

Tachysurus wuyueensis (Teleostei, Bagridae), a new species of catfish from the Qiantang-Jiang basin, southeast China

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Abstract

Tachysurus wuyueensis, new species, is described from the Qiantang-Jiang Basin, situated in Suichang County, Zhejiang Province and Xiuning County, Anhui Province, southeast China. The coastal basin drains into the East China Sea. The new species belongs to the *T. pratti*-*T. truncatus* group within the genus *Tachysurus* defined by having a smooth anterior margin of the pectoral-fin spine, short maxillary barbels not extending beyond the base of the pectoral-fin spine, short dorsal spine not exceeding two thirds of head length and an emarginated caudal fin. This new species is distinct from all other species of this group, *Tachysurus pratti* (Gunther, 1892), *T. truncatus* (Regan 1913), *T. gracilis* (Li, Chen & Chan, 2005) and *T. brachyrhabdion* (Cheng, Ishihara & Zhang, 2008), in having a shorter prepelvic body (length 40.0–46.4% of SL vs. 45.8–54.8%). It further differs from *T. pratti*, *T. truncatus* and *T. gracilis* in having more vertebrae (45–47 vs. 37–44) and more anal fin rays (21–25 vs. 14–20), from *T. brachyrhabdion* in having a more slender body (depth 10.1–13.5% of HL vs. 13.1–17.6%). Molecular phylogeny, based on the mitochondrial cytochrome *b* (cyt. *b*) gene confirms the validity of *T. wuyueensis* and the *T. pratti*-*T. truncatus* group. Furthermore, this study addresses the diagnostic traits distinguishing the *T. pratti*-*T. truncatus* group from the *T. tenuis*-*T. crassilabris* group which have historically been treated as a single species group due to morphological similarities.

Key Words

Caudal fin shape, new taxon, stream-dwelling species, taxonomy

Introduction

The genus *Tachysurus* Lacépède 1803 is a group of East Asian endemic catfish that is widely distributed throughout most of the East Asian continent (Ku et al. 2007; Watanabe 2010; Shao and Zhang 2023). It is also one of the most diversified catfish genus in China containing more than thirty species with strong differentiation in ecological niches (Shao et al. 2021; Shao and Zhang 2023). South China, which is characterised by high mountains, deep valleys and abundant precipitation (López-Pujol et al. 2011; Wang et al. 2018; Sun et al. 2021), harbours numerous *Tachysurus* species restricted to montane streams with fast-flowing high-oxygen waters and predominance of rocky substrate, for

example, *Tachysurus ondon* (Shaw 1930), *T. adiposalis* (Oshima 1919), *T. albomarginatus* (Rendahl 1928), *T. trilineatus* (Zheng 1979) and *T. tenuis* (Günther 1873). Unlike its congeners, species of *Tachysurus* always possess elongated bodies and rounded, truncated or slightly emarginated (round-tailed) caudal fins regarded herein as key adaptations for the torrent environments (Gosline 1997; Krishnadas et al. 2018). Moreover, the absence of diagnosable characters and ambiguous descriptions have obscured the species boundaries of these species (Ferraris 2007; Shao et al. 2021). For instance, *T. albomarginatus* has long been synonymised under *T. tenuis* (Zheng & Dai, 1999) until Cheng et al. (2021) resurrected the former species, based on morphometric and osteological analyses.

In addition, rheophilic (fast-water) fishes are always confined to a narrow distribution which limits their dispersal ability and contributes to their habitat fragmentation (Lima et al. 2017). Previous works have highlighted the underestimated diversity of *Tachysurus*, v.gr., *T. albomarginatus* that may be an assemblage of five species (Cheng et al. 2021; Shao et al. 2021). A similar scenario occurs in *T. adiposalis*, originally described by Oshima (1919) on a single specimen of 170 mm SL (standard length) collected from the Tamusui River in Taiwan. *T. adiposalis* has been treated as widespread species, with a distribution including Taiwan and river basins from the southern region of Chinese mainland, such as the mid-lower Yangtze, Pearl River and Qiantang River (= Qiantang-Jiang in Chinese) (Zheng and Dai 1999). The key characters useful in differentiating *Tachysurus* species are absent or obscured in the original description of *T. adiposalis*, which resulted in the taxonomic confusion. Recent studies have suggested that specimens from the Xi-Jiang (the Pearl River Basin) and the Yuan-Jiang (the middle Yangtze River Basin) belonging to *T. adiposalis* s.l. were determined as *Tachysurus gracilis* (Li, Chen & Chan, 2005) and *Tachysurus brachyrhabdion* (Cheng, Ishihara & Zhang, 2008). However, the taxonomic status of specimens from the Qiantang-Jiang which were also recognised as *Tachysurus adiposalis* has not been mentioned in previous studies and it potentially represents an undescribed species.

A fish field survey conducted by the authors in the Qiantang-Jiang Basin of Zhejiang and Anhui Provinces yielded 14 specimens initially identified as *T. adiposalis*. Careful morphological examination revealed that these were, in fact, not conspecific with any other known species of *Tachysurus* and represent a new species. The purpose of the present paper is to provide a formal description of this unnamed species, based on multiple lines of evidence containing morphological and phylogenetic datasets.

Materials and methods

Fourteen specimens of the new species were caught during two field surveys conducted, respectively, in September 2020 and May 2023 into the Qiantang-Jiang flowing into the East China Sea. Amongst them, six specimens were fixed in 10% formalin after removal of right-side pelvic-fin clips. These fin clips were stored in 95% ethyl alcohol and utilised for molecular analysis. The remaining caught specimens were directly preserved in 10% formalin preservative for morphological examination. Their voucher specimens are deposited in the Museum of Aquatic Organisms of the Institute of Hydrobiology (IHB), Chinese Academy of Sciences, Wuhan. Eight species, including *T. gracilis*, *T. truncatus*, *T. pratti*, *T. brachyrhabdion*, *T. crassilabris*,

T. albomarginatus, *T. adiposalis* and *T. tenuis*, were morphologically examined in this study, which came from the following collections: Museum of Aquatic Organisms of Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan (IHB), the Natural History Museum, London (BMNH) and French Museum of Natural History, Paris (FMNH).

Measurements were taken point to point with digital calipers linked to a data recording computer and data were recorded to the nearest 0.1 mm and made on the left side of each individual whenever possible, following the methods for Cheng et al. (2008). The head length and measurements of other parts of the body are estimated as percentages of the standard length (SL). Subunits of head are provided as percentages of the head length (HL). The number of rays from the dorsal- and anal fins were counted using the method by Watanabe (1995). Other fin rays were counted under a binocular dissecting microscope utilising transmitted light. Vertebral count was taken from X-ray photographs, with the anterior five vertebrae, namely the Weberian complex, not counted.

Morphometric measurements were subject to principal component analysis (PCA) in order to examine external morphological differentiation and determine the relative contributions of specific variables to morphological differences in the target species. PCA was run with SPSS 16 (SPSS, Chicago, IL, USA). Prior to the analysis, all morphometric measurements, except standard length, were normalised following the method of Reist (1985) to eliminate the influence of allometry of body parts and sample size.

Phylogenetic analysis was performed on cyt. *b* and the sequences uploaded to NCBI GenBank (Table 1). The thirty-eight cyt. *b* gene sequences, here amplified from twenty-five species of *Tachysurus*, were used for molecular phylogenetic analysis. *Tachysurus trilineatus* was used as the outgroup which is the basal lineage of *Tachysurus* genus (Ku et al. 2007). The sequences were revised manually and then aligned using ClustalW in MEGA7 (Kumar et al. 2016). Both Maximum Likelihood (ML) and Bayesian Inference (BI) methods were utilised to reconstruct the phylogenetic relationships. The optimal nucleotide substitution model was selected by ModelFinder (Kalyaanamoorthy et al. 2017) according to the Akaike Information Criterion. Maximum Likelihood analysis was run by IQ-tree (Nguyen et al. 2015), with the selected TIM3+F+I+G4 model and 1,000 non-parametric bootstrap replicates. Bayesian Inference was performed in MrBayes (Ronquist et al. 2012) under the selected GTR+F+I+G4 model. Two independent runs were carried out with four Monte Carlo Markov chains (three hot chains and one cold chain) for 20 million generations to calculate posterior probability. Trees were sampled every 1000 generations. The initial 25% of sampled trees were discarded as burn-in. Convergence of the runs was assessed by the average standard deviation of split frequencies (< 0.01).

Table 1. GenBank accession numbers for molecular phylogenetic analysis.

