



## A new newt of the genus *Cynops* (Caudata: Salamandridae) from Fujian Province, southeastern China

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### Abstract

A new species of fire-bellied newt, *Cynops fudingensis*, is described from northeastern Fujian Province, southeastern China. This species forms a well-supported clade with *C. orientalis* and *C. orphicus* based on molecular phylogenetic analysis of nucleotide sequences from mitochondrial DNA subunit two of NADH dehydrogenase and its two flanking tRNAs. Further, its genetic distance to each of the two previously described species is large. Principal-components analysis of external linear measurements differentiates the new species from *C. orientalis* and *C. orphicus* in morphological space. Geographically, *C. fudingensis* occupies the distribution gap between *C. orientalis* and *C. orphicus*.

**Key words:** Molecular phylogeny; taxonomy; Amphibia; salamanders; new species

### Introduction

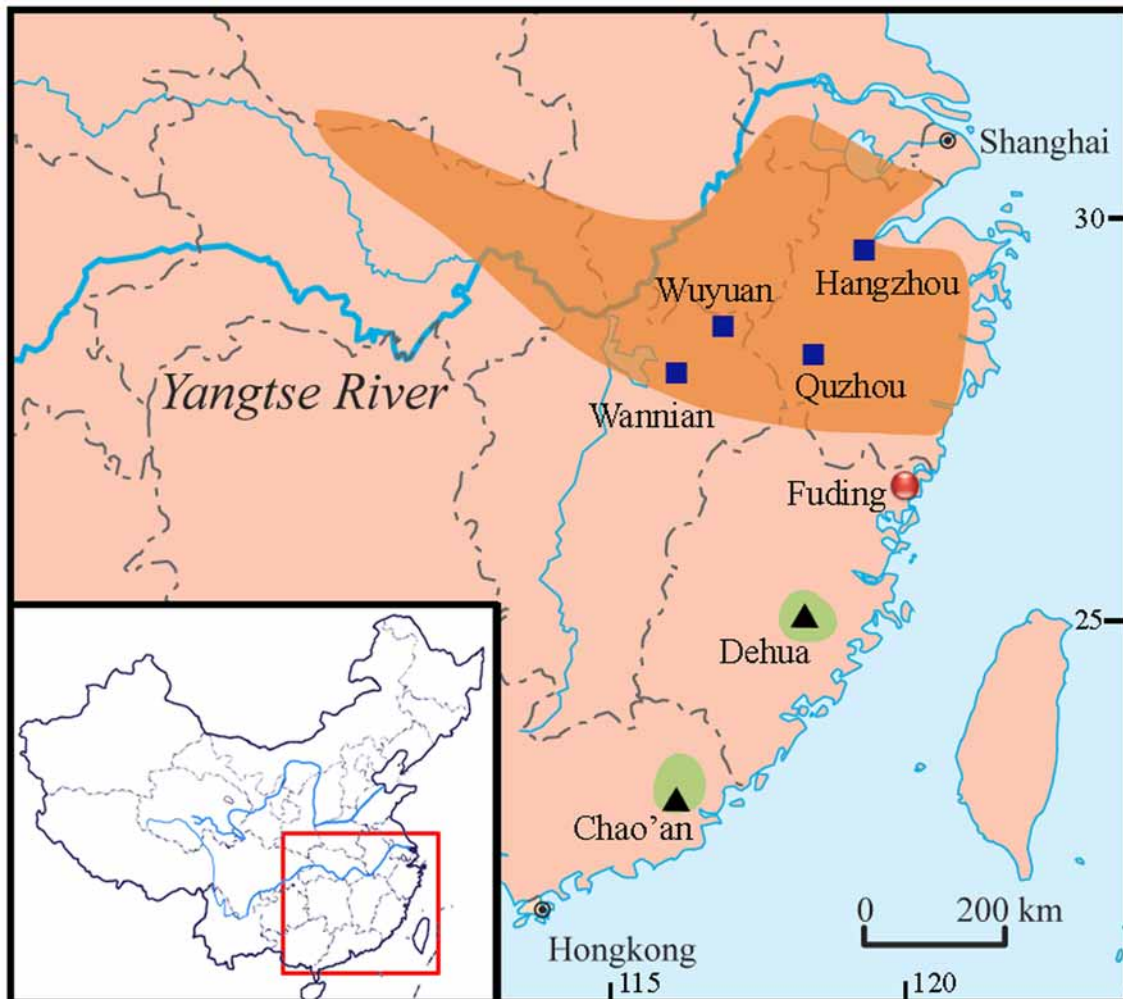
The genus *Cynops*, commonly known as the fire-bellied newts, is a member of the “modern Asian newts” clade, which also includes *Pachytriton* and *Paramesotriton* (Zhang *et al.* 2008). These three genera do not have a close relationship with other Asian salamandrids but instead are sister taxa to European newts, such as *Triturus*, *Mesotriton* and *Lissotriton* (Weisrock *et al.* 2006; Steinfartz *et al.* 2007; Zhang *et al.* 2008). Seven species of *Cynops* are recognized at this time, which constitute three species groups based on external morphology and osteology: the first group includes *C. ensicauda* Hallowell and *C. pyrrhogaster* Boie, which are restricted to a few Japanese islands; the second group comprises *C. chenggongensis* Kou and Xing, *C. cyanurus* Liu, Hu and Yang, and *C. wolterstorffi* Boulenger, three highland species that inhabit pools and lakes on the Yunnan-Guizhou Plateau of China; the third group consists of *C. orientalis* David and *C. orphicus* Risch, both from the foothills and mountainous regions of southeastern China (Zhao & Hu 1984; Dubois & Raffaëlli 2009; Frost 2009). The taxonomic status of *C. wolterstorffi*, a neotenic species that may represent a separate genus, is an ongoing controversy (e.g., Freytag 1962; Zhao & Hu 1984; Fei *et al.* 2006; Dubois & Raffaëlli 2009). The IUCN Red List of Threatened Species (2009) lists two species, *C. ensicauda* and *C. orphicus*, as endangered and a third, *C. chenggongensis*, as data deficient; *C. wolterstorffi* may already be extinct (Zhao 1998).

