

A new genus and species of gonideine freshwater mussel from Guizhou, China, with notes on a new synonym of *Cosmopseudodon resupinatus* (von Martens, 1902) (Bivalvia: Unionidae: Gonideinae)

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Abstract. A new genus and species of gonideine freshwater mussel, *Tenuiunio accuratus* n. gen. & n. sp., is described from the upper Yuanjiang River basin in Guizhou, China. It can be distinguished from all other genera of Gonideini by the irregularly oval and thin shell, and the almost invisible pseudocardinal teeth. The validity of the new genus is further supported by the molecular phylogenetic results based on *COI*, *16S* and *28S* sequences. Additionally, based on molecular phylogenetic results, morphological characteristics, and geographic distribution, we consider *Cosmopseudodon wenshanensis* Wu & Liu, 2024 to be a junior synonym of *C. resupinatus* (von Martens, 1902).

Key words. Biodiversity, molecular phylogeny, new taxa, new synonym, taxonomy

Introduction

The unionid subfamily Gonideinae Ortmann, 1916 exhibit a broad distribution across East and Southeast Asia and harbor considerable diversity (He & Zhuang, 2013; Guo, 2022; Graf & Cummings, 2025; MolluscaBase eds, 2025). In recent years, several new gonideine genera and species have been discovered in China (Dai et al., 2023, 2024; Wu et al., 2024). Tribe Gonideini Ortmann, 1916 is one of the most diverse groups of the subfamily, consist of 15 genera and more than 30 species (Dai et al., 2024; Graf & Cummings, 2025; MolluscaBase eds, 2025). The tribe is distinguished from other tribes of the subfamily by its relatively thin shell, the absence or presence of only vestigial hinge teeth, and a tetragenous brooding type (Dai et al. 2024). Here, we describe a new genus and species of Gonideini from Guizhou, China, and proposal of a new synonym of *Cosmopseudodon resupinatus* (von Martens, 1902).

Materials and methods

Living specimens were initially frozen at -20°C for 2 hours and subsequently thawed at room temperature for 1 hour to facilitate the extraction of animal parts. After photograph, the animal parts were then fixed in 95% ethanol. Empty shells were cleaned, dried, and preserved at room

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<http://zoobank.org/urn:lsid:zoobank.org:pub:E919A276-E65B-46C2-8396-AEB74C6440FF>

TABLE 1. GenBank accession numbers of sequences used in this paper.