	Taxon	Locality	Distribution	Accession number
	Ingroup			
(1)	<i>Tachysurus albomarginatus</i>	Zhejiang, China	Qiantang-Jiang	PP266663
(2)	<i>Tachysurus analis</i>	Jiangxi, China	Gan-Jiang of lower Yangtze River	PP266668
(3)	<i>Tachysurus argentivittatus</i>	Jiangxi, China	Gan-Jiang of lower Yangtze River	PP266678
(4)	<i>Tachysurus brachyrhabdion</i> 1	Guizhou, China	Yuan-Jiang of middle Yangtze River	PP266650
	<i>Tachysurus brachyrhabdion</i> 2	Guizhou, China		PP266651
	<i>Tachysurus brachyrhabdion</i> 3	Hunan, China		PP266652
(5)	<i>Tachysurus crassilabris</i>	Hunan, China	Xiang-Jiang of middle Yangtze River	PP266665
(6)	<i>Tachysurus dumerili</i>	Jiangsu, China	Lower Yangtze River	PP266661
(7)	<i>Tachysurus gracilis</i> 1	Guangxi, China	Xiang-Jiang of middle Yangtze River	PP266654
(8)	<i>Tachysurus gracilis</i> 2	Hunan, China	Lijiang River of Pearl River	PP266655
(9)	<i>Tachysurus intermedius</i>	Hainan, China	Nandu-Jiang	PP266676
(10)	<i>Tachysurus kyphus</i>	Guangxi, China	Fangcheng- Jiang	PP266671
(11)	<i>Tachysurus lani</i>	Guangxi, China	Gui-Jiang of the Pearl River	PP266662
(12)	<i>Tachysurus longispinalis</i>	Vietnam	Red River	PP266672
(13)	<i>Tachysurus nitidus</i>	Hunan, China	Xiang-Jiang of middle Yangtze River	PP266660
(14)	<i>Tachysurus ondon</i>	Zhejiang, China	Ou-Jiang	PP266677
(15)	<i>Tachysurus pratti</i> 1	Sichuan, China	Jinsha-Jiang of upper Yangtze River	PP266656
	<i>Tachysurus pratti</i> 2	Yunan, China		PP266657
(16)	<i>Tachysurus similis</i>	Fujian, China	Min-Jiang	PP266664
(17)	<i>Tachysurus sinensis</i>	Hubei, China	Middle Yangtze River	PP266674
(18)	<i>Tachysurus tenuis</i>	Zhejiang, China		PP266666
(19)	<i>Tachysurus truncatus</i> 1	Sichuan, China	Upper Yangtze River	PP266658
	<i>Tachysurus truncatus</i> 2	Shaanxi, China	Han-Jiang of middle Yangtze River	PP266659
(20)	<i>Tachysurus ussuriensis</i>	Heilongjiang, China	Heilong-Jiang	PP266669
(21)	<i>Tachysurus vachelli</i>	Hubei, China	Middle Yangtze River	PP266670
(22)	<i>Tachysurus virgatus</i>	Hainan, China	Jiajihe River	PP266673
(23)	<i>Tachysurus wuyueensis</i> (SUIC55690)	Zhejiang, China	Qiantang-Jiang	PP266644
	<i>Tachysurus wuyueensis</i> (SUIC55691)			PP266645
	<i>Tachysurus wuyueensis</i> (SUIC55692)			PP266646
	<i>Tachysurus wuyueensis</i> (XIUN65294)	Anhui, China		PP266647
	<i>Tachysurus wuyueensis</i> (XIUN65295)			PP266648
	<i>Tachysurus wuyueensis</i> (XIUN65296)			PP266649
(24)	<i>Tachysurus zhangfei</i>	Hunan, China	Yuan-Jiang of middle Yangtze River	PP266667
	Outgroup			
(25)	<i>Tachysurus trilineatus</i>	Guangdong, China	Dong-Jiang of Pearl River	PP266679

The genetic distances, based on cyt. *B*, were computed in MEGA 7 using the Kimura-2-parameter (K2P) model (Kimura 1980).

Results

Phylogenetic analysis

A total of 1092 bps were included in the aligned dataset of the cyt. *b* gene, with 668 conservative sites, 492 variable sites, 375 Parsim-informative sites and 117 singleton sites. The mean frequency of the four nucleotides in the sequences of *Tachysurus wuyueensis* are A = 29.1%, G = 15.6%, C = 27.7% and T = 28.5%. The phylogenetic trees reconstructed by ML and BI methods are identical in topology (Fig. 1). A monophyly formed by samples of *Tachysurus wuyueensis* was recovered with 100% posterior probabilities (pp) and 1.00 bs in ML and BI trees, respectively and belonged to a clade containing *T. gracilis*, *T. brachyrhabdion*, *T. truncatus* and *T. pratti*. *Tachysurus wuyueensis* is sister to a species pair consisting of *T. gracilis* and *T. brachyrhabdion*

and the above all are sister to another species pair: *T. truncatus* and *T. pratti*. Herein, these five species are designated as belonging to the *T. truncatus*-*T. pratti* group given their affinities in both morphology and molecular phylogeny.

The estimated K2P genetic distances of the cyt. *b* gene between *T. wuyueensis* and congeners range from 6.9% to 12.6% (Table 2). The distances between *T. wuyueensis* and members of the *T. pratti*-*T. truncatus* group are in a range of 6.9–8.3%. The paired species, *T. truncatus* and *T. pratti*, endemic to the upper Yangtze River Basin have a 1.4% genetic distance, while another paired species, *T. brachyrhabdion* and *T. gracilis*, displays a 4.1% distance. The range of intraspecific genetic distances within *T. wuyueensis* is 0.1%.

Table 2. K2P distances (%) for species within the *Tachysurus pratti*-*Tachysurus truncatus* group, based on the cyt. *b* gene.

	1	2	3	4
1. <i>T. wuyueensis</i> sp. nov.				
2. <i>T. pratti</i>	7.1			
3. <i>T. truncatus</i>	6.9	1.4		
4. <i>T. gracilis</i>	8.3	9.1	8.6	
5. <i>T. brachyrhabdion</i>	7.5	8.3	8.0	4.1

