length; IND, internarial distance; IOD, interorbital distance; UEW, upper eyelid width; ED, eye diameter; TD, tympanum diameter; DNE, distance between nostril and eye; FHL, forearm and hand length; TL, tibia length; TFL, length of foot and tarsus; FL, foot length.

Dorsal surface of body rough, covering with small tubercle; ventral surface of chest, body, and thighs covered with smooth tubercle; throat fine granular; specimen dorsal surface in life predominantly green with irregular brown spots; a light brown stripe extended from the snout tip along the canthal ridge, passing over the eyelid and extending to temporal fold; some male individual flanks mottled with bright yellow, faded in preservative; limbs with reticulated pattern of intermingled green and brown spots; throat, chest, ventral edge of limbs scattered with irregular light cloud-like black spots; ventral surface of webbing between fingers and toes yellow, dorsal surface

of webbing intermingled with same color pattern as the limbs; males have a single internal vocal sac, female without vocal sac openings; Iris yellowish-golden (Fig. 3).

Based on morphological comparisons, the collected specimens in Chongqing, China are consistent with the description of *Z. omeimontis* (Fei *et al.*, 2010).

Habit and ecology

During the surveys, the species was found inhabiting mountain streams, vines, and terraced fields at elevations exceeding 1,100 m in Fairy Mountain, Wulong District, Chongqing, China. Eggs were found in an artificial water reservoir (Fig. 4), and sparse calls of the *Z. omeimontis* were heard in May. *Polypedates braueri* (Vogt, 1911) and *Hyla tsinlingensis* Liu and Hu, 1966 in Hu *et al.* (1966) were also found at the same site.



Fig. 3. *Z. omeimontis* GXNU YU000805 in life. a, front view; b, lateral view; c, dorsal view; d, ventral view (wulong Fairy Mountain, Chongqing County, photoed by Yuanqiang Pan).



Fig. 4. Habitat of the *Z. omeimontis* in Wulong, Chongqing. A: Mountain stream, B: Farmland ditch, C: Foam nests found in an artificial reservoir, a-b: *Z. omeimontis* (A-B, a-b. Photo by Yuanqiang Pan, C Photos by Xiangjian Wu).

Table III. Morphological measurements of *Z. omeimontis* from Wulong, Chongqing (Unit: mm).

Item/mm	yu000804	Percent/ %	yu000805	Percent/ %	yu000806	Percent/ %	yu000807	Percent/ %	yu000808	Percent/ %
Character	M		M		M		F		M	
SVL	52.8		54.9		57.9		64.6		53.2	
HL	18.6	0.35	18.7	0.34	18.8	0.32	21	0.33	18.9	0.35
HW	18.8	0.36	19.3	0.35	20.9	0.36	24.4	0.38	19.6	0.37
SL	8.7	0.17	8.3	0.15	8.7	0.15	9.9	0.15	8.6	0.16
IND	5.9	0.11	5.2	0.1	5.7	0.1	6.8	0.11	5.9	0.11
IOD	5.9	0.11	6	0.11	6.7	0.12	6.6	0.1	6.1	0.11
UEW	4.5	0.08	4.2	0.08	5.1	0.09	5.1	0.08	4.7	0.09
ED	6.4	0.12	6.5	0.12	7.6	0.13	7.8	0.12	6.8	0.13
TD	4.2	0.08	4.6	0.08	4.4	0.08	4.7	0.07	4.7	0.09
DNE	4.1	0.08	4	0.07	4.7	0.08	5	0.08	4.7	0.09
FHL	33.9	0.64	33.5	0.61	36	0.62	42.8	0.66	33.7	0.63
TL	28.8	0.54	28.6	0.52	31.4	0.54	37.4	0.58	32.2	0.61
TFL	41.2	0.78	41.3	0.75	44.9	0.78	51.6	0.8	42.9	0.81
FL	26.7	0.51	27.5	0.5	28.1	0.49	34.8	0.54	28	0.53

For abbreviations, see Table II.

DISCUSSION

Zhangixalus omeimontis has been recorded widely in Sichuan, Chongqing, Yunnan (Zhaotong, Pingbian, and Lvchun), Guizhou, Hubei (Lichuan), Hunan (Yizhang and Changde), Guangxi (Jinxu and Longshen), Guangdong (Nanling National Nature Reserve), China and Lao Cai, Vietnam (Amphibia China, 2024). Previously, no atlases had recorded the distribution of *Z. omeimontis* in Chongqing. Although it was once included in some reports of biodiversity surveys, there has no photographs and molecular data (Luo *et al.*, 2012; Yang *et al.*, 2017). This study supplements morphological description of *Z. omeimontis* in Chongqing and sheds some light on the genetic structure of this species.

Morphologically, the specimens of *Z. omeimontis* collected from Chongqing exhibit some differences compared to the specimens from the type locality. The interorbital distance (IOD) is equal to internarial distance (IND) and wider than UEW in male individuals from Chongqing (vs. IOD equal to IND and shorter than UEW in specimens from the type locality); subarticular tubercles well developed and rounded, supernumerary tubercles small or undeveloped (vs. subarticular tubercles prominent, and rows of supernumerary tubercles on the fingers) (Fei *et al.*, 2012; Fei, 2020; Amphibia China, 2024).