*Cynops orientalis* remains abundant and has a broad geographic distribution that is centered at the lower reaches of the Yangtze River in China (Fig. 1). Based on molecular phylogenetic analysis of mitochondrial DNA (mtDNA) sequence data, *C. orientalis* is closely related to *C. orphicus* (Weisrock *et al.* 2006; Zhang *et al.* 2008), which differs morphologically by the presence of a conspicuous vertebral ridge and a bright ventral longitudinal stripe (Fei *et al.* 2006).

For a long time *C. orphicus* was known only from its type locality in the Shantou region in eastern Guangdong Province. Recently, however, a population of *C. orientalis* from Mt. Daiyun, Dehua, in central

Fujian Province was reassigned to *C. orphicus* (Fei *et al.* 2006), and this taxonomic change was confirmed by molecular analysis (Weisrock *et al.* 2006). As a result, the documented range of *C. orphicus* expanded northward to more closely approach the southern limit of *C. orientalis*.

In early April 2009, we collected specimens of a population of *Cynops* from a coastal mountain that is located between the known ranges of *C. orientalis* and *C. orphicus*. Our initial impression was that this new population could not be assigned confidently to either named species. Thus, we employed molecular markers and morphometric analyses to more fully resolve its taxonomic status within *Cynops*. Based on these results, herein we describe this population as a new species.



**FIGURE 1.** Geographic distribution of *Cynops fudingensis* sp. nov. (red dot), *C. orientalis* (orange shading) and *C. orphicus* (green shading) in southeastern China (adapted from Fei *et al.* 2006). Samples of the latter two species used in the molecular analysis are denoted by blue squares (*C. orientalis*) and black triangles (*C. orphicus*). Inset: red square shows the location of the focal area in China.

## Materials and methods

Thirteen specimens were collected from near Mt. Taimu, Fuding, in northeastern Fujian Province. Euthanized animals were fixed and preserved in 75% ethanol. Fresh liver or muscle samples from each specimen were preserved in 100% ethanol for genetic analyses. Congeneric specimens for morphological comparison were examined from the Chengdu Institute of Biology, the Chinese Academy of Sciences (CIB), the Museum of Comparative Zoology, Harvard University (MCZ), and the Museum of Vertebrate Zoology, University of California at Berkeley (MVZ). Specimens examined are listed after the species description. Osteological

features were examined on digital radiographs and cleared whole mounts that were differentially stained for bone and cartilage (Klymkowsky and Hanken 1991).

For the morphometric analysis, 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 anterior 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. *Cynops orientalis* from Anhui Province and Zhejiang Province and *C. orphicus* from Dehua, Fujian Province, were compared to the new population by principal-components analysis (PCA) in SPSS (ver. 16, Chicago, IL, USA). To control for the effect of body size in PCA, each measurement was divided by the corresponding SVL. Differences in total length among species were assessed by one-way analysis of variance (ANOVA) and Welch's test. Only adult females were used in the morphometric analysis to avoid the potentially confounding effects of sexual dimorphism, which is significant in *Cynops* (Fei *et al.* 2006).

Maternal relationships within *Cynops* were derived from an analysis of the mtDNA fragment that codes for subunit two of NADH dehydrogenase (ND2) and its flanking tRNAs. All known species were included except *C. chenggongensis* and *C. wolterstorffi* (Table 1); the latter two species have not been collected since the 1990s, and tissue samples for genetic analysis were not available. *Cynops orientalis* was sampled from four localities (plus one animal obtained from the commercial pet trade) to better represent the broad geographic range of this species. One of these samples—CIB 97919, collected near Quzhou, Zhejiang Province—was from near the type locality, which was originally reported as “Tche-san,” “near Chuchowfu” (an earlier name for Quzhou), “Chekiang” (an alternate English translation for Zhejiang; David 1873, 1875). We were unable to associate any current Chinese locality with the name “Tche-san.” *Pachytriton* and *Paramesotriton* were chosen as outgroup genera because of their close relationship to *Cynops* (Weisrock *et al.* 2006; Steinfartz *et al.* 2007; Zhang *et al.* 2008). Genomic DNA extraction, PCR and sequencing methods were performed as in Wu *et al.* (2009); PCR primers were available from Wu *et al.* (2010).