Species	COI	16S	28S
UNIONIDAE Rafinesque, 1820			
Gonodeinae Ortmann, 1916			
Gonideini Ortmann, 1916			
<i>Tenuiunio accuratus</i> n. gen. & n. sp. 1	PX724592	PX724523	PX724588
<i>Tenuiunio accuratus</i> n. gen. & n. sp. 2	PX724593	PX724524	PX724589
<i>Guiunio rarus</i> 1	PV368601	PV368859	PV368862
<i>Guiunio rarus</i> 2	PV368602	PV368860	PV368863
<i>Guiunio rarus</i> Chongzuo 1	PX724594	PX724525	PX724590
<i>Guiunio rarus</i> Chongzuo 2	PX724595	PX724526	PX724591
<i>Obovalis omiensis</i>	MT020684	LC223994	MT020830
<i>Ptychorhynchus pfisteri</i>	MG463036	KY067440	MG595564
<i>Parvasolenia rivularis</i>	MG463100	KX966393	MG595626
<i>Sinosolenia carinata</i>	MG463087	NC023250	MG595616
<i>Sinosolenia oleivora</i>	MG463090	NC022701	MG595617
<i>Sinosolenia iridinea</i>	MG463091	MT477834	MG595618
<i>Sinosolenia recognita</i>	MG463092	KY561653	MG595619
<i>Leguminaia wheatleyi</i>	MN402614	MN396725	MN396721
<i>Microcondylaea bonellii</i>	KX822652	KT966473	KX822609
<i>Gonidea angulata</i>	MN402615	MN396726	MN396722
<i>Koreosolenia sitgyensis</i>	MT020682	GQ451859	MT020817
<i>Postolata guangxiensis</i> 1	OP009379	OP020466	OP020470
<i>Postolata guangxiensis</i> 2	OP009380	OP020467	OP020470
<i>Postolata longjiangensis</i> 1	PP786557	PP786405	PP786407
<i>Postolata longjiangensis</i> 2	PP786557	PP786406	PP786407
<i>Pseudopostolata angula</i> 1	PQ189757	PQ201945	PQ201943
<i>Pseudopostolata angula</i> 2	PQ189757	PQ201945	PQ201944
<i>Cosmopseudodon resupinatus</i>	PP079436	PP079964	PP080006
<i>Cosmopseudodon</i> “wenshanensis”	PP079444	PP079972	PP080014
Pseudodontni Frierson, 1927			
<i>Pseudodon mekongi</i>	KX865861	KX865632	KX865733
<i>Pseudodon vondembuschianus</i>	KP795029	KP795052	MZ684028
<i>Pseudodon cambodjensis</i>	KP795028	NC044112	KP795011
<i>Bineurus loeensis</i>	KX865879	KX865650	KX865750
<i>Bineurus mouhotii</i>	KX865876	KX865647	KX865747
<i>Sundadontina tanintharyensis</i>	MN275057	MN307248	MN307189
<i>Sundadontina brandti</i>	MN275058	MN307249	MN307190
<i>Pilsbryoconcha exilis</i>	KP795024	NC044124	KP795007
<i>Pilsbryoconcha compressa</i>	KX865875	KX865646	KX865746
<i>Thaiconcha callifera</i>	KX865862	KX865633	KX865734
<i>Thaiconcha munelliptica</i>	MN275063	MN307252	MN307193
<i>Nyeinchanconcha nyeinchani</i>	KP795025	KP795050	KP795008
Lamprotulini Modell, 1942			
<i>Lamprotula caveata</i>	MG462991	NC030336	MG595518
<i>Lamprotula leaii</i>	MN402616	MN396727	MN396723
<i>Potomida littoralis</i>	MN402617	MN396728	MN396724
<i>Pronodularia japonensis</i>	KX822659	AB055625	KX822615
Chamberlainiini Bogan et al., 2017 in Lopes-Lima et al. 2017			
<i>Sinohyriopsis schlegelii</i>	MT020706	EF507846	MT020836
<i>Sinohyriopsis cumingii</i>	MG463086	NC011763	MG595613
<i>Chamberlainia hainesiana</i>	KX822635	NC044110	KX822592

TABLE 1. (Continued)

Species	COI	16S	28S
Rectidentini Modell, 1942			
<i>Hyriopsis bialata</i>	KX051274	MT993644	MT993697
<i>Ensidens ingallsianus</i>	MT993541	MT993687	MT993739
Contradentini Modell, 1942			
<i>Lens contradens</i>	MG581991	MT993693	MT993745
<i>Lens comptus</i>	KX865928	KX865682	KX865799
<i>Physunio superbus</i>	MG582020	MT993689	MT993741
Schepmaniini Lopes-Lima et al., 2021 in Zieritz et al., 2021			
<i>Schepmania sp.</i>	MZ678755	MZ684082	MZ684035
Ctenodesmini Pfeiffer et al., 2021 in Zieritz et al. 2021			
<i>Khairuloconcha lunbawangorum</i>	MN900790	MZ684078	MN902294
<i>Khairuloconcha sahanae</i>	MZ678752	MZ684079	MZ684024
Unioninae Rafinesque, 182			
<i>Anemina arcaeformis</i>	NC026674	NC026674	MG595457
<i>Cristaria plicata</i>	NC012716	NC012716	MG595484
<i>Sinanodonta woodiana</i>	HQ283346	HQ283346	MG595604
MARGARITIFERIDAE Henderson, 1929			
<i>Gibbosula laosensis</i>	JX497731	KC845943	KT343741
<i>Margaritifera margaritifera</i>	KX550089	KX550091	KX550093

temperature. Photographs were taken by Sony® A7C II and edited in Adobe Photoshop® CC 2025. Map was made in ArcGIS® Pro.