Phylogenetic analyses revealed that there are two

clades in *Z. omeimontis*, which is consistent with a previous study (Shui *et al.*, 2023). Populations of *Z. omeimontis* from Sichuan, Chongqing, and northeastern Yunnan (Zhaotong) form one clade (Clade 2), while populations from southern Yunnan (Pingbian and Lvchun), Guangdong, Guangxi, and northern Hunan (Changde) form another clade (Clade 1; Fig. 2). The genetic divergence between Clade 1 and Clade 2 is 2.1% (Supplementary Table SI). This level of divergence is nearly equal to the distances between some congeners (e.g., 2.4% between *Z. daweshanensis* and *Z. dorsoviridis*, 2.4% between *Z. nanshanensis* and *Z. dorsoviridis*, 2.1% between *Z. nanshanensis* and *Z. liushuiensis*, and 1.9% between *Z. duboisi* and *Z. puerensis*; Supplementary Table SI), implying that these two clades are probably not conspecific. However, no obvious geographical boundaries have been identified in the distribution pattern and no data of samples from Guizhou Province has been included in this and previous analyses. Therefore, more molecular and morphological studies based on wide sampling are needed to test for taxonomic status of the clade containing samples from southern Yunnan, Guangxi, Guangdong, and Hunan (Clade 1) and to unveil the genetic structure and its driving force in *Z. omeimontis*.

Recently, it was noted that *Z. duboisi* and *Z. omeimontis* are likely conspecifics on the basis of low divergence of 16S sequence (Dufresnes and Litvinchuk, 2022). However, in this study, we revealed that *Z. duboisi*

from the type locality (VNMN 4103 and VNMN 4104) is closer to *Z. puerensis* while *Z. omeimontis* is closer to *Z. franki*, which is consistent with Pan *et al.* (2025) and supports that *Z. duboisi* and *Z. omeimontis* are distinctive to each other. The distances between *Z. duboisi* and the two clades of *Z. omeimontis* are 5.0%–5.4%. The reason for the wrong taxonomic change in Dufresnes and Litvinchuk (2022) is that the nominal *Z. duboisi* used by Dufresnes and Litvinchuk (2022) was misidentified and actually belongs to *Z. omeimontis*. For instance, both the present study and Shui *et al.* (2023) found that the nominal *Z. duboisi* from Pingbian, Yunnan did not cluster together with topotypes of *Z. duboisi* (VNMN 4103 and VNMN 4104) but grouped in the clade of *Z. omeimontis*. The Pingbian population was once described as *Polypedates pingbianensis* (Kou *et al.*, 2001), which was synonymized with *Z. duboisi* by Orlov *et al.* (2002) and was synonymized with *Z. omeimontis* by Fei *et al.* (2009). Therefore, based on the phylogenetic analysis, we agree with Fei *et al.* (2009) that *P. pingbianensis* or *Z. duboisi* from Pingbian, Yunnan belongs to *Z. omeimontis*.

DECLARATIONS

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Generative AI and AI-assisted technology statement

The authors have declared that no generative AI or AI assisted technologies were used to create this manuscript.

Supplementary material

There is supplementary material associated with this article. Access the material online at: <https://dx.doi.org/10.17582/journal.pjz/20250530041021>

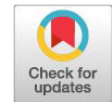
Statement of conflict of interest

The authors have declared no conflict of interest.

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Supplementary Material

First Morphological Description and Phylogenetic Analysis of *Zhangixalus omeimontis* (Anura: Rhacophoridae) from Chongqing, China

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Supplementary Table S1. Genetic distances of Clade1, Clade2, and some *Zhangixalus* species estimated from 16S rRNA genes based on Kimura two-parameter model.