Sequences were aligned manually in Se-Al 2.0 (Rambaut 1995) and compared to referential sequences from GenBank. No premature stop codon or indels were detected in the protein-coding region. Phylogenetic relationships within *Cynops* were reconstructed first under the maximum parsimony (MP) criterion in PAUP 4.0b10 (Swofford 2002); heuristic searches were performed for 1000 replicates of random sequence additions with tree-bisection-reconnection (TBR) as the branch-swapping algorithm. Bootstrap nodal support was calculated by 1000 replicates of the heuristic search, each of which included 10 replicates of random sequence additions. Reconstruction also was performed under the maximum likelihood (ML) criterion in Garli (Zwickl 2006), with the best-fitted evolutionary model determined by the Akaike Information Criterion (AIC) implemented in MODELTEST 3.7 (Posada & Crandall 1998). The search for the ML tree was terminated when the likelihood score had not been improved for 500,000 generations. Bootstrap values were calculated for 100 replicates with the termination threshold reduced to 100,000 generations. We further inferred the molecular phylogeny through Bayesian inference (BI) in MrBayes 3.1.2 (Huelsenbeck & Ronquist 2001). Sequence data were partitioned by tRNA and codon positions. Each partition was assigned an independent GTR+I+G model. Two independent runs were carried out for 2,000,000 generations. The first 1,200,000 generations were discarded as burn-in to insure an effective sample size.

## Results and discussion

Principal-components (PC) analysis differentiates the new population from *Cynops orientalis* and *C. orphicus* in morphological space by a combination of head and body proportions (Fig. 2). The first axis (PC 1) explains 87.4% of the total variance, with large positive loadings for TTL/SVL (0.997), TAL/SVL (0.992), HL/SVL

(0.537), EN/SVL (0.566), AL/SVL (0.541) and PL/SVL (0.612), and negative loading for AG/SVL (-0.451). This axis mainly distinguishes the new population from *C. orientalis*; the new population has a proportionately shorter trunk, longer tail, longer head and longer limbs. The second axis (PC 2) explains another 6.9% of the total variance and separates the new population from *C. orphicus*; the large positive PC 2 values of the new population denote its proportionately larger head, longer limbs and shorter trunk. One-way ANOVA and Welch's test both failed to detect any significant difference in total length among the three species ( $P > 0.05$ ). Summary statistics are given in Table 2 and the Appendix.

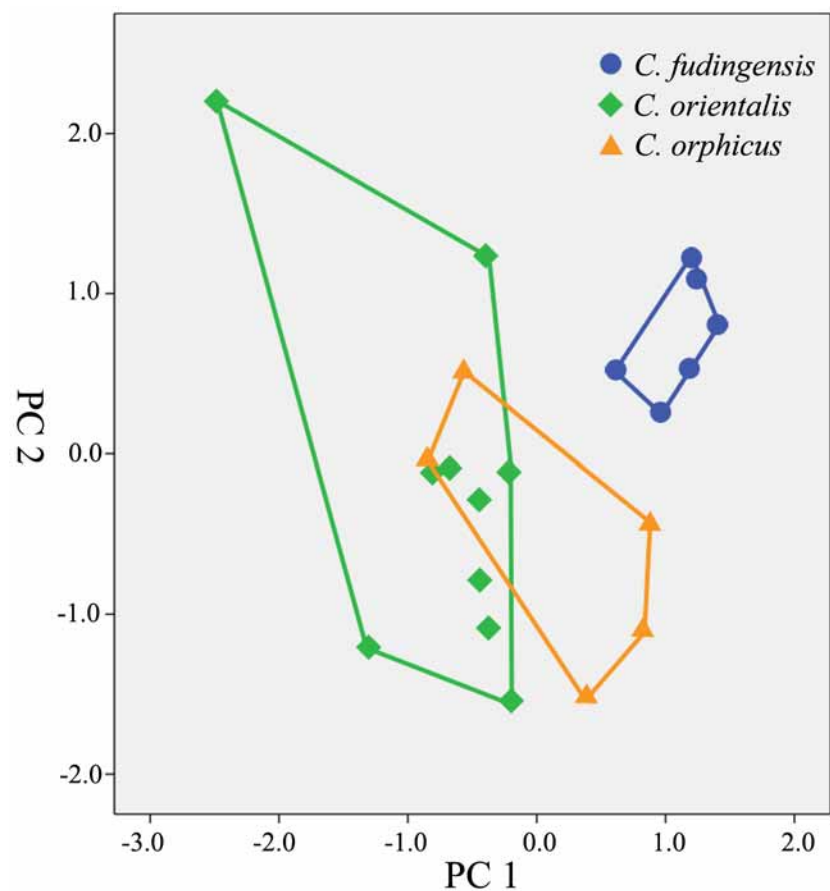
**TABLE 1.** Specimens included in the molecular phylogenetic analysis.

