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A new species of newt of the genus *Paramesotriton* (Salamandridae) from southwestern Guangdong, China, with a new northern record of *P. longliensis* from western Hubei

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Abstract

We report two previously unknown populations of Asian warty newts (Salamandridae: *Paramesotriton*) in China. The first population, from southwestern Guangdong, is described as a new species, which is closely related to *P. guangxiensis* based on morphological and molecular data. The second new population, from western Hubei, is assigned to *P. longliensis*, which extends the known range of this species 400 km northwards. Limited genetic differentiation between *P. longliensis* and *P. zhijinensis* suggests that these two names may refer to the same (single) species.

Key words: Amphibia; salamander; Mitochondrial DNA; phylogenetics; taxonomy

Introduction

The salamandrid genus *Paramesotriton* is popular in the international amphibian pet trade. Their peculiar warty skin and variable color pattern make these salamanders appealing to most herpetological hobbyists. Illegal field collections, however, may seriously threaten natural populations of some species of *Paramesotriton*, especially those with restricted ranges. Indeed, some scientists and conservationists advocate withholding the locality data for newly described species that are potentially valuable in commercial markets (Stuart *et al.* 2006).

Ten species of *Paramesotriton* are currently recognized from southern China, northern Laos and northern Vietnam: *P. caudopunctatus* Liu and Hu; *P. chinensis* Gray; *P. deloustali* Bourret; *P. ermizhaoi* Wu, Rovito, Papenfuss and Hanken; *P. fuzhongensis* Wen; *P. guangxiensis* Huang, Tang and Tang; *P. hongkongensis* Myers and Leviton; *P. laoensis* Stuart and Papenfuss; *P. longliensis* Li, Tian, Gu and Xiong; and *P. zhijinensis* Li, Tian and Gu. Recent studies suggest that *P. laoensis* constitutes a different lineage from *Paramesotriton* (Weisrock *et al.* 2006; Zhang *et al.* 2008), and a new monotypic genus, *Laotriton,* is proposed for this species (Dubois & Raffaëlli 2009). On the basis of external morphology and osteological characters, Freytag (1983) considered *P. caudopunctatus* to be distinct from congeners and proposed a new genus, *Allomesotriton*, to contain only this species. Freytag's proposed taxonomic change has not received wide acceptance from later workers, who instead recognize *Allomesotriton* as a subgenus or species group within *Paramesotriton* (Pang *et al.* 1992; Fei *et al.* 2006; Dubois & Raffaëlli 2009).

The first species of *Paramesotriton* was described 150 years ago (Gray 1859), and an additional five species were described over the next 140 years. Four new species, however, have been reported in just the last ten years (Stuart & Papenfuss 2002; Li *et al.* 2008a, b; Wu *et al.* 2009). This recent surge suggests that species-level diversity within *Paramesotriton* may remain underestimated, especially in poorly surveyed areas of Southeast Asia. Here we present a molecular and morphological analysis of the taxonomic status of two previously unreported populations of *Paramesotriton* from China. We describe one population as a new species and identify the other population as a new record of the recently described *P. longliensis*.

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Material and methods

Nine specimens from the first new population were collected from streams on Yunwu Mountain in southwestern Guangdong. Seven specimens from the second population were caught by seine net from a river in Xianfeng County, western Hubei. Euthanized newts were fixed and preserved in 75% ethanol. Freshly cut liver samples from each animal were preserved in 100% ethanol for molecular analyses. We took the following linear measurements from preserved specimens with a digital caliper: TTL, total length; SVL, snout-vent length, measured from the tip of the snout to the posterior edge of the vent; TAL, tail length, measured from the posterior edge of the vent to the tail tip; TAD, maximum tail depth; HL, head length, measured from the tip of the snout to the posterior edge of the parotoid gland; HW, maximum head width; IO, interocular distance, measured from the anterior corner of each eye; EN, distance from the anterior corner of the right eye to the right nostril; IN, internostril distance; AG, distance between the axilla and the groin along the left side of the body; AL, average length of both forelimbs; PL, average length of both hind limbs. Osteological features were assessed by dissection and digital radiography at the Museum of Comparative Zoology, Harvard University (MCZ). Material for morphological comparisons was examined from the Chengdu Institute of Biology, Chinese Academy of Sciences (CIB), the Museum of Vertebrate Zoology, University of California at Berkeley (MVZ), and the Kunming Institute of Zoology, Chinese Academy of Sciences (KIZ). We also incorporated data from the original descriptions of previously named species.

Phylogenetic relationships of the two new populations of *Paramesotriton* to congeneric species were derived from molecular genealogical reconstruction based on the mitochondrial ND2 fragment and flanking tRNAs. This work extended the analysis of Wu *et al.* (2009). Sequences were generated or retrieved from GenBank for all known species (Table 1) except *P. laoensis*, which exhibits closer affinity to the sister genus *Pachytriton*—our phylogenetic outgroup—than to other *Paramesotriton* on the basis of a mitogenomic analysis (Zhang *et al.* 2008). All taxa were sampled from or near their respective type localities (Fig. 1, Table 1). Genomic DNA extraction, PCR and sequencing methods were performed as in Wu *et al.* (2009); PCR primers were available from Wu *et al.* (2010).