Genomic DNA was extracted from muscle tissues preserved in 95% ethanol using a QIAamp DNA Blood Mini kit (Qiagen, Germany). The quality and concentration of the DNA were checked on 1% agarose gel electrophoresis and NanoDrop 2000 (Thermo Scientific, USA). Partial cytochrome c oxidase subunit 1 (CO I), 16S ribosomal RNA (16S) and 28S ribosomal RNA (28S) were amplified and sequenced for molecular phylogenetic analyses. Polymerase chain reaction (PCR) systems, conditions and primer pairs were followed Dai et al., (2024). The CO I sequences were aligned using MEGA v. 6.0 (Tamura et al., 2013), and the 16S and 28S sequences were aligned using MAFFT v. 7 (Katoh et al., 2019) by the Q-INS-i algorithm. The accession numbers of all sequences used in this study are given in Table 1.

Phylogenies reconstructed by the dataset combined three genes using Maximum Likelihood (ML) and Bayesian Inference (BI). Five species of Unioninae Rafinesque, 1820 (Unionidae) and Margaritiferidae Henderson, 1929 were used as the outgroups for rooting the trees. The best-fit model for each gene and gene partition was calculated by PartitionFinder2 v. 1.1 (Lanfear et al., 2017), based on the corrected Akaike Information Criterion (AICc) and using a heuristic search algorithm. The program proposed the division of the concatenated dataset into five partitions, comprising partitions for the 16S and 28S genes and each of the three codon positions of the COI gene. The best-fit model was determined to be GTR+I+G for the first and second codon positions of COI, as well as for 16S and 28S, while GTR+G was selected for the third position of COI. ML analyses were performed in IQ-TREE v. 1.6.12 (Minh et al., 2013) using the Ultrafast bootstrap approach (Minh et al., 2013) with 10,000 iterations. Bayesian inference (BI) analysis was conducted in MrBayes v. 3.2.6 (Ronquist et al., 2012). Four simultaneous runs with four independent Markov Chain Monte Carlo (MCMC) were implemented for 10 million generations, and trees were sampled every 10,000 generations with a burn-in of 25%. The convergence was checked with the average standard deviation of split frequencies <0.01 and the potential scale reduction factor (PSRF) ~ 1. Trees were visualized in