Species	Voucher No.	Locality information	GenBank Acc. No.	Reference
<b>Ingroup</b>				
<i>Cynops fudingensis</i>	CIB 97874	Fuding, Fujian, China	GU301785	this study
	CIB 97875	Fuding, Fujian, China	GU301786	this study
	CIB 97876	Fuding, Fujian, China	GU301787	this study
<i>Cynops orientalis</i>	CIB 97919	Quzhou, Zhejiang, China <sup>T</sup>	GU301790	this study
	CIB 97867	Wannian, Jiangxi, China	GU301788	this study
	CIB 97864	Wuyuan, Jiangxi, China	GU301789	this study
	CIB 88167	Pet-trade, Fuzhou, Fujian, China	GU301783	this study
	MVZ 230344	Hanzhou, Zhejiang, China	DQ517770	Weisrock <i>et al.</i> (2006)
	MVZ 230345	Hanzhou, Zhejiang, China	EU880311	Zhang <i>et al.</i> (2008)
	MVZ 231158	Dehua, Fujian, China	DQ517771	Weisrock <i>et al.</i> (2006)
<i>Cynops orphicus</i>	MVZ 241427	Chao'an, Guangdong, China <sup>T</sup>	DQ571772	Weisrock <i>et al.</i> (2006)
	MVZ 241428	Chao'an, Guangdong, China <sup>T</sup>	EU880312	Zhang <i>et al.</i> (2008)
<i>Cynops cyanurus</i>	CIB 95897	Shuicheng, Guizhou, China <sup>T</sup>	GU301784	this study
	MVZ 219759	Chuxiong, Yunnan, China	DQ517768	Weisrock <i>et al.</i> (2006)
	TJP 30104	Kunming, Yunnan, China	EU880309	Zhang <i>et al.</i> (2008)
<i>Cynops ensicauda</i>	MVZ 238580	Tokashiki-jima, Ryukyu Islands, Japan	DQ517769	Weisrock <i>et al.</i> (2006)
<i>Cynops pyrrhogaster</i>	MVZ 263718	Chiba Prefecture, Japan	DQ517773	Weisrock <i>et al.</i> (2006)
<b>Outgroup</b>				
<i>Pachytriton brevipes</i>	MVZ 231167	Dehua, Fujian, China	EU880324	Zhang <i>et al.</i> (2008)
<i>Pachytriton labiatus</i>	MVZ 230355	Yixian, Anhui, China	EU880325	Zhang <i>et al.</i> (2008)
<i>Paramesotriton guangxiensis</i>	MVZ 220905	Linming, Guangxi, China	DQ517804	Weisrock <i>et al.</i> (2006)
<i>Paramesotriton deloustali</i>	MVZ 223628	Tam Dao, Vinh Phu, Vietnam	EU880327	Zhang <i>et al.</i> (2008)