Mitochondrial sequences were aligned manually in Se-Al 2.0 (Rambaut 1995). No premature stop codons or indels were found in the protein-coding region. We inferred the matriarchal genealogical relationships within *Paramesotriton* using both maximum likelihood (ML) and Bayesian inference (BI) methods. The optimal evolutionary model was determined by the Akaike Information Criterion (AIC) implemented in MODELTEST 3.7 (Posada & Crandall 1998); the ML analysis was conducted in Garli v.0.951 (Zwickl 2006). The search for the ML tree was continued until the ML had not been improved by 0.01 for 500,000 generations. Bootstrap values were calculated for 100 replicates with the termination threshold reduced to 100,000 generations. Bayesian inference was executed in MrBayes 3.1.2 (Huelsenbeck & Ronquist 2001). Sequence data were partitioned according to tRNA and codon positions because a mitogenomic study on plethodontid salamanders suggests significant improvement of model likelihoods by defining more partitions (Muller *et al.* 2004). Independent GTR+I+G models were assigned to each data partition. Two independent runs with three heated chains and one cold chain were carried out for four million generations. Parameter convergence was assessed by the average standard deviation of split frequencies. The first two million generations were discarded as burn-in. To assess the effect of data partitioning on nodal support, we also conducted an unpartitioned analysis, which, with other conditions unchanged, applied one GTR+I+G model to the entire mtDNA sequence. Harmonic means of model likelihood were compared between the partitioned and unpartitioned strategy using Bayes Factor (BF). A BF > 10 indicates strong evidence favoring the better model (Kass & Raftery 1995). Additionally, we performed a maximum parsimony (MP) analysis in PAUP* 4.0b10 (Swofford 2002). A heuristic search was carried out for 1000 random-sequence-addition replicates; the MP bootstrap support was calculated by 1000 nonparametric pseudo-replicates. Interspecific divergences were assessed through uncorrected pairwise genetic distances (*p*-distance) in PAUP*; sequences retrieved from Lu *et al.* (2004) were excluded due to the large amount of missing data.

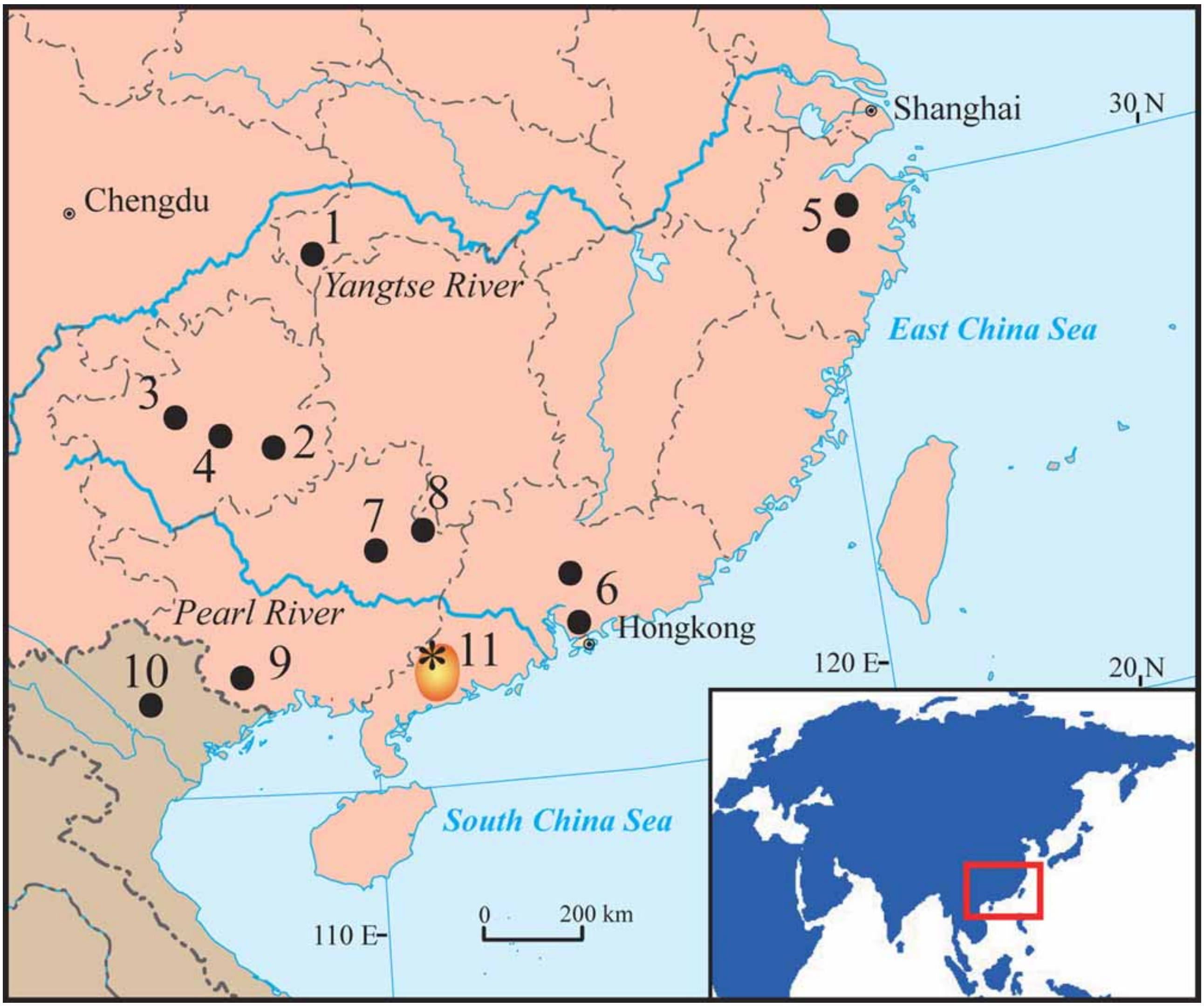

FIGURE 1. Sample localities. 1: *Paramesotriton* sp. (western Hubei); 2: *P. caudopunctatus*; 3: *P. zhijinensis*; 4: *P. longliensis*; 5: *P. chinensis*; 6: *P. hongkongensis*; 7: *P. ermizhaoi*; 8: *P. fuzhongensis*; 9: *P. guangxiensis*; 10: *P. deloustali*. Asterisk (11) denotes the type locality of *P. yunwuensis* **sp. nov.** The Yunwu Mountains are shaded orange. Inset: red square shows the focal area in Asia.