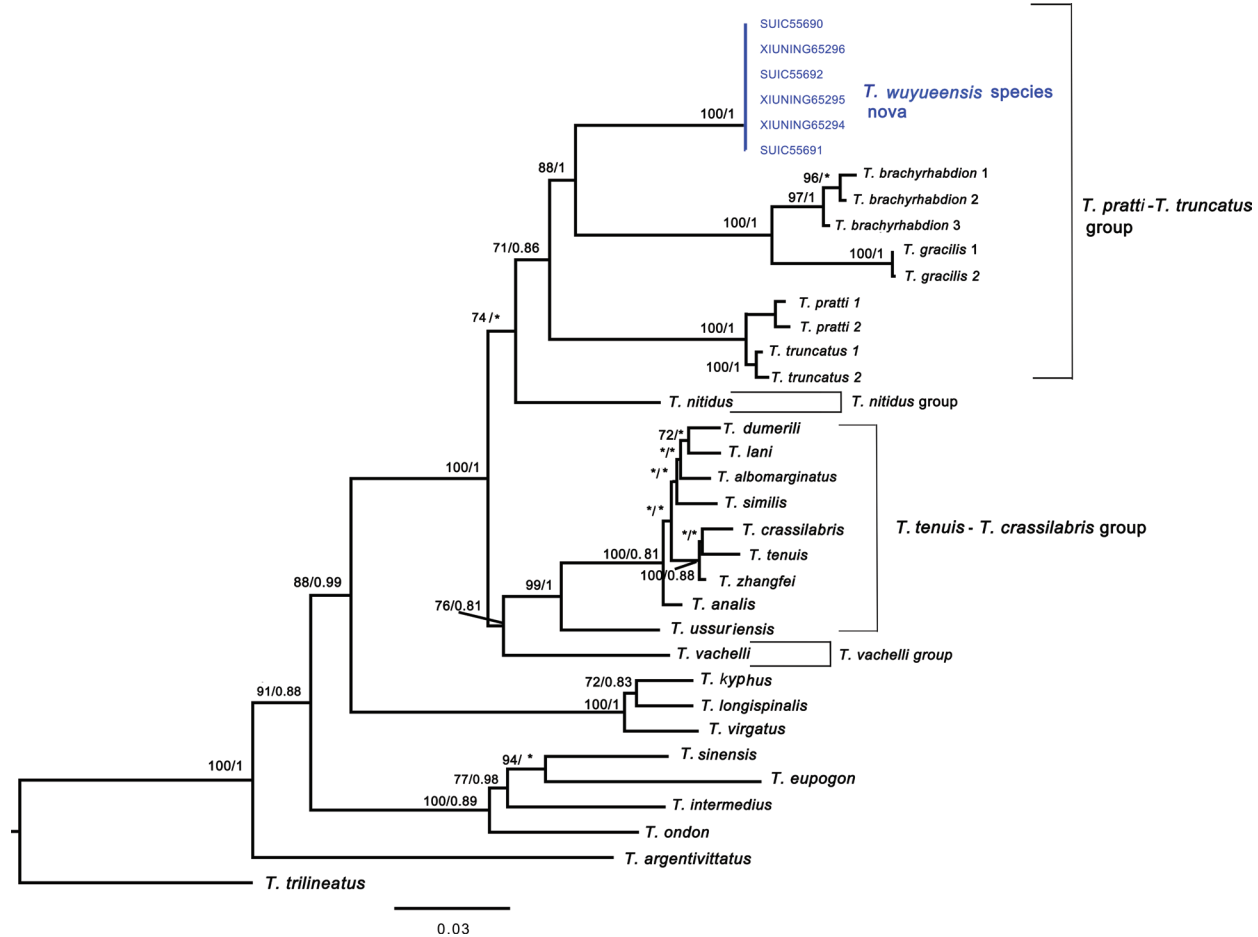


Figure 1. Phylogenetic tree of *Tachysurus* species inferred from cyt. *b* using Bayesian Inference and Maximum Likelihood methods. Bayesian posterior probabilities (> 0.8) and Maximum Likelihood bootstrap values (> 70%) are shown, respectively.

Principal component analysis

The *T. truncatus*-*T. pratti* group can be differentiated from all other *Tachysurus* species by having a smooth anterior margin of the pectoral spine, short dorsal spine not exceeding two-thirds of head length and short maxillary barbels not extending beyond the base of the pectoral spine.

Amongst these five species, excluding *T. pratti* which has a deeply forked caudal fin (Fig. 2), the other four round-tailed species were included in the principal component analysis performed on the variance-covariance matrix of log-transformed measurements (Table 3; Fig. 3). The results show that the combination of PC1 against PC3 and PC2 against PC3 enabled the separation of *T. wuyueensis* from *T. truncatus*, *T. gracilis* and *T. brachyrhabdion*. Characters with main loadings in PC1 were the adipose to caudal distance and body depth at anus; in PC2, they were the outer mandibular barbel length, anal-fin base length, nasal-barbel length and maxillary barbel length; and, in PC3, they were the inner mandibular barbel length, eye diameter and interorbital width (Table 3).

Morphological comparisons

Amongst the characters displaying main loading in PCA, some exhibit stable variations between species and can

Table 3. Loadings on the first three principal components extracted from morphometric data for *T. wuyueensis*, *T. truncatus*, *T. brachyrhabdion* and *T. gracilis*.

	PC1	PC2	PC3
Standard length	21.2	18.5	7.8
Body depth at anus	21.3	5.6	26.4
Predorsal length	19.4	7.0	6.7
Pre-anal length	21.1	9.6	9.1
Prepelvic length	20.7	9.3	7.5
Prepectoral length	18.0	3.6	14.0
Length of dorsal-fin spine	15.8	14.2	8.5
Length of dorsal-fin base	20.3	2.2	6.8
Length of pectoral-fin spine	16.1	17.2	1.7
Length of anal-fin base	19.6	41.2	29.2
Height of adipose fin	16.5	13.7	20.2
Adipose to caudal distance	23.9	19.1	13.8
Length of caudal peduncle	24.7	21.9	24.2
Depth of caudal peduncle	19.7	4.2	23.5
Head length at latera	19.0	1.2	5.5
Head depth	18.3	0.08	12.2
Head width	19.8	3.0	18.0
Snout length	18.5	0.9	14.7
Interorbital width	20.2	8.8	30.2
Eye diameter	12.9	22.6	36.2
Mouth width	20.4	7.7	12.2
Length of nasal barbel	21.8	37.6	23.4
Length of maxillary barbel	22.6	36.3	3.8
Length of inner mandibular barbel	21.4	24.7	45.9
Length of outer mandibular barbel	22.7	46.2	19.5

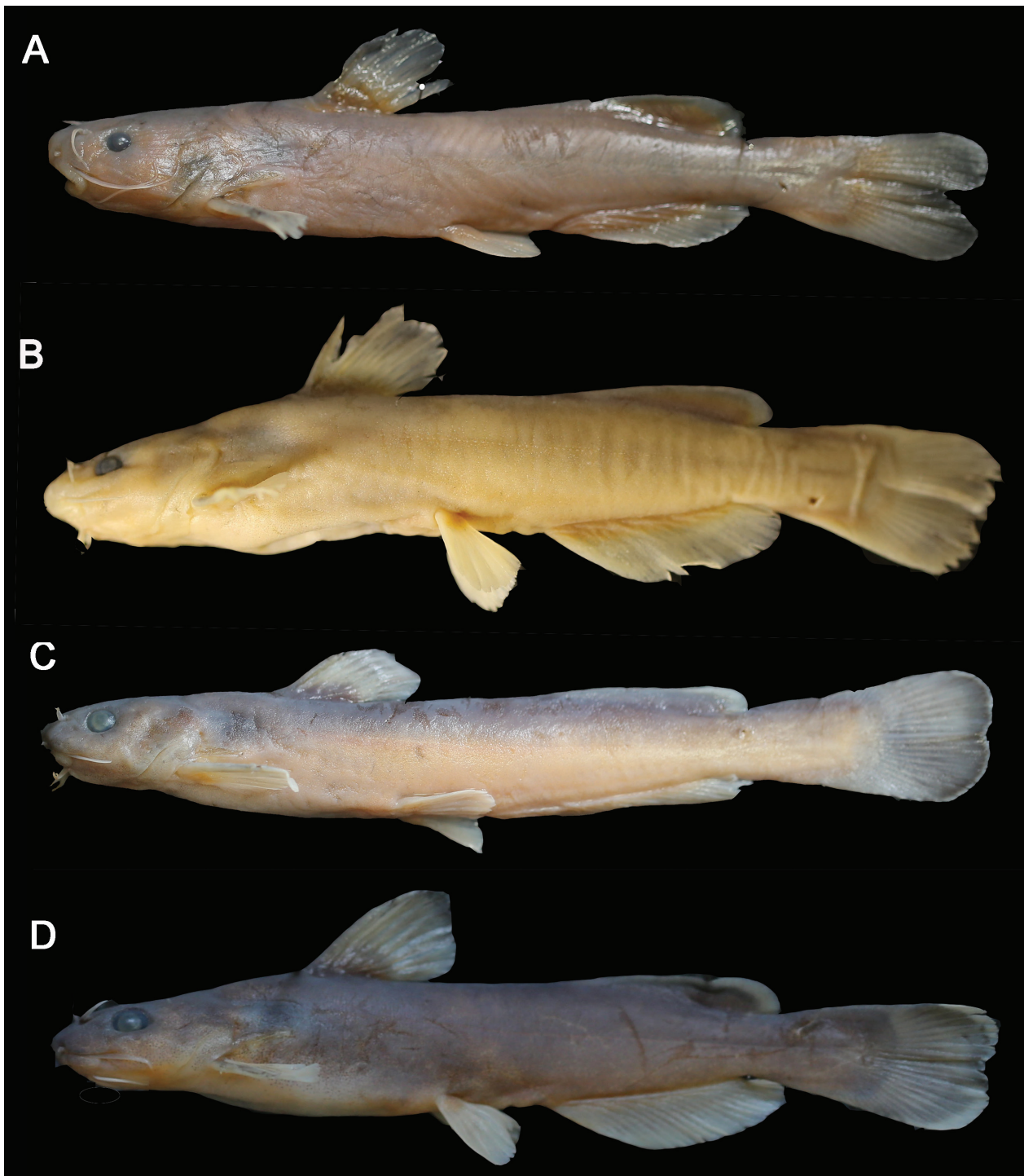


Figure 2. Lateral view of *T. pratti* (A) for IHB201909013758, 114.2 mm SL, Huili County, Sichuan Province, *T. truncatus* (B) for IHB201812028889, 79.5 mm SL, Qianwei County, Sichuan Province, *T. brachyrhabdion* (C) for IHB 2017090539, 120.8 mm SL, Songtao County, Guizhou Province, *T. gracilis* (D) for IHB 201803023401, 98.2 mm SL, Guanyang County, Guangxi Zhuang Autonomous Region.

be used to distinguish between them (Fig. 4). *Tachysurus wuyueensis* is distinct from the other three species in having a shorter prepelvic body (length 40.0–46.4% of HL vs. 45.8–54.8%; see Fig. 4A), from *T. truncatus* and *T. gracilis* in having more anal-fin rays (21–25 vs. 17–20) and vertebrae (45–47 vs. 37–43) (Fig. 5), from *T. truncatus* and *T. brachyrhabdion* in having a more slender body (depth 10.1–13.5% of HL vs. 13.1–20.6%; see Fig-

ure 4B). It further differs from *T. truncatus* in having a shorter pre-anal length (53.0–60.1% vs. 61.0–67.7%; Fig. 4C), longer anal-fin base (length 25.4–31.1% SL vs. 19.1–25.5%, Fig. 4D), narrower mouth (width 8.1–10.6% SL vs. 10.0–13.7%; Fig. 4E), narrower interorbital space (width 5.0–7.9% SL vs. 8.7–10.5%; Fig. 4F) and from *T. gracilis* in having longer inner mandibular barbels (length 4.9–6.0% of SL vs. 3.2–5.0%; Fig. 4G).