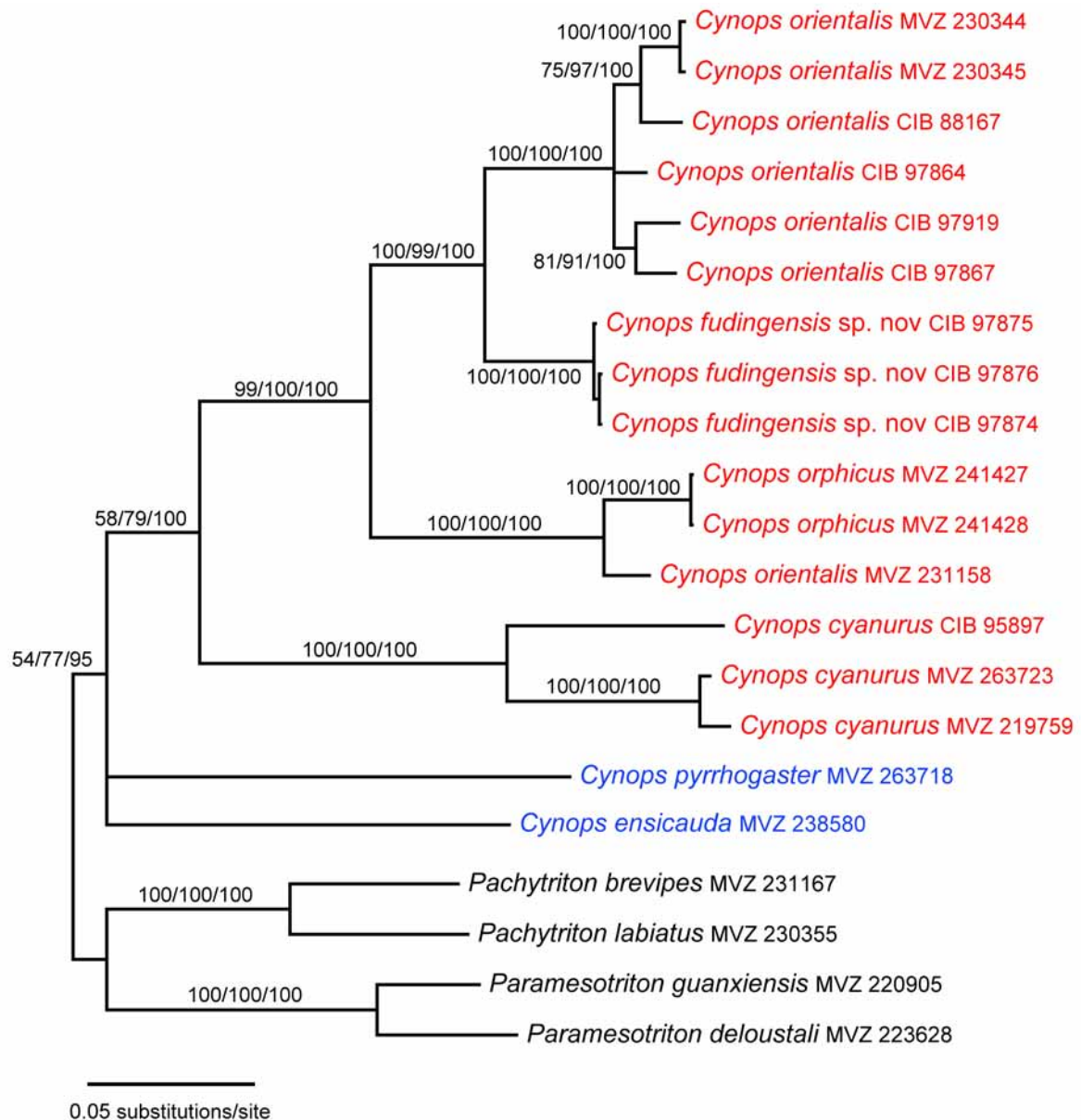
T—type locality.

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

Measurements	Holotype	Females (N = 6)		Males (N = 4)	
	(CIB 97879)	Range	Mean $\pm$ SE	Range	Mean $\pm$ SE
SVL	40.1	40.1–48.2	44.1 $\pm$ 1.3	39.1–40.3	39.8 $\pm$ 0.3
TTL	79.7	79.7–94.9	86.8 $\pm$ 2.3	71.8–76.9	75.2 $\pm$ 1.2
TAL	36.3	36.3–44.7	40.1 $\pm$ 1.2	30.3–33.1	32.1 $\pm$ 0.6
HL	13.3	12.9–15.2	13.6 $\pm$ 0.4	12.0–13.2	12.8 $\pm$ 0.3
HW	8.6	8.3–9.8	9.0 $\pm$ 0.2	8.1–9.0	8.5 $\pm$ 0.2
EN	3.3	3.2–3.9	3.4 $\pm$ 0.1	3.1–3.4	3.3 $\pm$ 0.1
IO	5.3	5.0–6.0	5.5 $\pm$ 0.2	4.9–5.3	5.1 $\pm$ 0.1
IN	2.2	2.2–2.7	2.4 $\pm$ 0.1	2.3–2.7	2.5 $\pm$ 0.1
AG	20.3	20.3–23.0	21.6 $\pm$ 0.6	17.9–18.6	18.3 $\pm$ 0.1
TAD	5.5	4.6–6.9	5.5 $\pm$ 0.4	5.1–5.7	5.5 $\pm$ 0.1
AL	14.2	14.2–15.7	14.7 $\pm$ 0.2	13.3–15.0	14.2 $\pm$ 0.4
PL	14.9	14.9–16.1	15.7 $\pm$ 0.2	13.9–15.6	14.8 $\pm$ 0.4



**FIGURE 2.** Principal-components (PC) scores of *Cynops fudingensis* sp. nov., *C. orientalis* and *C. orphicus*. Positive PC 1 scores mean a proportionately shorter trunk, longer tail, longer head and longer limbs. Positive PC 2 scores correspond to a proportionately larger head, longer limbs and shorter trunk. All body measurements were divided by SVL before principal-components analysis, and thus represent proportions.



**FIGURE 3.** Bayesian inference (BI) tree based on ND2 and flanking tRNA sequences. Maximum parsimony (MP) and maximum likelihood (ML) analyses yielded similar topologies. Numbers on branches: bootstrap support from MP analysis/bootstrap support from ML analysis/Bayesian posterior probability (%). For *Cynops*, Chinese taxa are coded in red; Japanese species are in green. *Cynops orientalis* from Dehua, Fujian Province (MVZ 231158) should be reassigned to *C. orphicus*. The tree is rooted by species of the sister genera *Pachytriton* and *Paramesotriton*.