Results and discussion

Mitochondrial ND2 and flanking tRNA sequences yield an alignment for 33 specimens that contains 1216 nucleotide sites; 432 of these are variable and 356 are potentially parsimony-informative. Two single-site indels at the tRNA-Trp region are present in the sequences from *Pachytriton* (outgroup), and a single-site deletion is fixed at the tRNA-Ala region in the new population of *Paramesotriton* from southwestern Guangdong. TrN+G is the optimal evolutionary model for the ML analysis (alpha = 0.2876). Branch lengths from BI are unrealistically long (nearly ten times longer than those from ML), which results from the dependence of branch length estimation on branch length prior (Marshall 2010). Deleting sequences that contain a large amount of missing data or reducing the number of partitions ameliorates the long-branch problem. The partitioned-BI yields very similar posterior probabilities compared to the unpartitioned analysis. But the partitioned strategy is strongly favored (BF = 436.36). Tree topologies from the ML, BI (partitioned and unpartitioned) and MP analyses are fully congruent. Therefore, we depict only the ML tree here (Fig. 2).

TABLE 1. Specimens included in the molecular phylogenetic analysis.

Species	Voucher no.	Locality	GenBank acc. no.	Reference
Ingroup				
Paramesotriton yunwuensis	CIB 97854	Luoding, Guangdong, China	GU980579	this study
	CIB 97855	Luoding, Guangdong, China	GU980577	this study
	CIB 97856	Luoding, Guangdong, China	GU980578	this study
Paramesotriton guangxiensis	MVZ 220905	Ningming, Guangxi, China*	DQ517804	Weisrock *et al.* (2006)
	SN 02053	Ningming, Guangxi, China*	AY233166	Lu *et al.* (2004)
	unknown	unknown	FJ169604	GenBank direct submission
Paramesotriton fuzhongensis	MVZ 230363	Xiling, Guangxi, China	DQ517803	Weisrock *et al.* (2006)
	SN 02011	Fuchuan, Guangxi, China	AY233162	Lu *et al.* (2004)
	unknown	unknown	FJ169605	GenBank direct submission
Paramesotriton deloustali	MVZ 223627	Tam Dao, Vinh Phu, Vietnam*	DQ517802	Weisrock *et al.* (2006)
	MVZ 223628	Tam Dao, Vinh Phu, Vietnam*	FJ744599	Wu *et al.* (2009)
	MVZ 223629	Tam Dao, Vinh Phu, Vietnam*	FJ744600	Wu *et al.* (2009)
Paramesotriton chinensis	CIB 95899	Ningbo, Zhejiang, China*	FJ744603	Wu *et al.* (2009)
	CIB 95911	Jinhua, Zhejiang, China	FJ744604	Wu *et al.* (2009)
	CIB 95910	Jinhua, Zhejiang, China	FJ744605	Wu *et al.* (2009)
Paramesotriton hongkongensis	MVZ 230366	Hongkong, China*	GU980581	this study
	MVZ 230368	Hongkong, China*	GU980582	this study
	CIB 97898	Huizhou, Guangdong, China	GU980580	this study
Paramesotriton ermizhaoi	CIB 88140	Jinxiu, Guangxi, China*	FJ744602	Wu *et al.* (2009)
	CIB 88141	Jinxiu, Guangxi, China*	FJ744601	Wu *et al.* (2009)
	MVZ 230616	Jinxiu, Guangxi, China*	DQ517801	Weisrock *et al.* (2006)
Paramesotriton longliensis	KIZ-GZH 081025	Longli, Guizhou, China*	GU980576	this study
	unknown	unknown	FJ169608	GenBank direct submission
Paramesotriton zhijinensis	KIZ-GZH 081026	Zhijin, Guizhou, China*	GU980575	this study
	unknown	unknown	FJ169609	GenBank direct submission
Paramesotriton sp.	CIB 97881	Xianfeng, Hubei, China	GU980572	this study

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TABLE 1 (continued)

Species	Voucher no.	Locality	GenBank acc. no.	Reference
	CIB 97883	Xianfeng, Hubei, China	GU980573	this study
	CIB 97885	Xianfeng, Hubei, China	GU980574	this study
Paramesotriton caudopunctatus	MVZ 236250	Leishan, Guizhou, China*	DQ517799	Weisrock *et al.* (2006)
	MVZ 236252	Leishan, Guizhou, China*	EU880326	Zhang *et al.* (2008)
Outgroup				
Pachytriton archospotus	CIB 95949	Guidong, Hunan, China*	GQ303630	Wu *et al.* (2010a)
Pachytriton brevipes	CIB 95926	Nanfeng, Jiangxi, China*	GQ303626	Wu *et al.* (2010a)
Pachytriton labiatus	CIB 95946	Jinxiu, Guangxi, China*	GU980583	this study