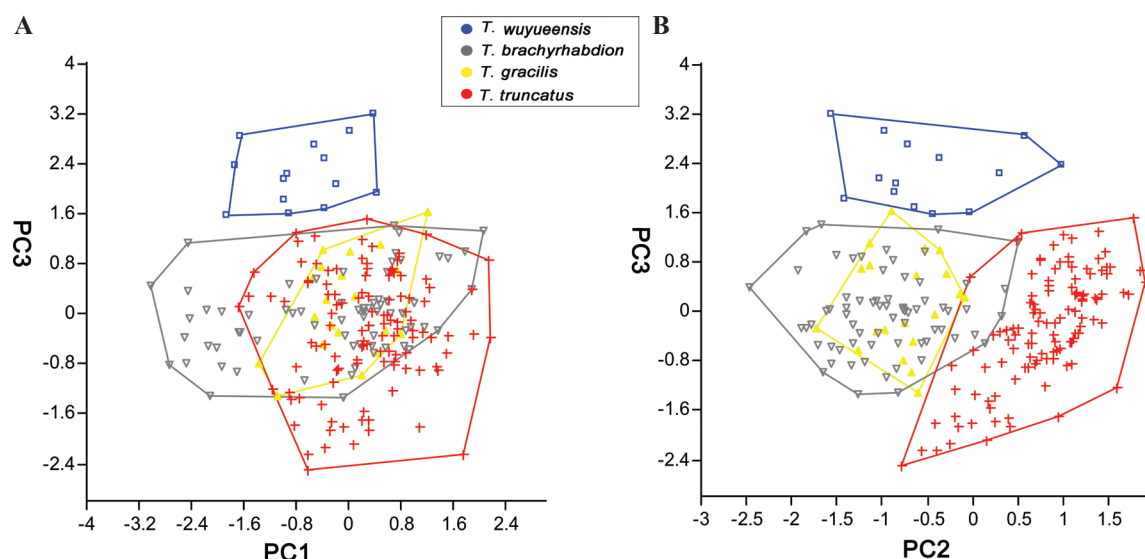


Figure 3. Scatter plot of **A.** PC2 against PC3 and **B.** PC1 against PC2 extracted from morphometric data for *T. wuyueensis*, *T. truncatus*, *T. brachyrhabdion* and *T. gracilis*

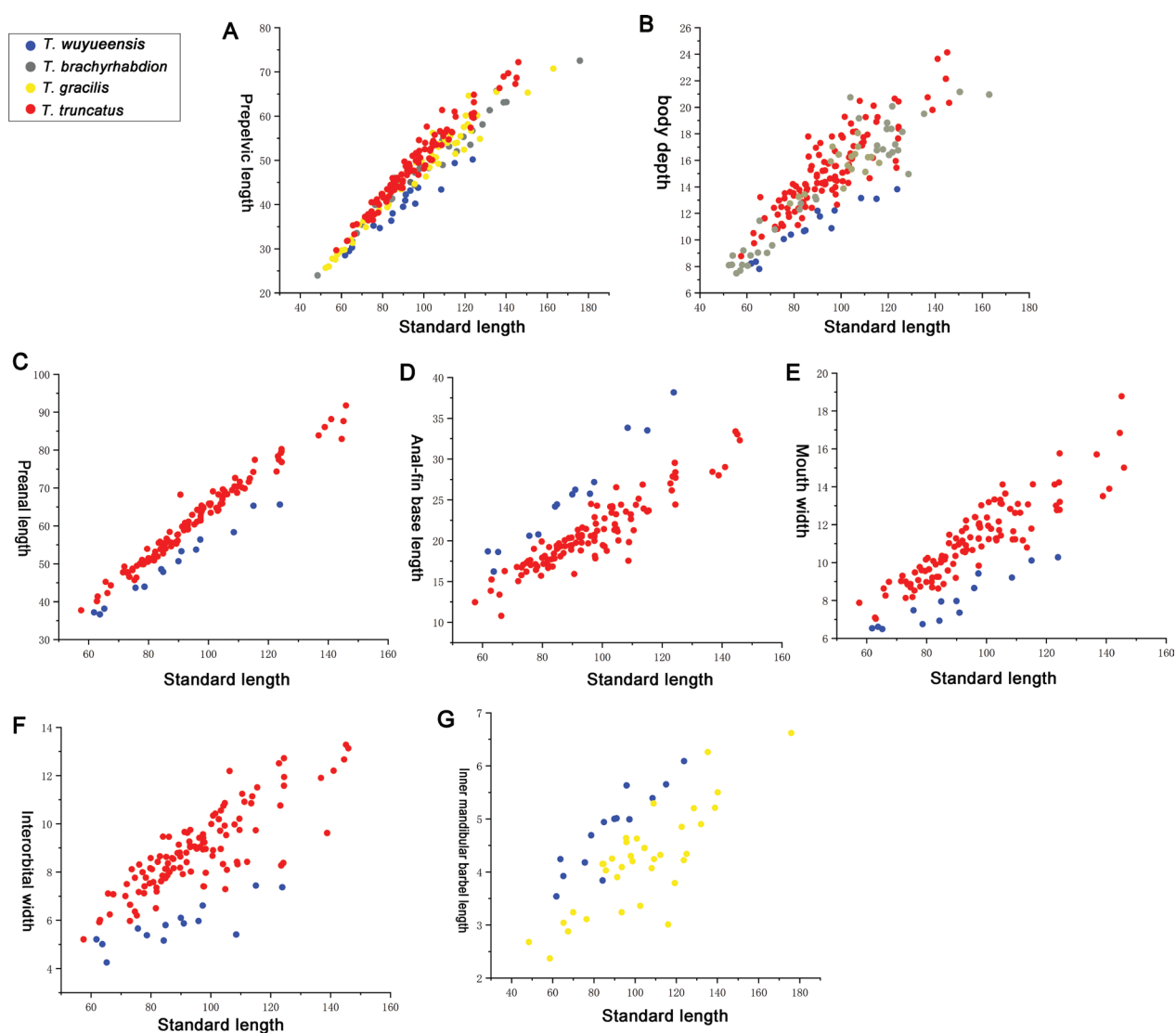


Figure 4. Relationship between **A.** Prepelvic length and SL for *T. wuyueensis*, *T. truncatus*, *T. brachyrhabdion* and *T. gracilis*; relationship between; **B.** Body depth and SL for *T. wuyueensis*, *T. truncatus* and *T. brachyrhabdion*; relationship between; **C.** Pre-anal length and SL; **D.** Anal fin base length and SL; **E.** Mouth width and SL; **F.** Interorbital width and SL for *T. wuyueensis* and *T. truncatus*; relationship between; **G.** Inner mandibular barbel length and SL for *T. wuyueensis* and *T. gracilis*.