The molecular analysis, which was based on 21 specimens, yielded a sequence alignment of 1219 nucleotide positions, of which 406 were potentially parsimony-informative and 739 were constant. The best-fitted model in the maximum likelihood (ML) analysis was chosen as TrN+I+G (I = 0.4993, G = 2.2453). The reconstructed topologies are very similar under different criteria; only the Bayesian inference tree is shown here (Fig. 3).

The maternal genealogical relationships we recovered within *Cynops* are concordant with those of both Weisrock *et al.* (2006) and Zhang *et al.* (2008). Whereas *Cynops* is recovered as monophyletic, it receives low statistical support in both MP and ML analyses, but higher support in BI (posterior probability = 95%). Indeed, even using the entire mitochondrial genome does not yield strong support for the monophyly of this genus (Zhang *et al.* 2008). Based on these earlier studies, Dubois & Raffaëlli (2009) assign Japanese and Chinese species to two different genera. Our analysis, however, does not group the two Japanese newts

together, but instead resolves *C. pyrrhogaster*, *C. ensicauda* and the monophyletic Chinese clade as a probable trichotomy at the base of *Cynops*. Within the Chinese clade, two groups are resolved based on geographic distribution. First, *Cynops cyanurus*, from the Yunan-Guizhou Plateau in southwestern China, is the sister group of the three species found in southeastern China—*C. orientalis*, *C. orphicus* and the new population. The two unavailable species, *C. chenggongensis* and *C. wolterstorffi*, which occur on the same plateau, might form a clade with *C. cyanurus* on the basis of phenotypic similarities, such as the characteristic postocular orange spot (Zhao & Hu 1984).

The newly discovered population, along with *C. orientalis* and *C. orphicus*, forms the second group within the Chinese clade. Specimens of *C. orientalis* collected from Zhejiang Province and Jiangxi Province group with those from the commercial pet trade. In contrast, specimens from Dehua, Fujian Province, cluster with *C. orphicus* and they should be reassigned to that species (Fei *et al.* 2006). The new population is the sister taxon of *C. orientalis*, but it differs by 7.1–7.2% in uncorrected pairwise distance from *C. orientalis* from near the type locality and by 6.6–7.6% from all sampled *C. orientalis*. This population is further diverged from Dehua specimens by 10.2–10.3% and from *C. orphicus* near its type locality by 11.2–11.3%. These levels of divergence are comparable to some interspecific distances in the closely related genera *Paramesotriton* and *Pachytriton* (Wu *et al.* 2009; Wu *et al.* 2010). Even though our molecular phylogeny groups the new population with *C. orientalis*, the new population exhibits several phenotypic similarities with *C. orphicus*, including finely granulated skin, a conspicuous vertebral ridge, and black spots on the tail. These data suggest that the new population is genetically isolated and, consequently, it should be recognized as a new species.

#### ***Cynops fudingensis* species nov. (Fig. 4 ABCDE)**

**Holotype:** CIB 97879, an adult female collected near Mt. Taimu (27°07'N, 120°10'E; elevation 718 m), Fuding, Fujian Province, P. R. China, by Xin Chen and Wenxiao Dong on 9 April 2009.