* Type locality

Monophyly of the genus *Paramesotriton* excluding *P. laoensis* is strongly supported. This result is congruent with Lu *et al.* (2004) and Weisrock *et al.* (2006). Moreover, each species represented by multiple samples forms a single lineage. *Paramesotriton* comprises two reciprocally monophyletic groups. Basal relationships of group A are resolved only in the ML analysis, where they receive low statistical support, and the positions of *P. ermizhaoi*, *P. chinensis* and *P. hongkongensis* are ambiguous within this group. These three species constitute a single clade in Wu *et al.* (2009). The new population from southwestern Guangdong constitutes the sister taxon to *P. guangxiensis*. Together, they form the sister clade to *P. fuzhongensis*. Genetic divergences between the new population and *P. guangxiensis* and *P. fuzhongensis* are similar (4.04–4.21% and 3.95–4.29%, respectively) but they slightly exceed distances between *P. guangxiensis* and *P. fuzhongensis* (3.95–4.04%). *Paramesotriton deloustali* from northern Vietnam is more divergent, with distances of 4.69–4.94% to *P. fuzhongensis*, 5.38–5.68% to *P. guangxiensis*, and 5.11–5.52% to the population from southwestern Guangdong. These distances are generally lower than other pairwise interspecific divergences within *Paramesotriton,* as well as those within the closely related genera *Pachytriton* and *Cynops* (Wu *et al.* 2009; Wu *et al.* 2010a, b). Nevertheless, these levels of divergence are comparable to those between some European salamandrids, such as *Lissotriton montandoni* and *L. vulgaris* (Babik *et al.* 2005), and to those within true *Triturus* (Steinfartz *et al.* 2007). Even though the population from southwestern Guangdong, *P. fuzhongensis*, *P. guangxiensis* and *P. deloustali* resemble each other morphologically, each species can be diagnosed based on phenotypic characters (see below). Moreover, all sampled mitochondrial haplotypes from southwestern Guangdong have a unique single-site deletion near the 3’-end of the tRNA-Ala sequence, which we regard as further evidence that this population is distinct from congeneric species. In doing so, we embrace an integrative taxonomy perspective (Padial *et al.* 2009) consistent with the view that each species is a metapopulation lineage that evolves separately from other such lineages (de Queiroz 2005, 2007).

Group B in the matriarchal genealogy is well resolved and supported by all reconstruction methods. *Paramesotriton caudopunctatus* diverges early in the history of the clade, but recently described *P. zhijinensis* and *P. longliensis* are separated by only a modest genetic distance. Unexpectedly, the second new population of *Paramesotriton* from western Hubei clusters with and is only slightly differentiated from *P. longliensis* (*p*-distance < 1.23%), despite the large geographic distance between sampling localities (ca. 400 km; Fig. 1). Both morphology and external coloration of this new population are consistent with the original description of *P. longliensis*, although the new population has a distinct caudal coloration and occupies a different aquatic habitat (see below). Thus, we assign the western Hubei population to *P. longliensis.* Before the description of

P. longliensis (Li *et al.* 2008b), specimens of *Paramesotriton* were collected in southeastern Chongqing, which is geographically intermediate between western Hubei and the type locality of *P. longliensis* in central Guizhou. These specimens, which were identified initially as *P. chinensis* (Xie *et al.* 2004), are morphologically similar to those from western Hubei and may belong to the same species. Therefore, the geographic range of *P. longliensis* likely extends from central Guizhou to western Hubei.