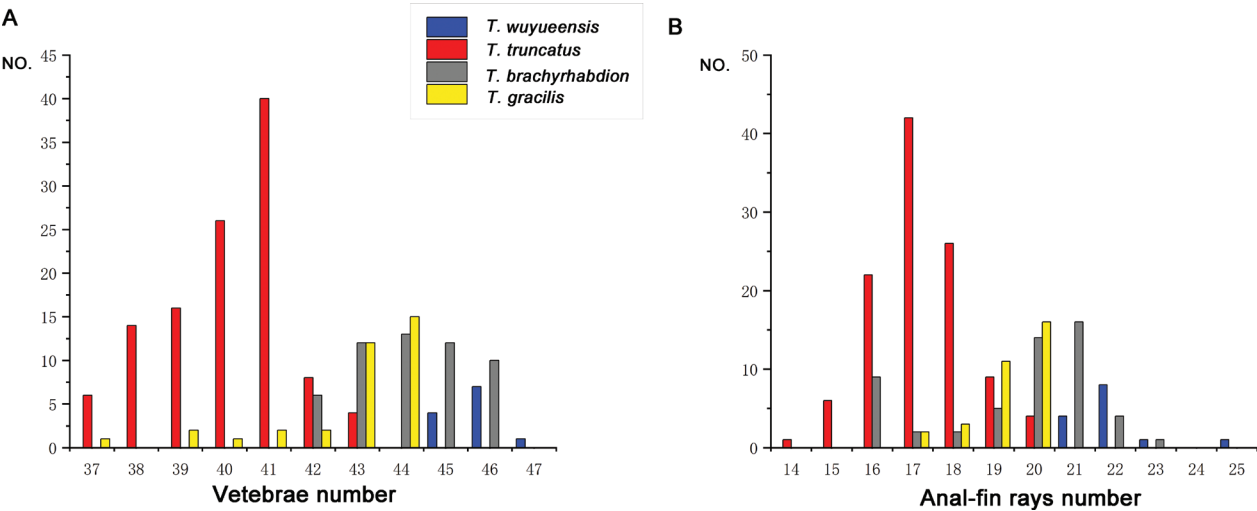


Figure 5. Meristic counts difference amongst *T. wuyueensis*, *T. truncatus*, *T. brachyrhabdion* and *T. gracilis* in vertebrae number (A) and anal fin ray number (B).

***Tachysurus wuyueensis* Zhou, Yuan & Shao, sp. nov.**

<https://zoobank.org/18A16B30-C113-4285-8A76-058999C3D0E1>

Fig. 6

Pseudobagrus adiposis: Mao 1991: 169 (coastal rivers in Zhejiang Province).

Type materials. *Holotype*. IHB 202009055690, 70.7 mm SL, South China: Zhejiang Prov.: Suichang County: the Qiantang-Jiang at Jiulongshan National Natural Reserve (28°23'38"N, 118°53'41"E) (Fig. 7); collected by Zhi-Gang Xie in Sept 2020.

Paratypes. IHB 202009055691-2, two ex., 63.8–65.2 mm SL; other data same as holotype. IHB202212165294-304, 11 ex., 61.8–123.9 mm SL, south China: Anhui Prov.: Xiuning County: the Qiantang-Jiang at Liukou Township (29°48'57"N, 117°53'11"E) (Fig. 7); collected by Wei-Han Shao in May 2023.

Diagnosis. Distinguished from its congeners by the following combination of characters: a smooth anterior margin of the pectoral-fin spine, short maxillary barbels not extending beyond the base of the pectoral-fin spine, short dorsal spine not exceeding two-thirds of head length, prepelvic length 40.0–46.4% SL, 45–47 vertebrae, 21–25 anal-fin rays, body depth 10.1–13.5% SL, a slightly emarginated caudal fin.

Description. Morphometric measurements taken from the holotype (78.7 mm SL) and 13 paratypes (61.8–123.9 mm SL) summarised in Table 4.

Body elongated, anteriorly cylindrical and slightly compressed posteriorly. Dorsal profile rising gradually from snout tip to dorsal-fin origin, then sloping evenly from there to posterior end of adipose-fin base, and gradually increasing to dorsal origin of procurrent caudal-fin rays. Ventral surface of head flattened; ventral profile of body straight or slightly rounded from head to anal-fin origin, decreasing evenly from posterior end of anal-fin base to origin of ventral procurrent caudal-fin rays. Lateral line complete, straight and mid-lateral in position. Vertebrae 5 + 45 (46, 47).

Table 4. Morphometric data for *Tachysurus wuyueensis* species nova.

	Holotype	Paratypes (n = 13)	
		Range	Mean ± SD
Standard length	78.7	61.8–115.1	69.7 ± 14.3
%SL			
Body depth at anus	13.2	10.1–13.5	13.1 ± 1.5
Predorsal length	32.6	27.2–35.3	32.5 ± 2.8
Pre-anal length	55.8	53.0–60.1	57.6 ± 1.9
Prepelvic length	44.1	40.0–46.6	44.0 ± 1.4
Prepectoral length	20.9	16.1–23.1	20.8 ± 2.1
Length of dorsal-fin spine	59.2	46.4–63.8	59.2 ± 3.3
Length of dorsal-fin base	11.4	8.6–11.7	11.3 ± 1.3
Length of pectoral-fin spine	14.7	10.7–15.5	14.7 ± 2.2
Length of anal-fin base	26.4	25.4–30.8	27.0 ± 1.6
Height of adipose fin	3.1	2.4–5.1	4.1 ± 0.9
Adipose to caudal distance	13.9	13.2–16.8	15.3 ± 2.1
Length of caudal peduncle	16.4	16.0–18.1	17.3 ± 0.9
Depth of caudal peduncle	7.9	6.5–8.0	7.6 ± 0.3
Head length at latera	22.8	17.9–24.8	23.7 ± 2.5
Head depth	11.7	9.0–13.2	12.3 ± 1.5
Head width	14.2	13.1–15.7	15.2 ± 1.1
Snout length	5.5	4.2–8.7	6.0 ± 1.9
Interorbital width	6.8	5.0–8.4	7.7 ± 1.3
Eye diameter	4.5	4.3–5.6	4.9 ± 0.3
Mouth width	8.6	8.1–10.4	10.1 ± 1.0
Length of nasal barbel	6.5	5.2–7.5	7.1 ± 1.4
Length of maxillary barbel	14.5	8.6–13.7	13.1 ± 3.8
Length of inner mandibular barbel	6.0	4.6–6.6	6.1 ± 0.7
Length of outer mandibular barbel	9.5	5.9–10.7	9.6 ± 2.1

Head depressed, broad, and covered with thin skin. Supra-occipital process slender, with evenly converging sides and pointed tip, separated from nuchal plate by a broad interspace. Snout slightly pointed in dorsal view and obtuse or blunt in lateral view, longer than eye diameter. Interorbital space moderately space wide and slightly flattish. Eyes moderately large, elliptical, covered with thick membrane and anterolateral in head, visible when viewed dorsally, but not ventrally, with slightly convex and comparatively narrow inter-orbital space.