**Paratypes:** CIB 97869–78, 97851–52; same collection date and locality as the holotype.

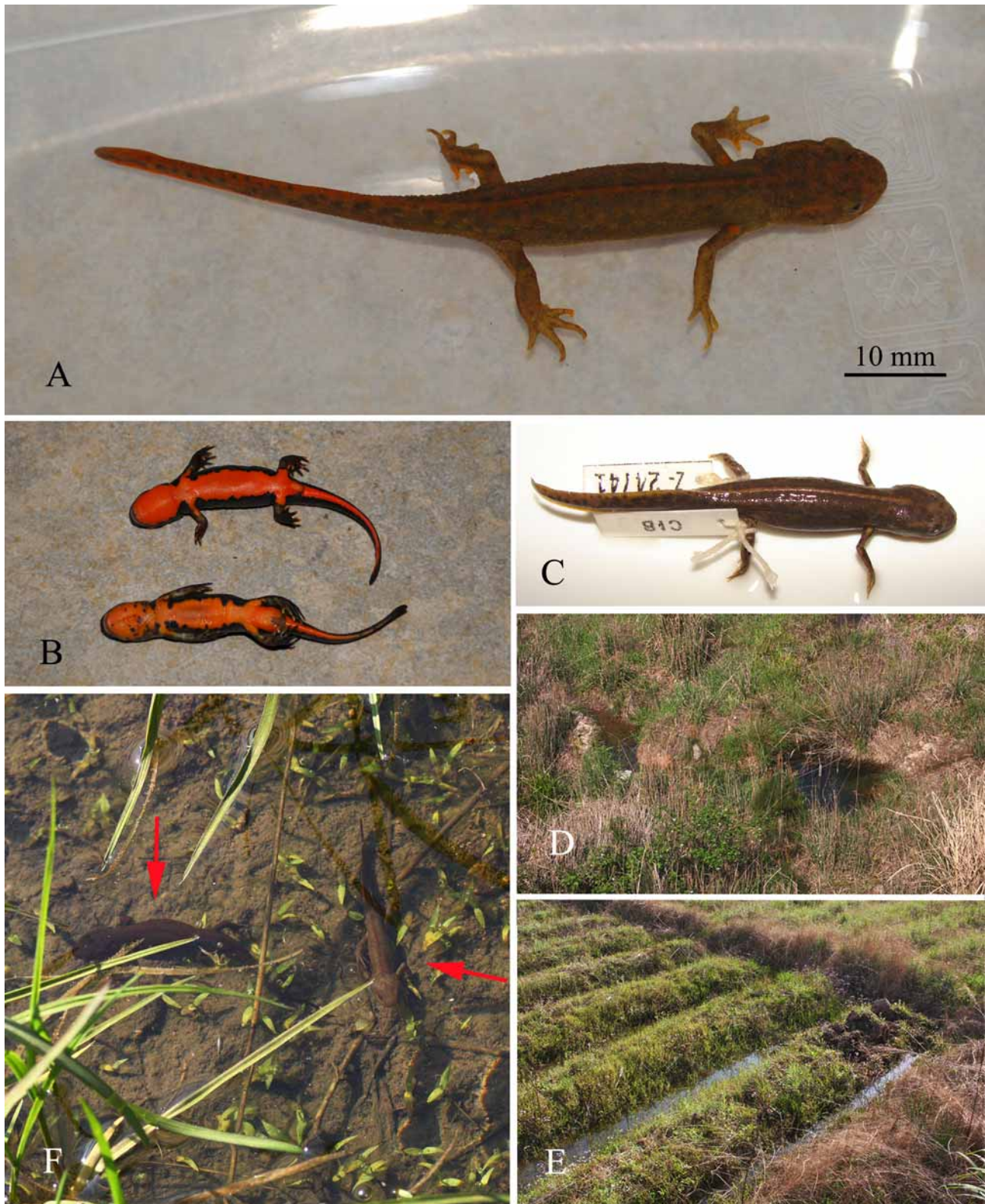
**Diagnosis:** *Cynops fudingensis* is assigned to the genus *Cynops* by its molecular phylogenetic position and the following phenotypic characters: total length normally less than 100 mm; bony or warty ridge absent on head; skin finely granulated; vertebral ridge conspicuous; digits elongate and slender. The species is differentiated from congeners by the following combination of characters: postocular orange spot absent; parotoid gland poorly developed; vertebral ridge conspicuous; venter and chin bright orange without dark blotches, but a few small black dots may be present; two dark ventral spots on the shoulder and axilla of each side, but spots from opposite sides do not connect at the midline; transverse black gular stripe absent; irregular black spots on tail.

**Description of the holotype:** This is a small newt; SVL = 40.1 mm. Head shape oval in dorsal view. Snout truncate, projects slightly beyond mandible. Nostril on snout tip. Eye large. Labial fold well developed on posterior part of upper jaw. An inconspicuous longitudinal ridge posterior to each eye. Skull relatively narrow; length / width = 1.21. Posterior tip of maxillary bone lies anterior to and does not contact the pterygoid bone. Fronto-squamosal arch robust. Tongue elongate, enlarged anteriorly, with free lateral margin. Vomerine tooth patch  $\wedge$ -shaped; tooth rows converge anteriorly and slightly exceed anterior limit of choanae. Parotoid gland poorly developed, gill remnants absent. Gular fold absent. Skin finely granulated on head, dorsum, flanks, limbs and tail; venter and underside of limbs smooth. A few longitudinal wrinkles on chin. Vertebral ridge elevated and conspicuous. Four fingers and five toes, all slender and elongated, lack webbing. Relative length of fingers,  $1 < 4 < 2 < 3$ ; relative length of toes,  $1 < 5 < 2 < 4 < 3$ . Tail laterally compressed, tapers posteriorly; caudal fin distinct; tail tip bluntly pointed. Cloacal opening olive-shaped, slightly protruded; no papillae on cloacal wall.

**Color of holotype:** Dorsum brownish yellow. Obscure black flecks on head and dorsum. Vertebral ridge dark orange. Venter bright orange with irregular lateral margin and a single black dot near groin. Chin bright orange without black dots; orange color continuous onto venter. Underside of axillae and all digit tips orange.

Orange dot on dorsal side of forelimb base. Base of first digits of forelimbs and hind limbs light orange. Orange red on cloaca, continuing to underside of tail.

In preservative, dorsum brownish black, vertebral ridge brown. All bright orange coloration fades to yellowish white. Obscure black spots remain visible on snout and tail.



**FIGURE 4.** A: Dorsal view of *Cynops fudingensis* sp. nov. in life (CIB 97879, holotype: ♀); B: Ventral view of *C. fudingensis* sp. nov. in life (lower—CIB 97851, paratype: ♂; upper—CIB 97852, paratype: ♀). C: Dorsal view of the holotype in preservative. D, E: Water puddles and ditches in the deserted agricultural field at the type locality. F: Two newts crawling in a submerged ditch. Photographs A–C were prepared by Yunke Wu, and D–F by Wenxiao Dong.