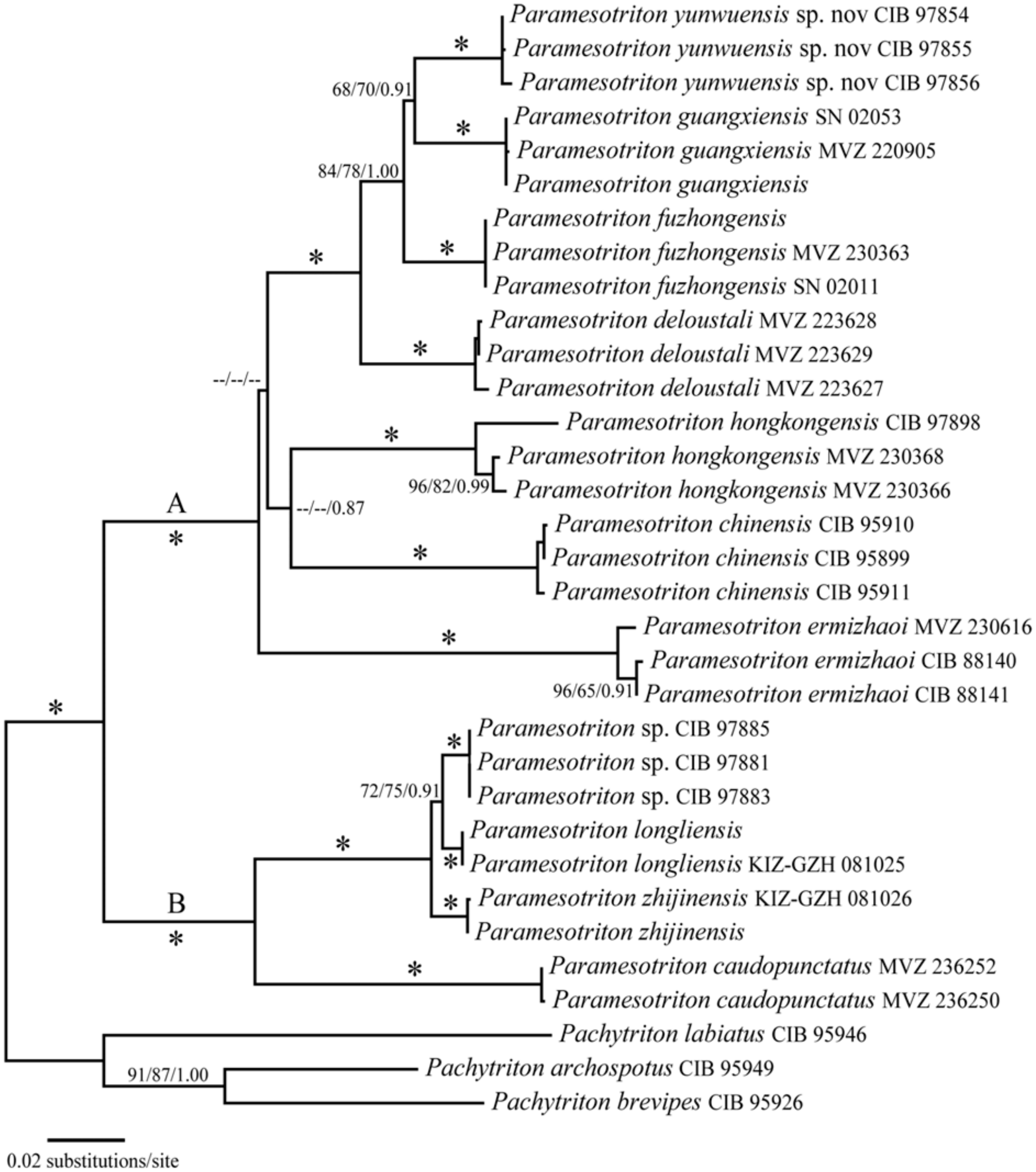

FIGURE 2. Maximum-likelihood (ML) tree based on mitochondrial ND2 and flanking tRNA sequences. Bayesian inference (BI) and maximum parsimony (MP) analyses produced consistent but less-well-resolved topologies. Sequences without any museum numbers are from GenBank direct submissions. *Paramesotriton* sp. is the new population from western Hubei. Numbers on branches are MP bootstrap values; ML bootstrap values; Bayesian posterior probabilities. Asterisks indicate > 95% support in both MP and MP analyses and > 99% support in the partitioned-BI; double-dashes denote < 50% support. The sister genus *Pachytriton* (*P. brevipes*, *P. archospotus* and *P. labiatus*) is chosen as the outgroup taxon.

Our DNA sequence data provide no evidence of long-term divergence between *Paramesotriton longliensis* and *P. zhijinensis* (*p*-distance < 1.84%). The most characteristic trait of *P. zhijinensis* is the presence of vestigial gills in breeding adults (Li *et al.* 2008a; Zhao *et al.* 2008). Close examination of cephalic morphology reveals that the same, likely neotenic trait is present both in *P. longliensis* from the type locality (Li *et al.* 2008b) and in specimens from western Hubei. *Paramesotriton longliensis* also shares with *P. zhijinensis* the presence of two non-continuous yellow dorsolateral stripes, although less conspicuous (only the dorsolateral warts are tinted yellow) in *P. longliensis* (Li *et al.* 2008b). Yellow dorsolateral stripes are a likely synapomorphy of group B, as they also are present in *P. caudopunctatus* (Fei *et al.* 2006). Limited genetic differentiation, similar phenotypes and short geographic distance between type localities (126 km; Fig. 1) constitute evidence against the recognition of *P. longliensis* and *P. zhijinensis* as distinct species.

In conclusion, molecular phylogenetic analyses support recognition of a newly discovered population of *Paramesotriton* from southwestern Guangdong as a new species, which we describe below. A second population from western Hubei is interpreted as a geographically remote component of the recently described species *P. longliensis*.

***Paramesotriton yunwuensis* species nov.**

(Fig. 3 A–G; Fig. 4)

Holotype: CIB 97854, an adult male collected from a pool along a montane stream (22°37’N, 111°10’E; 525 m elevation) near Nanchong village, Fuhe, Luoding city, Guangdong province, P. R. China, by Yunke Wu and Ke Jiang on May 8, 2009.

Paratypes: CIB 95336–95339, 97853, 97855–97856, 97950; same collection date and locality as the holotype.

Diagnosis: *Paramesotriton yunwuensis* is assigned to the genus *Paramesotriton* by its phylogenetic position and the following characters: warts covering dorsal and lateral surfaces; bright orange blotches present on ventral surface; large body size; laterally compressed tail with rounded tip. This species can be diagnosed from congeners by a combination of adult characters: large body size; robust habitus, especially in males; head large and broad; corner of mouth located well posterior to caudal margin of eye; skin rough, warts cover dorsum of head and large warts on dorsolateral ridges; cephalic bony ridges present but not prominent; dorsal vertebral ridge flat to low, not highly protuberant; forelimb short, when extended anteriorly does not reach the caudal margin of eye; palm and tarsus of adpressed limbs do not overlap; tail long, but not deep; bright ventral blotches irregular without a network of black lines; males with bluish-white stripe on posterior half of tail in breeding season.