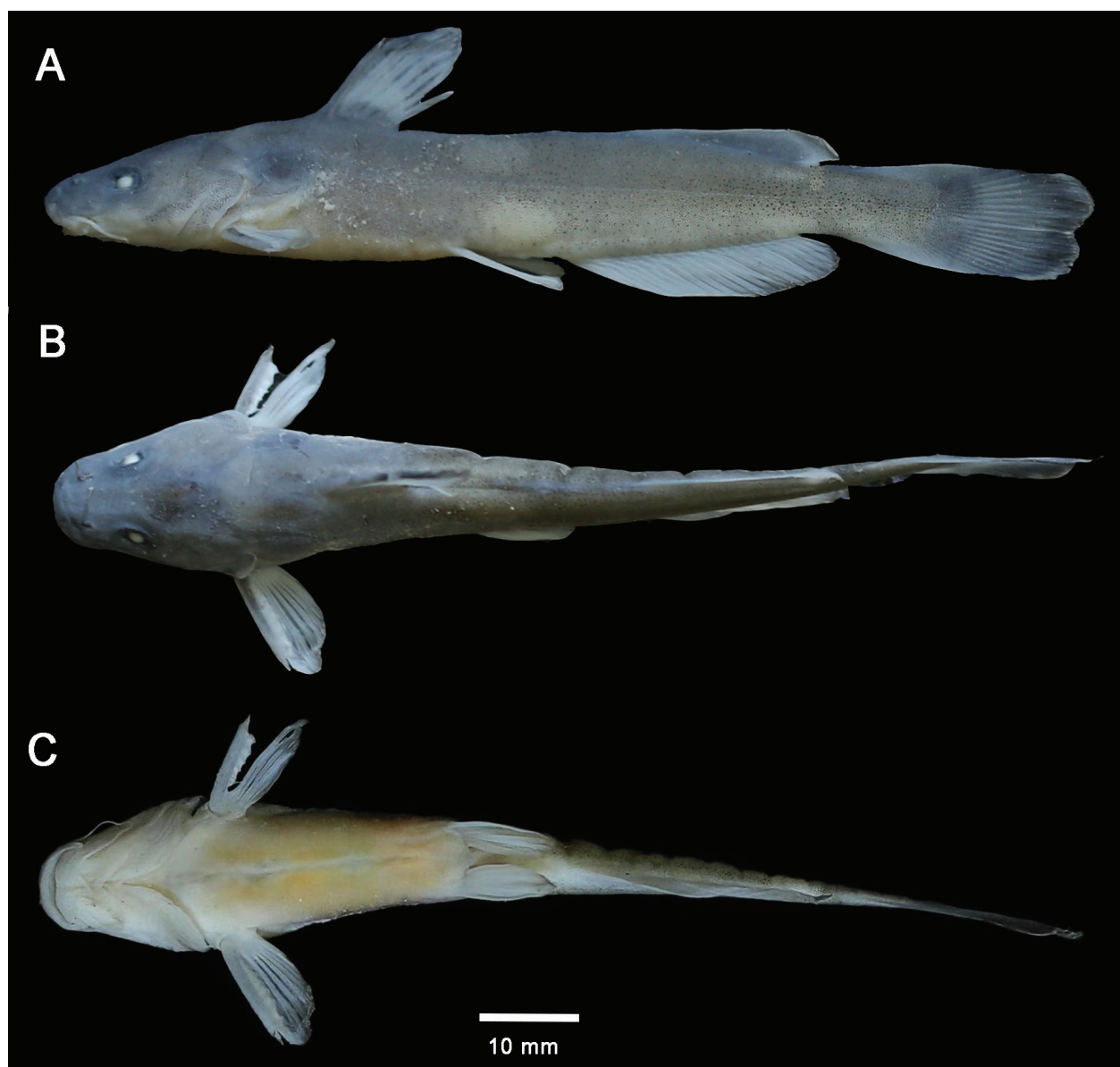


Figure 6. Lateral (A), dorsal (B) and ventral (C) views of *Tachysurus wuyueensis* species nova, IHB202009055690, holotype, 70.7 mm SL.

Mouth subterminal, transverse. Upper jaw anteriorly protruded, longer than lower jaw in length; interorbital space narrower than mouth opening. Teeth villiform, in irregular rows on all tooth-bearing surfaces. Premaxillary tooth plates broad, of equal width throughout. Dentary tooth plates arched, broadest at symphysis and narrowing laterally, of same width at symphysis as premaxillary tooth plates. Vomerine tooth plate unpaired, continuous across mid-line, slightly curved anteriorly and much narrower than premaxillary plate. Gill opening wide, extending from the post-temporal region to beyond isthmus.

Barbels in four pairs; nasal barbels small, thread-like, not reaching beyond posterior margin of eye; maxillary barbels slender, slightly exceeding posterior margin of eye; mandibular barbels in two pairs, thick, short, inner barbels positioned in transverse row at level of posterior naris, extending beyond mid-point of eye, outer barbels

rooted posterolateral to inner mandibular barbel, just extending to posterior margin of eye.

Dorsal fin with a spinelet, one spine and seven soft branched rays. Dorsal-fin origin equidistant to pectoral-fin insertion and ventrally to pelvic-fin insertion, also equidistant to anal-fin origin and snout tip. Spinelet flattened, with long blunt distal tip. Dorsal-fin spine slender, with smooth anterior margin and slightly serrated distal posterior margin, equal to or slightly longer than pectoral-fin spine. First dorsal-fin soft ray longest, surpassing tip of last ray. Distal margin of dorsal-fin rays nearly straight. Nuchal plate triangular, with anterior pointed tip anteriorly.

Adipose fin inserted slightly behind vertical through pectoral-fin origin, with convex distal margin along entire length and deeply incised posterior part to form rounded apex. Adipose fin base moderately long, equal to or slightly longer than anal fin base length.

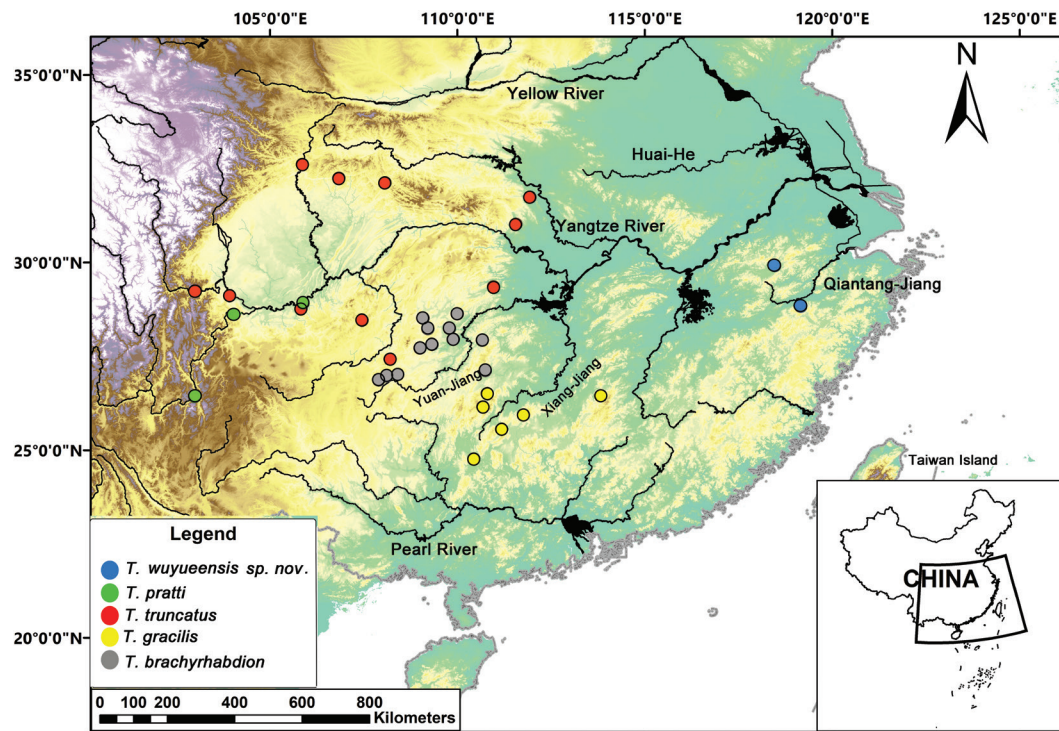


Figure 7. Map showing distributions of five species of *Tachysurus* in China: *T. wuyueensis* species nova, *T. pratti*, *T. truncatus*, *T. brachyrhabdion* and *T. gracilis*.

Pectoral fin with one spine and seven (or eight) soft branched rays, inserted slightly anterior or at level of posteriormost point of opercle, not reaching halfway to pelvic-fin insertion. Pectoral-fin spine very stout, sharply pointed at tip, equidistant to or slightly longer than dorsal-fin spine, with a smooth anterior margin and 8 (9, mean 8.3) strong serrations along posterior margin. Cleithral process triangular with a sharp pointed tip, extending for half of pectoral fin spine length.

Pelvic fin with one unbranched and five branched soft rays, inserted closer to tip of snout than to posterior end of anal fin base, closer to depressed tip of dorsal fin than to anterior end of anal fin base. Tip of depressed pelvic fin reaching or slightly extending beyond anal fin origin. Pelvic fin distal margin convex. Anus and urogenital opening nearer to anal fin origin than to posterior end of pelvic fin base. Males with a conical genital papilla not reaching base of first anal fin soft ray.

Anal fin long, with 21 (22, 23, 25) branched rays; adipose fin posterior margin away from caudal fin. Anal fin origin to caudal fin than to tip of snout. Distal margin of anal fin convex; anterior rays shortest.

Caudal fin with 9+10 principal rays, slightly emarginated, with middle rays longer than two-thirds of longest rays; both lobes rounded, with upper lobe slightly longer than lower lobe; procurent rays slightly extending from anterior to fin base. Lowest point of caudal peduncle behind posterior end of anal fin base.

Colouration. Body yellowish-grey with three obscured and broad vertical brown blotches in smaller individuals (the first one below the dorsal fin, the second one closely above the anal fin and the third occupying the

caudal peduncle) (Fig. 6) and fading to a more uniform yellow or brown in larger individuals (Fig. 8). Adipose fin brownish, with a yellow anterodorsal margin and a slightly transparent posterodorsal margin. Dorsal fin transparent for anterior two-thirds, rest of fin greyish-brown. Caudal fin greyish in posterior third, rest of fin transparent with a slightly white margin in smaller individuals. Pectoral, pelvic and anal fins transparent.

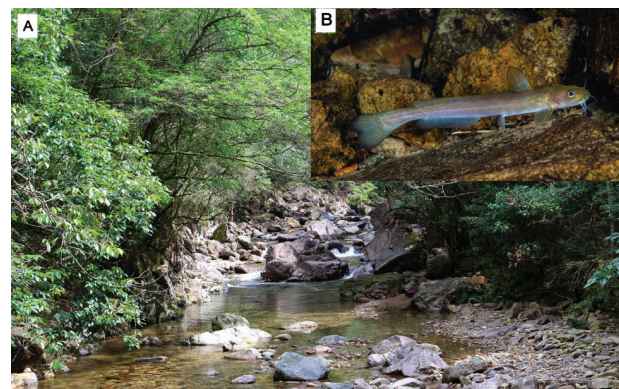


Figure 8. A. Habitat of *Tachysurus wuyueensis*; B. *T. wuyueensis* in situ.