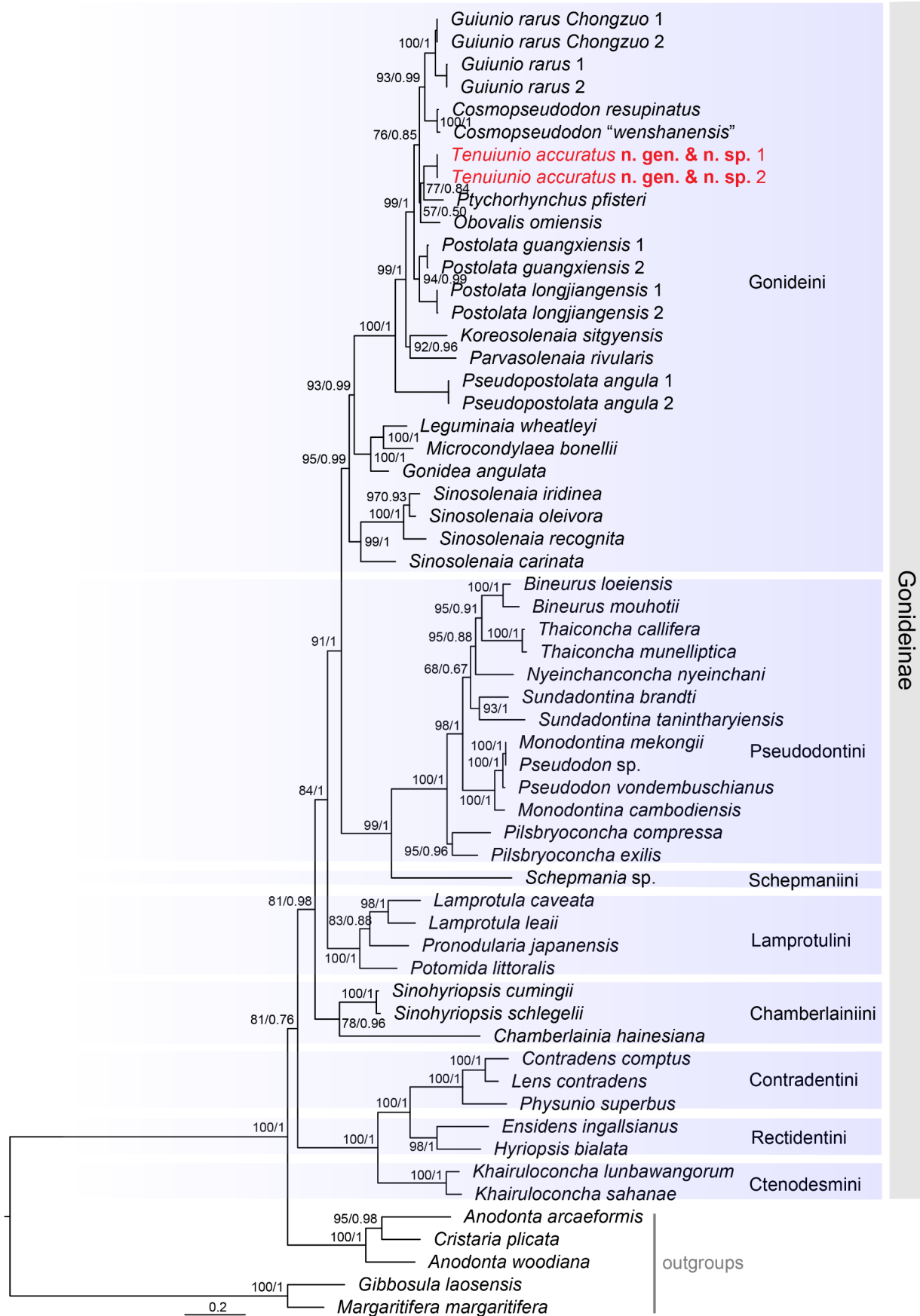


FIGURE 1. Maximum Likelihood tree and Bayesian inference tree inferred from *COI*, *16S* and *28S* genes sequences.

FigTree v.1.4.3 (<http://tree.bio.ed.ac.uk/software/figtree/>) and Adobe Illustrator® 2025.

Abbreviations. NCUMB: Museum of Biology, Nanchang University (Nanchang, China); ZGCC: Collection of Zhong-Guang Chen (Chengdu, China); MCZ: Museum of Comparative Zoology (Cambridge, USA); SMF: Senckenberg Museum (Frankfurt, Germany); UMMZ: University of Michigan Museum of Zoology (Ann Arbor, USA).

Results

Phylogenetic analyses

The sequence dataset consisting of 58 concatenated COI, 16S and 28S sequences from 51 species, including with five outgroup taxa, was employed for phylogenetic analyses (Table 1). The alignments of COI, 16S and 28S genes had a length of 606, 517 and 457 characters, respectively. Within these alignments, 258, 234 and 168 sites were variable, and 237, 200 and 154 sites were parsimony informative. The Bayesian and Maximum Likelihood analyses produced same phylogenies (Fig. 1). The subfamily Gonideinae comprise eight well-supported tribes as the same topology recovered by Dai et al. (2023, 2024). The new genus, along with *Cosmopseudodon* Haas, 1920, is assigned to the tribe Gonideini. The new genus forms a sister group with genus *Ptychorhynchus* Simpson, 1900 with moderate support rate (BS/PP = 77/0.84). *Cosmopseudodon wenshanensis* Wu & Liu, 2024 in Wu et al. (2024) forms a sister group with *C. resupinatus* (BS/PP = 100/1). However, these two species exhibit remarkably low genetic divergence, rendering them nearly indistinguishable.

Systematics

Family **Unionidae** Rafinesque, 1820

Subfamily **Gonideinae** Ortmann, 1916

Tribe **Gonideini** Ortmann, 1916

Genus ***Tenuiunio* n. gen.**

薄壳蚌属 (Pinyin: báo ké bàng shǔ)

Type species. *Tenuiunio accuratus* n. sp.

Diagnosis. The new genus is closely related to the genera *Ptychorhynchus* and *Obovalis* Simpson, 1900, but can be distinguished by the irregularly oval and comparatively thin shell, with a shell thickness comparable to that of *Parvasolenia rivularis* (Heude, 1877), as well as by the almost invisible pseudocardinal teeth.