**Variation:** Linear measurements are summarized in Table 2. The cloaca is wider and more swollen in males than in females, with papillae on the cloacal wall. The tail also is proportionally shorter in males. Tail tip rounded in males, bluntly pointed in females. Gular fold present in only a few specimens. In life, dorsal coloration varies from dark brown to lighter brown; ventral color ranges from yellowish orange to reddish orange. Number and position of ventral black dots vary among individuals; some specimens have black dots on the chin. Posterior limit of cloaca may be black.

**Etymology:** The specific name *fudingensis* is an adjective after the type and only known locality for this species, in Fuding, northeastern Fujian Province, southeastern China.

**Habitat and distribution:** The population was found in small, still-water puddles and ditches of a deserted agricultural field on a hillside, about 1 km from Mt. Taimu (Fig. 4C, D, E). Water is shallow (< 15 cm in depth) but clear, with abundant aquatic plants and arthropods. The aquatic substrate is composed of soft earth and decomposing vegetation. Weeds grow densely in the field. Newts were active during daytime, crawling on the bottom. Another site that used to contain *C. fudingensis* is near the Jinfeng Temple on Mt. Taimu; newts were once found in ditches there in large numbers. However, human-released bullfrogs (*Lithobates catesbeianus*) and red-eared slider turtles (*Trachemy scripta elegans*) may have devastated this population (X. Chen, pers. comm.). Currently, *C. fudingensis* is known only from the Mt. Taimu region in Fuding.

**Conservation status:** *Cynops fudingensis* likely suffers from habitat destruction associated with tourism, introduction of invasive predators and collection by herpetological hobbyists. We therefore urge efforts to protect and conserve this species in its restricted geographic range in the Fuding area. Creation of a natural reserve could potentially reduce pollution from human waste and illegal collection, while local education and regular monitoring could detect and remove introduced predators (e.g., bullfrogs, slider turtles and domestic fowls) from the species' natural habitat.

**Comparative material examined:** *Cynops chenggongensis* (CIB 18434–39, from Yunnan Province, China), *C. cyanurus* (CIB 95897, from Guizhou Province, China), *C. ensicauda* (MCZ A26601–02, A26605, A26610, A26615–6 and A26624, from Ryukyu Islands, Japan), *C. orientalis* (CIB 19584, 19619, 19622, 19636, 19671, 19677, 19698, 19712, 19717 and 19727, from Anhui Province, China; CIB 20347, 20353–4, 20356, 20366, 20371–2, 20374 and 20376–7, from Zhejiang Province, China), *C. orphicus* (labeled as *C. orientalis*, CIB 19450, 19470, 19476, 19516, 19520, 19525, 19544, 19562, 19577 and 19606, from Fujian Province, China), *C. orphicus* (CIB 95898, MVZ 22472, 22503 and 241426–8, from Guangdong Province, China), *C. pyrrhogaster* (MCZ A125121–4 and A125130–6, from Kanagawa, Japan) and *C. wolterstorffi* (MVZ A7170–4, from Yunnan Province, China).

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**APPENDIX.** Linear measurements (in mm) of *Cynops orientalis* (Anhui Province and Zhejiang Province) and *Cynops orphicus* (Fujian Province) used in principal-components analysis. Only females are included.

Measurements	<i>Cynops orientalis</i> (N = 10)		<i>Cynops orphicus</i> (N = 5)	
	Range	Mean $\pm$ SE	Range	Mean $\pm$ SE
SVL	40.7–52.8	44.8 $\pm$ 1.3	44.4–52.7	47.4 $\pm$ 1.5
TTL	66.2–98.0	86.7 $\pm$ 2.7	87.1–94.0	88.9 $\pm$ 1.3
TAL	23.4–42.8	33.8 $\pm$ 1.5	36.8–40.9	39.4 $\pm$ 0.7
HL	11.0–13.6	12.1 $\pm$ 0.2	12.0–13.6	12.8 $\pm$ 0.3
HW	8.2–10.0	8.9 $\pm$ 0.2	8.6–10.1	9.5 $\pm$ 0.2
EN	2.4–3.2	2.6 $\pm$ 0.1	2.4–3.3	2.7 $\pm$ 0.1
IO	4.6–5.6	5.0 $\pm$ 0.1	4.7–5.7	5.1 $\pm$ 0.2
IN	2.2–2.7	2.4 $\pm$ 0.1	2.3–2.7	2.5 $\pm$ 0.1
AG	19.9–29.5	24.2 $\pm$ 1.0	23.2–26.2	24.4 $\pm$ 0.6
TAD	4.3–6.9	5.5 $\pm$ 0.3	5.8–6.6	6.2 $\pm$ 0.1
AL	12.7–14.9	13.5 $\pm$ 0.2	13.4–15.5	14.2 $\pm$ 0.4
PL	12.9–15.3	14.0 $\pm$ 0.2	13.9–15.8	14.8 $\pm$ 0.3