Distribution and habitat. Currently only known from the Qiantang-Jiang in Suichang County, Zhejiang Province and Xiuning County, Anhui Province, south China (Fig. 7). *T. wuyueensis* is found in montane streams of this river basin (Fig. 8), co-existing with *Acrossocheilus fasciatus*, *Pseudogastromyzon fasciatus*, *Rhinogobius niger* and *Tachysurus albomarginatus*.

Etymology. The specific epithet is based on the two rival states Wu and Yue which were bordered by the Qiantang-Jiang in southeast China more than 2000 years ago. The onomatopoeic Chinese sound of this species is “Wu Yue Ni Chang”.

Discussion

Shao and Zhang (2023) erected the *Tachysurus pratti* group using morphological characters, such as smooth anterior margin of the pectoral spine, short maxillary-barbel not extending to the base of pectoral-fin, fewer than 20 anal-fins and uniform yellow or brown body in adults. Under this taxonomic treatment, the *T. pratti* group is the largest group within the genus, with more than twenty species. However, the monophyly of the *T. pratti* group was not supported under the molecular scrutiny in this study (Fig. 1), indicating these species were wrongly clustered due to retention of conservative morphological features, common in catfishes (Zhou et al. 2016). Members in the *T. pratti* group formed two distinct phylogenetic entities in our analyses: *T. wuyueensis* clustering with *T. truncatus*, *T. pratti*, *T. gracilis* and *T. brachyrhabdion* form a well-supported monophyletic clade, namely the *T. pratti*-*T. truncatus* group, that is sister to *T. nitidus*. The remaining species of the “*T. pratti* group” form another monophyly here defined as the *T. tenuis*-*T. crassilabris* group, sister to *T. vachelli*. In addition, the *T. pratti*-*T. truncatus* group plus *T. nitidus* appears to be sister to a clade with *T. vachelli* and *T. tenuis*-*T. crassilabris* group.

Although the morphological similarities between these two newly-erected species groups are numerous, there are some distinguishing features that can be used to diagnose them. The *T. pratti*-*T. truncatus* group differs from the *T. tenuis*-*T. crassilabris* group in having a shorter dorsal spine (length not longer than vs. longer than two-thirds of HL) (Figs 2, 9, 10). Differences in colour patterns were also found to be apparent between the two clades. The body colour of the *T. pratti*-*T. truncatus* group is yellowish-brown (Fig. 2), but dark brown in the *T. tenuis*-*T. crassilabris* group (Fig. 10). The distinction in colouration of the abdomen is conspicuous with numerous dark spots in the *T. tenuis*-*T. crassilabris* group, but is absent in the *T. pratti*-*T. truncatus* group (Fig. 11). In addition, the caudal-fin colouration of round-tailed species can be used as another diagnostic character between these two clades. Except for *T. tenuis*, the white or yellowish caudal-fin margin is broad in the *T. tenuis*-*T. crassilabris* group (Fig. 10), but which is narrow or absent in the *T. pratti*-*T. truncatus* group (Fig. 2). The *T. pratti*-*T. truncatus* group can also be distinguished from other species groups of *Tachysurus* in the external morphology. It differs from the *T. aurantiacus* group, the *T. vachelli* group and the *T. trilineatus* group in having short maxillary barbels not extending to (vs. extending beyond or reaching) the base of pectoral fin, from the *T. nitidus* group, the *T. vachelli* group and *T. virgatus* group in having a dorsal fin spine shorter (vs. longer) than two-thirds of HL.

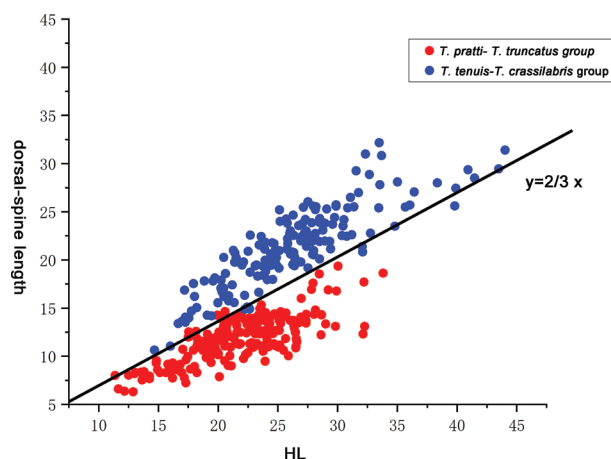


Figure 9. Relationship between dorsal spine length and HL for the *T. pratti*-*T. truncatus* group (including *T. wuyueensis*, *T. pratti*, *T. truncatus*, *T. brachyrhabdion*, *T. gracilis*) and the *T. tenuis*-*T. crassilabris* group (including *T. tenuis*, *T. albomarginatus*, *T. analis*, *T. lani*, *T. zhangfei*, *T. ussuriensis*, *T. crassilabris*).

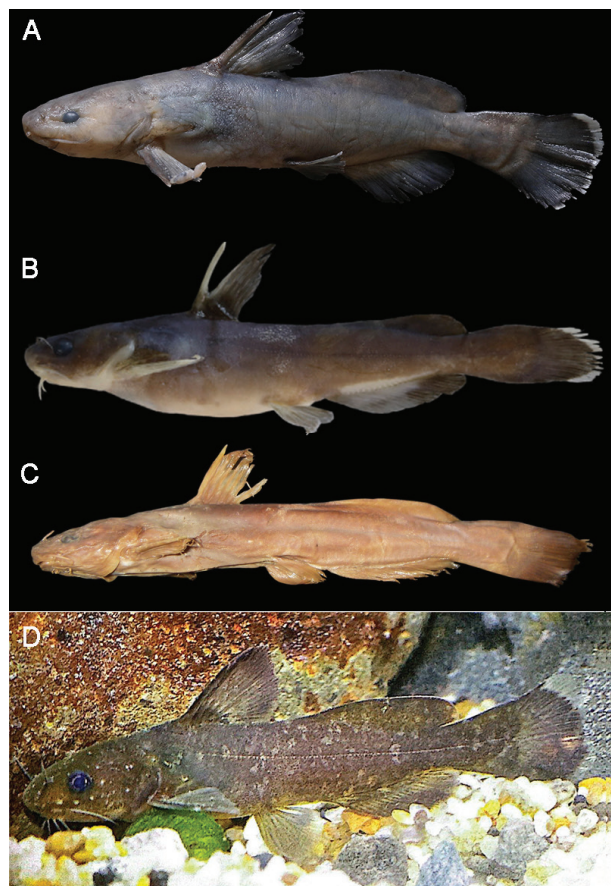


Figure 10. Lateral view of *T. albomarginatus* (A) for IHB 202110025885, 133.5 mm SL, Macheng County, Hubei Province; *T. analis* (B) for IHB201707014311, 124.2 mm SL, Yudu County, Jiangxi Province, in Gan-Jiang; *T. adiposalis* (C) for FMNH 59079, holotype, 172 mm SL, Tamusui River, Taiwan Island; (D) Colour in life of adult of *T. adiposalis*, cited from Zhou and Gao (2011).