Etymology. The genus name is formed from the Latin *tenuis*, meaning “thin”, and *Unio*, the type genus of Unionidae. The name refers to the distinctly thin shell of this genus. The gender of the genus is masculine.

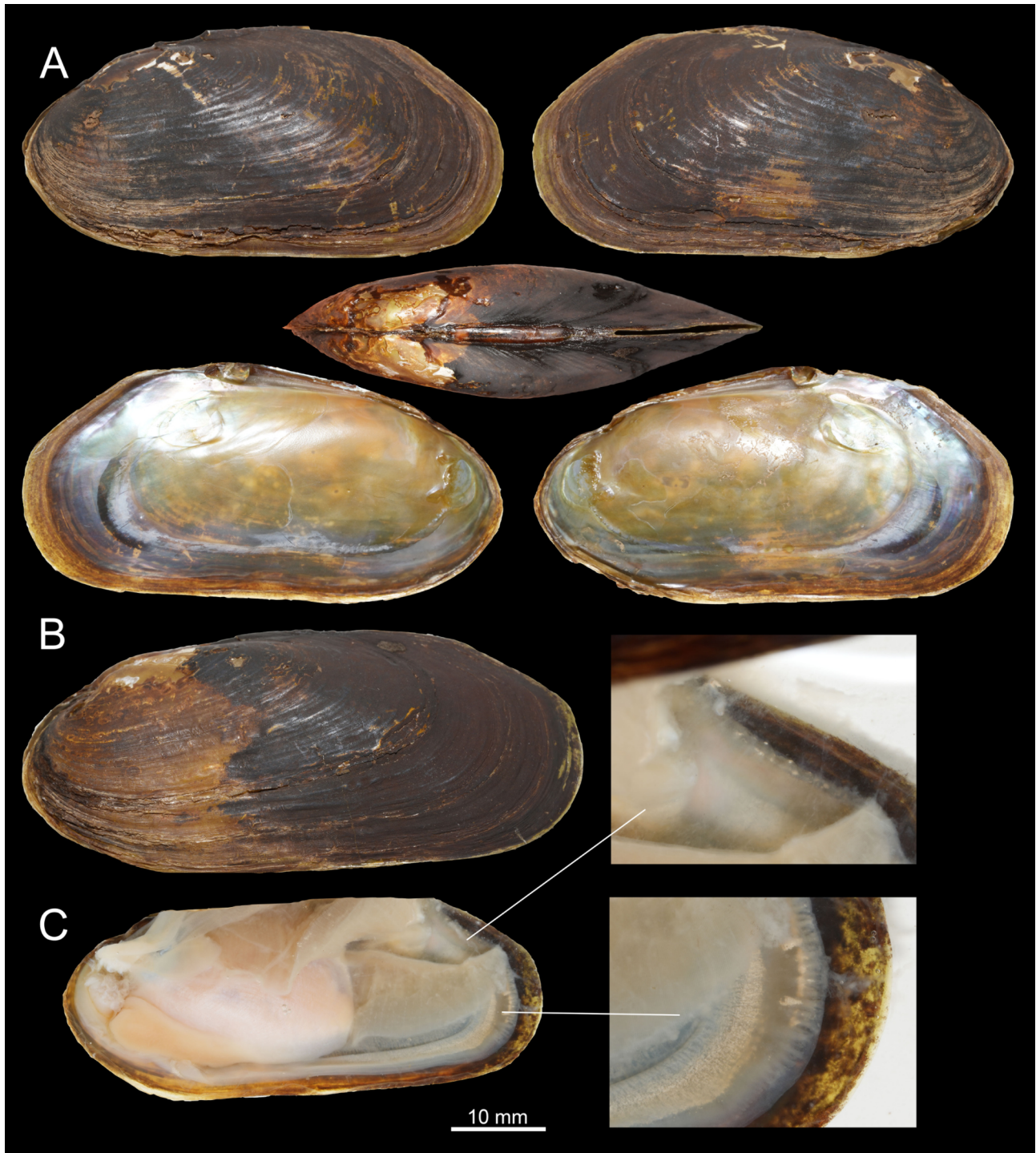


FIGURE 2. *Tenuiunio accuratus* n. gen. & n. sp. A. holotype. B. paratype. C. animal anatomy of the holotype.