Description of the holotype: This is a large newt; SVL equals 100.8 mm. Habitus very robust. Head large, much wider than neck. Head longer than broad. Snout truncate, projects beyond mandible. Head slopes steeply downward anteriorly in lateral view. Skull very broad; length / width = 1.06. Labial fold well developed on lateral side of upper jaw. Vomerine tooth patch ʌ-shaped; tooth rows converge anteriorly and extend slightly beyond anterior limit of choanae. Tongue elliptical, adheres to mouth floor but with free lateral margins. Frontosquamosal arch complete and robust. Posterior tip of maxillary bone articulates posteriorly with the pterygoid bone. Epibranchial bones elongated posteriorly and flared dorsolaterally. Parotoid gland prominent. Gular fold present, numerous longitudinal wrinkles on throat. Vertebral ridge flat and inconspicuous. Numerous transverse wrinkles on flanks, venter and lateral sides of tail base. Large warts present on head and dorsolateral ridges. Forelimb very short; when extended rostrally barely reaches posterior margin of eye. When forelimb and hind limb are adpressed against flank, digits tips meet but palm and tarsus do not overlap. Four fingers and five toes, no interdigital webbing. Relative length of fingers, 1 < 4 < 2 < 3; relative length of toes, 1 < 5 < 2 < 4 < 3. Tail laterally compressed; dorsal caudal fin evident on posterior half of tail; ventral caudal fin inconspicuous. Tail tip rounded. Cloaca swollen, with transverse wrinkles; few papillae on cloacal wall.

FIGURE 3. A & B: dorsal and ventral views of male *Paramesotriton yunwuensis* **sp. nov.** (CIB 97854, holotype). C & D: ventral and dorsal views of female *P. yunwuensis* (CIB 97950, paratype). E & F: ventral and dorsal views of a subadult (CIB 97856, paratype). G: the holotype in preservative.

TABLE 2. Linear measurements (in mm) of *Paramesotriton yunwuensis* **sp. nov.** See text for abbreviations. The holotype is included in the summary statistics for males.

	Holotype	Females (N = 5)		Males (N = 3)		Subadult
Measurements	(CIB 97854)	Range	Mean ± SE	Range	Mean ± SE	(CIB 97856)
SVL	100.8	73.4–87.8	82.9 ± 2.7	93.0–104.8	99.5 ± 3.5	66.6
TTL	186.0	145.0–161.0	155.3 ± 2.8	165.1–186.0	177.2 ± 6.2	124.0
TAL	85.2	68.4–76.5	72.4 ± 1.3	72.1–85.2	77.6 ± 3.9	57.4
HL	30.7	23.1–27.6	25.2 ± 0.8	29.9–31.6	30.7 ± 0.5	20.5
HW	26.2	17.9–21.4	19.4 ± 0.6	23.3–27.1	25.6 ± 1.2	14.5
EN	8.7	6.3–7.3	6.8 ± 0.2	8.3–9.3	8.8 ± 0.3	5.6
IO	14.5	9.8–11.5	10.8 ± 0.3	12.9–15.1	14.1 ± 0.7	9.0
IN	6.9	4.9–5.9	5.4 ± 0.2	6.5–7.1	6.8 ± 0.2	4.8
AG	43.9	31.9–40.4	36.2 ± 1.5	36.4–44.2	41.5 ± 2.5	27.5
TAD	13.5	9.9–11.8	11.0 ± 0.3	13.5–15.4	14.3 ± 0.6	8.4
AL	26.5	22.0–23.8	22.9 ± 0.3	21.4–26.5	23.5 ± 1.5	20.2
PL	27.8	21.7–24.1	23.3 ± 0.4	26.2–28.8	27.6 ± 0.8	20.7

TABLE 3. Linear measurements (in mm) of *Paramesotriton longliensis* from western Hubei Province. See text for abbreviations.

	Females (N = 3)		Males (N = 4)	
Measurements	Range	Mean ± SE	Range	Mean ± SE
SVL	66.3–89.8	78.8 ± 6.8	69.9–82.7	77.3 ± 2.7
TTL	130.0–165.3	150.0 ± 10.4	128.2–146.0	138.5 ± 3.9
TAL	63.7–75.5	70.7 ± 3.6	58.3–63.3	61.2 ± 1.4
HL	20.7–26.7	23.5 ± 1.4	21.4–23.9	23.1 ± 0.6
HW	16.8–19.7	18.1 ± 0.9	17.3–18.7	18.3 ± 0.3
EN	5.4–7.8	6.3 ± 0.7	5.7–6.6	6.2 ± 0.2
IO	9.1–10.4	9.6 ± 0.4	9.3–10.4	9.8 ± 0.2
IN	4.4–5.4	4.9 ± 0.3	4.8–5.6	5.3 ± 0.2
AG	30.5–38.8	35.4 ± 2.5	31.1–36.1	33.2 ± 1.1
TAD	9.9–13.3	11.4 ± 1.0	11.4–14.8	13.5 ± 0.7
AL	22.6–28.5	25.4 ± 1.7	22.8–24.9	23.6 ± 0.5
PL	22.6–29.4	26.1 ± 2.0	23.6–26.2	24.8 ± 0.5

Color of the holotype: Dorsum olive brown. Vertebral ridge darker brown with fine black margin. Venter dark orange with a few large irregular pale-orange blotches and small black flecks. Each blotch has a black margin. Chin pale-orange with dense black flecks. Anterior portion of cloaca, underside of limbs and tail orange. A single pale-orange blotch is present on the ventral surface of each limb base. A bluish-white caudal stripe on posterior half of tail.

In preservative, dorsum chocolate brown, vertebral ridge dark orange. Ventral orange coloration fades to milky white, and caudal stripe to pale white.

FIGURE 4. Left: montane pools at the type locality of *P. yunwuensis* near Nanchong village. Right: the stream that connects a cascade of pools at the same site.