Species	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	30	31
Clade 2																															
Clade 1																															
2.1																															
<i>Z. dziewishiensis</i>	5.2	5.8																													
<i>Z. nanshanensis</i>	4.1	5.3	3.3																												
<i>Z. duboisi</i>	5.0	5.4	5.6	5.3																											
<i>Z. schlegelii</i>	5.9	7.1	6.8	6.5	6.3																										
<i>Z. zhoutaiyae</i>	4.6	5.2	3.8	2.2	6.1	6.8																									
<i>Z. melanoleucus</i>	8.9	9.6	9.4	10.1	6.7	9.6	9.9																								
<i>Z. diliensis</i>	11.8	13.8	13.7	13.1	8.1	14.3	12.9	15.2																							
<i>Z. hongchiensis</i>	5.3	6.2	7.0	5.9	3.1	6.4	6.5	10.9	14.2																						
<i>Z. nigropunctatus</i>	8.2	9.3	9.1	10.3	7.7	9.8	10.2	5.4	14.7	11.0																					
<i>Z. thaore</i>	7.9	9.0	9.1	9.5	7.4	9.9	9.3	6.7	14.3	10.4	5.8																				
<i>Z. dorsovirens</i>	4.4	5.0	2.4	2.4	6.0	6.7	3.0	8.8	11.9	5.9	9.0	8.3																			
<i>Z. minimus</i>	5.3	6.2	6.4	6.0	3.6	7.3	6.8	10.7	13.8	3.6	10.5	9.4	6.1																		
<i>Z. pachyproctus</i>	9.1	10.7	9.5	9.9	6.8	9.8	10.0	12.2	14.6	10.9	12.0	11.5	9.2	10.7																	
<i>Z. smaragdinus</i>	9.9	11.5	10.6	9.4	9.2	9.9	9.4	12.2	14.3	10.8	11.9	11.6	9.6	11.0	9.4																
<i>Z. hui</i>	4.5	5.5	6.1	5.1	2.8	6.1	5.5	9.8	12.5	3.6	9.9	9.2	5.6	3.6	10.2	9.6															
<i>Z. yaoshanensis</i>	8.8	9.9	9.8	9.9	8.3	10.1	9.7	7.0	15.3	11.4	6.1	3.8	8.9	10.5	12.2	12.1	10.1														
<i>Z. pinglongensis</i>	8.2	8.9	9.4	9.6	6.9	10.0	9.4	7.0	15.3	11.0	6.1	3.3	8.5	10.0	11.8	11.9	9.9	3.6													
<i>Z. yunnanensis</i>	8.5	9.8	9.7	9.5	6.6	9.6	9.5	5.1	14.9	10.8	5.1	6.5	8.4	11.0	11.8	11.3	9.5	6.6	6.7												
<i>Z. dennysi</i>	9.0	10.3	9.3	8.8	7.1	10.2	9.0	12.5	15.5	10.8	12.4	11.9	8.7	10.2	11.6	10.6	9.8	11.7	11.8	11.9											
<i>Z. feae</i>	7.7	9.6	8.4	7.8	5.1	8.0	7.8	9.8	12.8	8.4	9.7	9.8	7.5	9.3	8.7	9.0	7.8	10.9	9.7	9.4	9.3										
<i>Z. dugritei</i>	4.8	5.7	6.5	5.3	3.1	6.6	5.9	9.5	12.9	3.6	9.6	8.9	5.7	3.8	10.3	9.8	0.6	9.8	9.7	9.3	10.1	8.2									
<i>Z. chenfui</i>	9.3	10.3	9.7	10.3	6.8	10.8	10.5	8.6	15.9	11.4	8.2	8.2	9.3	11.5	12.2	12.4	9.9	8.7	8.4	7.7	13.1	10.4	9.8								
<i>Z. hungfuensis</i>	4.9	5.9	6.0	5.2	3.1	6.7	6.1	10.4	14.0	3.5	10.5	9.7	5.5	3.6	10.9	10.2	3.8	10.5	10.0	10.4	10.4	9.0	4.0	11.3							
<i>Z. burmanus</i>	3.2	4.2	4.9	4.0	5.1	5.8	4.3	9.4	12.9	5.0	9.2	8.4	4.4	5.0	9.5	9.5	4.3	9.1	8.9	9.1	9.1	7.4	4.4	9.2	5.4						
<i>Z. puerensis</i>	4.7	6.3	5.9	5.7	1.9	6.2	6.1	10.3	12.9	4.5	9.9	8.9	5.7	5.0	9.9	9.8	3.8	10.1	9.6	9.5	9.6	7.6	3.9	9.5	4.8	5.0					
<i>Z. moltrechti</i>	5.7	7.0	7.5	6.4	4.3	6.7	6.9	10.4	13.1	6.6	9.3	8.7	6.5	6.9	10.6	9.5	5.0	9.9	9.9	10.0	10.5	7.9	5.3	10.6	6.7	5.8	5.7				
<i>Z. franki</i>	3.0	3.6	5.2	4.8	4.8	6.3	4.9	7.7	13.6	5.7	7.9	8.1	4.8	5.4	10.3	11.3	4.9	8.5	8.1	8.1	9.8	8.6	5.2	8.9	5.0	3.0	5.3	6.4			
<i>Zhangixalus</i> sp.	4.5	4.4	5.5	5.7	6.6	7.7	7.1	4.5	6.7	5.5	3.5	1.1	5.5	5.0	7.5	9.6	5.0	2.6	2.0	5.0	7.7	4.5	5.2	7.2	5.2	4.0	5.5	5.0	3.7		
<i>Z. jodiae</i>	8.0	10.6	11.7	10.0	4.2	10.5	9.2	8.3	18.4	11.5	6.1	4.3	8.3	10.6	13.1	11.9	10.0	5.3	4.2	6.8	12.2	11.1	9.5	8.0	10.8	9.5	9.2	9.6	10.2	0.0	
<i>Z. tishuensis</i>	4.6	5.5	3.6	2.1	5.7	6.9	1.0	10.1	13.4	6.5	10.4	9.5	3.0	6.6	10.2	9.6	5.8	9.7	9.2	9.7	8.9	7.7	6.0	10.5	5.9	4.0	6.0	7.0	4.8	6.7	9.8