***Tenuiunio accuratus* n. sp.**

严谨薄壳蚌 (Pinyin: yán jǐn báo ké bàng)

(Figure 2)

Type materials. *Holotype.* NCUMB B2601001, Liping County [黎平县], Qiandongnan Miao and Dong Autonomous Prefecture [黔东南苗族侗族自治州], Guizhou Province [贵州省], China, leg. local people, ex. coll. Zhong-Guang Chen, December 2025. *Paratype.* ZGCC/1, other information

same as holotype.

Diagnosis. Same as the genus.

Description. Shell irregularly oval, medium-sized, very thin, flat, long, sub-glossy, rather smooth, edge semi-transparent. Anterior small, rounded and short; posterior expanded, wide and long. Dorsal margin slightly curved downwards; ventral margin weakly retuse. Umbo lower than the hinge line, located at 1/5 of the dorsal margin, smooth. Periostracum brown with thin growth lines, usually covered by black sediment. Ligament short and weak. Beak cavities shallow, open. Anterior adductor muscle scars irregularly rounded, shallow, smooth; posterior adductor muscle scars long oval, smooth. Pseudocardinal teeth of both shells degenerated, almost invisible. Lateral teeth of both shells short and thin. Nacre light orange to white.

Mantle and aperture margins off-white, papillae on flap margin highly degraded. Gills off-white, inner and outer gills are almost equal in length. Labial palps brown, oval. Visceral mass and foot light orange.

Measurements. Holotype: shell length 51.0 mm, height 25.0 mm, width 14.3 mm. Paratype: shell length 59.5 mm, height 25.8 mm, width 15.2 mm.

Etymology. The species is named after the Latin *accuratus*, meaning “rigorous”, referring to the need for rigor in taxonomic studies of Chinese freshwater mussels, as insufficiently careful work may lead to the repeated description of junior synonyms.

Distribution and ecology. The species is restricted to a small tributary of the Yuanjiang River in Liping (Fig. 3). It inhabits flowing streams with pebble and sandy substrates, where it occurs alongside *Pseudocuneopsis liuovatus* (He & Zhuang, 2013) (Fig. 4). The population size appears to be very small (Yu-Chen Wang, pers. comm.).



FIGURE 3. Distribution of *Tenuiunio accuratus* n. gen. & n. sp. Star shows the type locality.



FIGURE 4. Habitat of *Tenuiunio accuratus* n. gen. & n. sp. The shells are empty shells. © Yu-Chen Wang.

Remarks. The survival of the new species is under severe threat. Under the guise of scientific research, some individuals have reportedly commissioned local collectors to conduct intensive and destructive harvesting across the type locality, followed by the commercial sale of specimens at high prices. In addition to direct overharvesting, the collection methods employed by local collectors have also caused physical damage to the habitat itself. Such combined pressures have very likely exceeded the carrying capacity of the population and have caused a severe impact on the persistence of the species. As a consequence of this overexploitation and habitat disturbance, subsequent field surveys failed to locate any living individuals at the type locality, including a follow-up survey conducted only one month later (Yu-Chen Wang, pers. comm.). Under these circumstances, the authors were compelled to rely on specimens derived from the same distorted source above for the present study. Such practices are strongly condemned here, and we call for their firm rejection, together with an appeal for responsible and ethical shell collecting practices that prioritise species conservation over commercial or personal interests.

Genus *Cosmopseudodon* Haas, 1920

Type species. *Pseudodon resupinatus* E. von Martens, 1902, by original designation.