Variation: Morphology of paratypes resembles that of the holotype with the following exceptions. Adult females have a more conspicuous vertebral ridge, a smaller and shorter cloacal opening, and no papillae on the cloacal wall. In subadults, the skin is more densely granulated; the dorsal vertebral ridge is highly elevated; the forelimbs are relatively long and extend beyond the anterior margin of the eye when extended forward; the palm and tarsus overlap when the forelimb and hind limb are adpressed against the flank. The number of caudal vertebrae varies among specimens; the posterior tip of the maxillary bone is slightly separated from the pterygoid bone in a few specimens. Linear measurements are summarized in Table 2. Adult dorsal coloration ranges from reddish brown to olive brown; ventral color pattern varies from black background with a few orange blotches to orange background with numerous small black flecks. Arrangement of blotches and flecks is subject to individual variation. The white caudal stripe is absent in females. Subadults are black dorsally, with rounded orange blotches on a black venter.

Etymology: The specific epithet *yunwuensis* is derived from the name of the mountain range, Yunwu, in southwestern Guangdong.

Habitat and distribution: *Paramesotriton yunwuensis* is found in large pools (max. 4 × 4 m) along a montane stream at mid-elevation of the mountain near Nanchong village. Maximum water depth reaches about 3 m. Submerged boulders, small rocks and coarse gravel constitute the pool substrate. Pools are connected by currents of water that course over giant granite boulders. The water is cold, clear and slow-moving. Several species of stream fishes coexist with the newt. Broadleaf forests flourish along the site, but the stream is not covered by the canopy. Newts can be seen crawling actively on the deep pool bottom at midday and they can be found at shallower pool edges at night. Sightings of similar newts in nearby mountains are affirmed by local people. Therefore, we suggest that this species likely occurs in many montane streams in the Yunwu Mountains.

Remarks: Morphologically, *Paramesotriton yunwuensis* resembles but is nevertheless distinct from *P. deloustali*, *P. guangxiensis* and *P. fuzhongensis*. Adult *P. yunwuensis* have a flat or low vertebral ridge and lightly granular warts and the other three species have a high vertebral ridge and densely granulated warts (Bourret 1934; Huang *et al.* 1983; Wen 1989). The new species also has short limbs. For example, when the forelimb is stretched forward in *P. yunwuensis* it does not reach the posterior margin of the eye. In *P. deloustali* the extended forelimb reaches the midpoint of the eye and in *P. fuzhongensis* it reaches even further anteriorly to a point midway between the eye and the nostril (Wen 1989). When the forelimb and hind limb are adpressed against the flank in *P. yunwuensis* only the digit tips overlap. In contrast, the palm and tarsus overlap in *P. fuzhongensis* (Wen 1989). The new species is readily differentiated from *P. guangxiensis* by its larger body size (SVL females 73.4–87.8 mm, males 93.0–104.8 mm), robust habitus, and long and relatively shallow tail. *Paramesotriton guangxiensis* is smaller (SVL female 71.0 mm, males 67.8–75.5 mm), more gracile (e.g., the trunk is relatively flat in cross-section, versus square or round in *P. yunwuensis*), and its tail is short and deep (Huang *et al.* 1983).

The type locality of *P. yunwuensis* lies within a small scenic park. Local villagers use baited fishing line (e.g., earthworms) as well as electrofishing equipment to catch newts and sell them to tourists as juvenile *Andrias davidianus* (Chinese giant salamander). It is unlikely that these human activities associated with tourism are sustainable. According to the IUCN Red List Categories and Criteria version 3.1 (http://www.iucnredlist.org), we consider this species as near threatened. Appropriate conservation measures should be implemented to prevent extirpation of *P. yunwuensis* from its type locality and other naturally occurring populations.

A new population of *Paramesotriton longliensis*

(Fig. 5 A–F)

Seven specimens of *P. longliensis* (CIB 97880–97886) were collected by seine net from a river at night (29°37´N, 109°05´E; 787 m elevation) near Shizilu village, Xianfeng county, Hubei, P. R. China, by Yunke Wu on June 17, 2009. Linear measurements are summarized in Table 3.

This species is characterized by a combination of the following characters: knob-like, fleshy protuberance present in branchial (gill) region; skin very rough, warts densely covering much of the dorsal and lateral surfaces; warts on dorsolateral ridge with yellow or orange tint and sometimes form discontinuous dorsolateral stripes; cloaca prominent in females, conically shaped. Frontosquamosal arch complete and moderately robust; posterior tip of maxillary bone approaches or articulates with the pterygoid bone posteriorly; epibranchial bones elongate and attenuate posteriorly, flared laterally, and extend to the parotoid gland dorsally.

Adults from the newly discovered population are larger than those from the original type series (Li *et al.* 2008b: SVL females 59.0–79.9 mm, males 57.6–73.6 mm; *cf*. Table 3). Although our collection date was close to the early May of Li *et al.* (2008b), we observed a pair of yellowish-white caudal stripes in both males and females from the new population, whereas Li *et al.* (2008b) mention only that the posterior part of the tail in males is light purple without spots or stripes. In the new population, the caudal stripes are continuous anteriorly with the discontinuous dorsolateral stripes. Posteriorly, the caudal stripes are very conspicuous and almost reach the tail tip in males; they are less evident and do not approach the tail tip in females.