The topotypes of *T. adiposalis* were not available in this study, but our photographic examination on the type (FMNH59079) confirmed that *T. adiposalis* has a long dor-

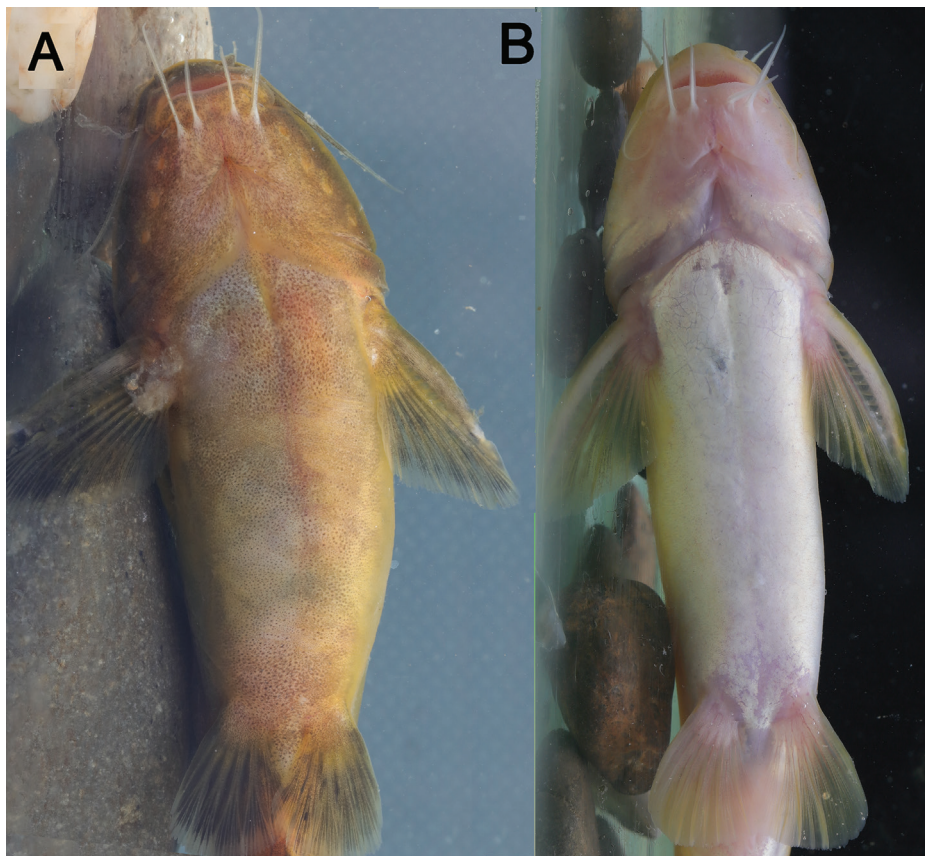


Figure 11. Ventral view of *T. zhangfei* (A) and *T. gracilis* (B) that belong to the *T. tenuis*-*T. crassilabris* group and the *T. pratti*-*T. truncatus* group, respectively.

sal-fin spine (longer than two-thirds of HL) and 19 anal-fin rays (Fig. 10C), which is distinct from *T. wuyueensis*. Based on data from Taiwan, the dark brown body and wide white margin in the caudal fin are present in a living specimen of *T. adiposalis* (Fig. 10D) (Zhou and Gao 2011), suggesting this species may belong to the *T. tenuis*-*T. crassilabris* group. Moreover, a phylogenetic analysis, based on a short segment of mtDNA, showed the specimens of *T. adiposalis* collected from Taiwan are closely related to *T. ussuriensis* of the *T. tenuis*-*T. crassilabris* group. These data confirm our conclusion (Watanabe et al. 2007).

High levels of inter-specific variations in the shape of the caudal fin occur in the *T. pratti*-*T. truncatus* group; for example, *T. pratti* has a deeply forked caudal fin, but the remaining species of the group have round-tailed caudal fins. A similar scenario also occurs in the *T. tenuis*-*T. crassilabris* group. It suggests the convergent evolution of caudal fin morphology in *Tachysurus*. There is a tight link between the shape of the caudal fin and habitat preference: round-tailed species present habitat affinities to montane streams, while fork-tailed species are restricted to rivers' main stream and lakes. The observation describes the effects of ecological niches by shaping the caudal fin in *Tachysurus*.

Comparative materials examined

1. *T. adiposalis*: FMNH59079, 170 mm SL, China: Tamsui River in Taiwan Island.
2. *Tachysurus albomarginatus*: IHB200605264–7, 200605269–86, 220605268 72.1–128.5 mm SL, topotypes, China: Anhui Province: Dangtu County: the lower Yangtze River.
3. *Tachysurus brachyrhabdion*: IHB2017090535–9, 107.6–121.8 mm SL, China: Guizhou Province: Songtao County, the Yuan-Jiang of middle Yangtze River Basin; IHB2017090522–31, China: Chongqing City: Xiushan County, the Yuan-Jiang of the middle Yangtze River Basin; IHB2016106554, 6, 7, China: Hunan Province: Jishou County, the Yuan-Jiang of the middle Yangtze River Basin; IHB2017090548–58, 588, China: Guizhou Province: Tongren City, the Yuan-Jiang of the middle Yangtze River Basin; IHB 201906012028–31, 104.0–127.3 mm SL, China: Hunan Province: Xupu County, the Yuan-Jiang of the middle Yangtze River Basin; IHB2016106295–500, 104.4–124.2 mm SL, China: Hunan Province: Mayang County, the Yuan-Jiang of the middle Yangtze River Basin; IHB2017090495–6, 135.3–150.1 mm SL, China: Guizhou Province: Jiangkou County, the Yuan-Jiang of the middle Yangtze River Basin; IHB2017090427–34, 65.4–89.4 mm SL, China: Guizhou Province: Huangping County, the Yuan-Jiang of the middle Yangtze River Basin.
4. *Tachysurus crassilabris* (Günther 1864): BMNH 1864.7.9.9 (holotype), 155.2 mm SL, China (photograph and X-ray examined); IHB 201909034566–9,

- 97.1–107.2 mm SL, China: Sichuan Province: Huili County: the Jinsha Jiang of the upper Yangtze River; IHB201909017347–61, 69.1–120.5 mm SL, China: Jiangsu Province: Nanjing City: the lower Yangtze River.
5. *T. gracilis*: IHB201803023394–403, 93.6–140.1 mm SL, China: Guangxi Zhuang Autonomous Region: Guanyang County: the middle Yangtze River Basin; IHB2017122195, 2017090542–6, 84.1–119.3 mm SL, China: Guangxi Zhuang Autonomous Region: Yangshuo County: the Pearl River Basin; IHB201909019374–83, 69.9–112.3 mm SL, China: Hunan Province: Shuangpai County: the Xiang-Jiang of the middle Yangtze River Basin; IHB201906011312, 175.9 mm SL, China: Hunan Province: Xinning County: the Zi-shui of the middle Yangtze River Basin; IHB201906011084, 132.0 mm SL, China: Hunan Province, Dongkou County, the Zi-shui of the middle Yangtze River Basin; IHB201906011497–503, 100.8–125.0 mm SL, China: Guangxi Zhuang Autonomous Region: Ziyuan County: the Zi-shui of the middle Yangtze River Basin; IHB201809019719–22, 201809019850–1, 48.4–138.8 mm SL, China: Yanling County, the Xiang-Jiang of the middle Yangtze River Basin.
 6. *Tachysurus tenuis*: IHB201909113617–13629, 124.5–159.6 mm SL, China: Zhejiang Province: Jiaxing City, the Qiantang-Jiang.
 7. *Tachysurus truncatus*: IHB201909038001–10, 84.9–109.5 mm SL, China: Sichuan Province: Wanyuan County, the Jialing-Jiang of the upper Yangtze River; IHB2019090112599–613, 76.0–111.2 mm SL, China: Sichuan Province: Nanjiang County, the Jialing-Jiang of the upper Yangtze River; IHB201909037495–506, 20210505666–70, 73.6–123.5 mm SL, China: Hubei Province: Yuan'an County, the Qing-Jiang of the middle Yangtze River; IHB201904028989–96, 71.5–138.8 mm SL, China: Hubei Province: Nanzhang County, the Han-Jiang of the middle Yangtze River Basin; IHB2015030702–7, 70.6–124.2 mm SL, China: Hunan Province: Cili County, the Li-Shui of the middle Yangtze River Basin; IHB2017090517–21, 91.2–101.5 mm SL, China: Sichuan Province: Leshan City, the Tuo-Jiang of the upper Yangtze River Basin; IHB201812028889–94, 65.7–124.4 mm SL, China: Qianwei County, the Tuo-Jiang of the upper Yangtze River Basin; IHB2019090212127–45, 81.90–145.92 mm SL, China: Sichuan Province: Hejiang County, the Chishui-He of the upper Yangtze River.
 8. *Tachysurus pratti*: IHB202009013755–64, 81.4–143.8 mm SL, China: Sichuan Province: Huili County, the Jinsha-Jiang of the upper Yangtze River Basin; IHB2019090212149–55, 80.8–138.1 mm SL, China: Sichuan Province: Hejiang County, the Chishui-He of the upper Yangtze River Basin; IHB201909034750, 57.3 mm SL, Shuifu County, the Jinsha-Jiang of the upper Yangtze River Basin; IHB202009016033–6, 48.8–56.0 mm, SL, China: Yunnan Province: Binchuan County, the Jinsha-Jiang of upper Yangtze River Basin.

Conflict of interest

The authors declare that they have no conflict of interest.

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Authors' contributions

Jia-Jun Zhou designed the study and revised the manuscript. Yuan Le-Yang extracted the genomic DNA and performed the molecular analysis. Wei-Han Shao examined the specimens and prepared the manuscript. All authors read and approved the final version of the manuscript.

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