***Cosmopseudodon resupinatus* (von Martens, 1902)**

稀褶饰拟齿蚌 (Pinyin: xī zhě shì nǐ chǐ bàng)

Pseudodon resupinatus von Martens, 1902: 131.*Pseudodon* (*Cosmopseudodon*) *resupinatus* – Haas, 1920: 310.*Ptychorhynchus resupinatus* – Bolotov *et al.*, 2023.*Cosmopseudodon resupinatus* – Wu *et al.*, 2024: 11, figs 1, 3a1–a3.*Cosmopseudodon wenshanensis* – Wu *et al.*, 2024: 11, figs 1, 3b1–b3. **New synonym.**

Material examined. Lectotype. MCZ 167671, Than Moi, Tonkin, French Indo China (photo examined). Paratype: MCZ 167672, other information same as lectotype (photo examined). SMF 13785/5, Than-Moi, Tonkin (photo examined). UMMZ 110156/3, Tonkin, French Indo China (photo examined). ZGCC/10, Yongfu County [永福县], Guilin City [桂林市], Guangxi Zhuang Autonomous Region [广西壮族自治区], China, leg. Zhong-Guang Chen & Yu-Ting Dai, March 2023. ZGCC/5, Panlonghe River [盘龙河], Wenshan Zhuang and Miao Autonomous Prefecture [文山壮族苗族自治州], Yunnan Province [云南省], China, leg. local people, ex. Zhong-Guang Chen, May 2023.

Remarks. Molecular phylogenetic analyses revealed an extremely limited genetic divergence between *C. resupinatus* and *C. wenshanensis*, with a COI gene distance of merely 1.82% between two geographically distant populations (based on online BLAST results from NCBI). We propose that the morphological distinctions between these two nominal species reflect ecotypic variation rather than interspecific divergence. Specifically, *C. wenshanensis* represents a stream-dwelling ecotype of *C. resupinatus*. Such ecotype-related morphological plasticity is well-documented in freshwater mussels, where numerous Chinese species exhibit pronounced conchological variation across habitats. Examples include *Lamprotula caveata* (Heude, 1877), *Lanceolaria triformis* (Heude, 1877), and *Inversidens rentianensis* Wu & Wu, 2021 in Wu *et al.* (2021) (Z.-G. Chen, unpublished data), among others. Consistently, conspecific individuals from stream environments often display shell morphologies distinct from those inhabiting large rivers. Historically, such ecologically mediated variation has frequently been misinterpreted as evidence for interspecific differentiation (Wu *et al.*, 2020, 2022). Furthermore, the *C. resupinatus* specimens sequenced by Wu *et al.* (2024) originated from the Pearl River basin, while their *C. wenshanensis* specimens were collected from the Red River basin. It is noteworthy that the type locality of *C. resupinatus* is situated within the Red River basin (von Martens, 1902). Thus, the *C. wenshanensis* specimens can be considered a near-topotype of *C. resupinatus*. Additionally, the shell morphology of the lectotype and paratype of *C. resupinatus* (illustrated in Graf & Cummings, 2025) appears intermediate between that of the *C. wenshanensis* and the Pearl River population of *C. resupinatus*. Another set of topotypic specimens of *C. resupinatus* (SMF 13785, illustrated in Graf & Cummings, 2025), collected from Than-Moi, Tonkin (around Hanoi, Vietnam), exhibited virtually no distinguishable morphological differences from *C. wenshanensis*. Based on this combined molecular, morphological, and biogeographic evidence, we treat *C. wenshanensis* as a junior synonym of *C. resupinatus*.

Acknowledgements

We thank the editor-in-chief and an anonymous reviewer for their very helpful suggestions to the manuscript; Yu-Chen Wang for providing photos of the habitat. This study was supported by the National Natural Science Foundation of China under Grant No.32360132 and the National Scholarship to Z.-G. Chen.

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贵州省隆脊蚌亚科一新属新种，兼论稀褶饰拟齿蚌一新异名 (双壳纲：蚌科：隆脊蚌亚科)

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摘 要

本文描述了产自中国贵州沅江上游的河蚌新属新种：严谨薄壳蚌 *Tenuiunio accuratus* **n. gen. & n. sp.**。该属可依据以下特征与所有同族其他属区分：贝壳薄且为不规则的椭圆形；拟主齿几乎不可见。其有效性也被基于*COI*、*16S*和*28S*序列的分子系统发育结果所证实。此外，基于分子系统发育结果、形态学特征和地理分布，我们将文山饰拟齿蚌 *Cosmopseudodon wenshanensis* Wu & Liu, 2024修订为稀褶饰拟齿蚌 *C. resupinatus* (von Martens, 1902)的次异名。

关键词：生物多样性，分子系统发育，新阶元，新异名，分类学