The new population inhabits a large river (ca. 10–20 m wide, 1–2 m deep) in a narrow valley. Water current is slow. A thick layer of algae grows on huge flat rocks that are semi-submerged. The newts are readily found on silty substrate. The newts are also found near river banks during or after rains. Local fishermen accidentally catch them in seines. This habitat differs from that reported from the original type series, which were taken from large ponds (Li *et al.* 2008b), but is identical to the report from Xie *et al.* (2004).

Comparative material examined: *Paramesotriton caudopunctatus* (MVZ 236252–236254 and 204295, from Guizhou, China), *P. chinensis* (CIB 95899 and 95907–95911, from Zhejiang, China), *P. deloustali* (MVZ 222122, 225135 and 223627–223628, from Tam Dao, Vietnam), *P. ermizhaoi* (CIB 88140–88141 and 95998–96000, from Guangxi Zhuang Autonomous Region, China), *P. fuzhongensis* (MVZ 230622–230625, from Guangxi Zhuang Autonomous Region, China), *P. guangxiensis* (MVZ 220905–220906, from Guangxi

Zhuang Autonomous Region, China), *P. hongkongensis* (MVZ 230365–230370, from Hong Kong, China) and *P. zhijinensis* (KIZ-GZH 081026, from Guizhou, China).

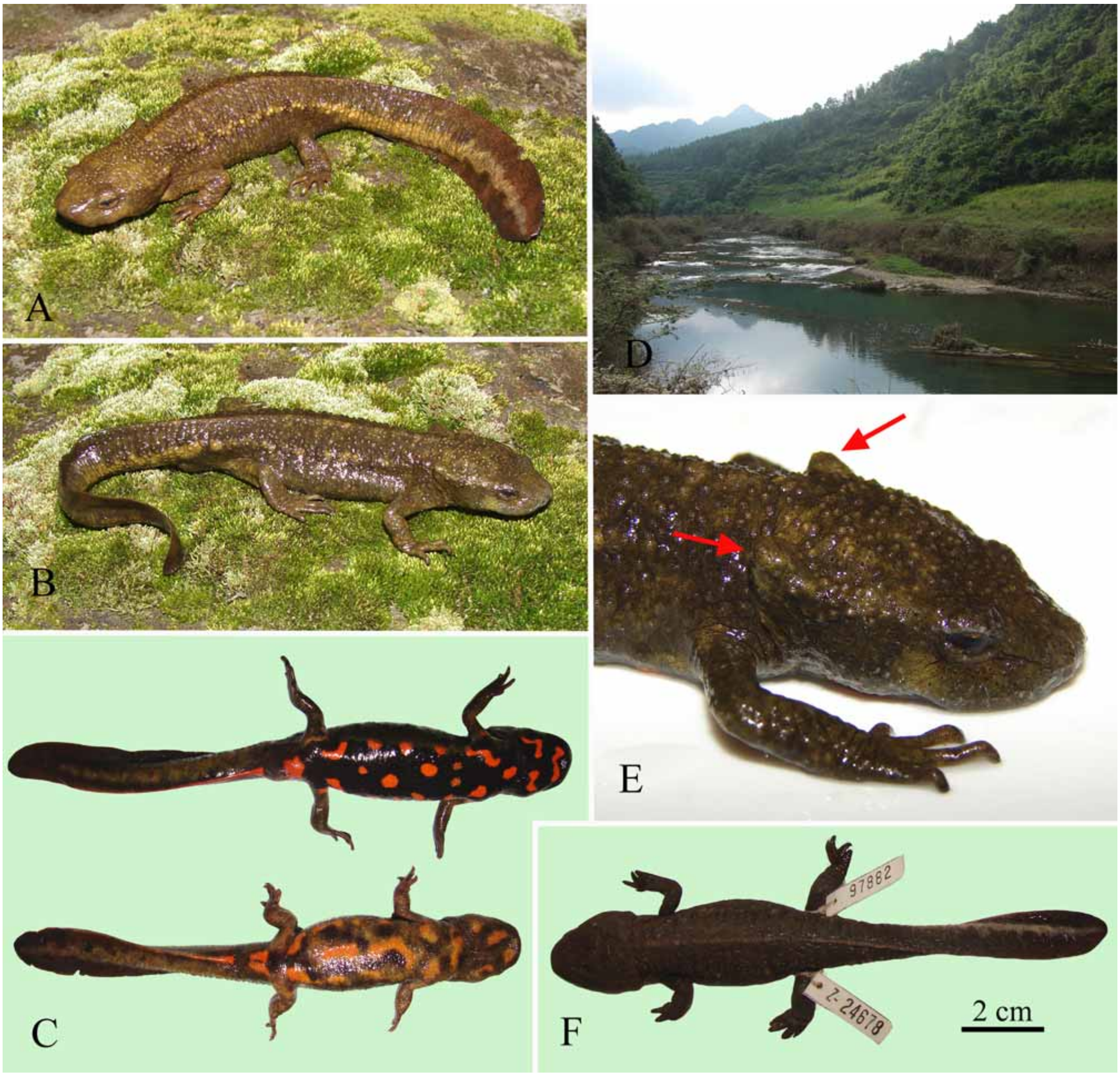

FIGURE 5. A: dorsal view of male *Paramesotriton longliensis* from western Hubei (CIB 97885). B: dorsal view of female *P. longliensis* from the same locality (CIB 97884); both males and females have a pair of yellowish-white caudal stripes that are continuous with the dorsolateral stripes anteriorly. C: ventral view of the same male (lower) and female (upper). D: river where the new *P. longliensis* population is found. E: close-up of the head region (CIB 97884), showing the knob-like protuberance (red arrows). F: A male *P. longliensis* (CIB 97882) in preservative.

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