

Hidden diversity in China's Sky Islands: Three new freshwater snail species of Erhaiidae (Gastropoda, Truncatelloidea) from the Yunnan-Guizhou Plateau

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Abstract

Alpine freshwater ecosystems in southwestern China, particularly those exhibiting sky-island characteristics (geographically isolated high-elevation habitats surrounded by contrasting lowlands), represent critical yet understudied hotspots for aquatic biodiversity evolution. The minute gastropod genus *Erhaia* (<3 mm shell height) exemplifies this pattern, with species distributed across fragmented high-elevation streams from the Himalayas to eastern China. Despite 20 described species, the group's diversity is likely underestimated due to their small size, collection neglect, and the lack of recent records—including the type species, *E. daliensis*, which has not been recollected since its original description. During field surveys conducted in 2023–2024, we re-discovered *E. daliensis* at its type locality in Yunnan, China, and identified three new species: *E. xiaoboqiani* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, **sp. nov.**, *Erhaia guizhouensis* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, **sp. nov.**, and *Erhaia bailong* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, **sp. nov.** from mountain streams in Yunnan and Guizhou. Combining morphological and molecular evidence (mitochondrial COI, 16S; nuclear 18S, 28S), we formally describe these taxa and discuss their biogeographic implications for understanding diversification in sky-island-like freshwater systems.

Key Words

Asian uplift, biogeography, Erhaiidae, molecular phylogeny, sky islands, species diversification

Introduction

Alpine freshwater ecosystems, particularly those situated in topographically isolated mountain regions, often exhibit “sky island” dynamics, making them critical hotspots for biodiversity evolution (Heald 1951; Moore et al. 2013; He and Jiang 2014; Zhang et al. 2019). The genus *Erhaia* provides a compelling case study of such isolation in montane freshwater systems. These minute gastropods (typically < 3 mm shell height) (Davis et al.

1985; Gittenberger et al. 2017; Gittenberger et al. 2020; Gittenberger et al. 2022) inhabit high-elevation streams across the Himalayas (Bhutan, Nepal) to eastern China (Yunnan, Guizhou, Hubei, and Fujian), displaying a classic insular distribution pattern in which populations are isolated by arid lowland valleys (Gittenberger et al. 2022; Gyeltshen et al. 2023; Sitnikova et al. 2023). Although 21 species have been formally described, the group's diversity remains severely underestimated due to their inconspicuous size leading to collection neglect, the type

species *E. daliensis* and most congeners not being recollected since their original descriptions, and a consequent research paucity (Gittenberger et al. 2022; Sitnikova et al. 2023). This knowledge gap persists despite their significance for understanding montane freshwater biogeography and sky island diversification processes.

During field surveys conducted between 2023 and 2024, we collected live specimens of *Erhaia daliensis* from its type locality, a montane tributary stream of Lake Erhai in Dali City, Yunnan Province, China. Additionally, we discovered three new *Erhaia* species: *E. bailong* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, sp. nov., *E. guizhouensis* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, sp. nov., and *E. xiaoboqiani* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, sp. nov. from Yunnan and Guizhou provinces. Herein, we formally describe these new species based on morphological and molecular evidence and discuss the role of *Erhaia* in understanding freshwater sky island biogeography in Asia.

Materials and methods

Materials and morphological examination

All specimens were collected in August 2023 and December 2024 from Guiyang City in Guizhou Province and from Yuxi City and Dali City in Yunnan Province, China (Fig. 1). The specimens were preserved in 95% ethanol and deposited at the Museum of Biology, Nanchang University (NCUMB), China. Shells were cleaned with a fine brush, rinsed with distilled water, and photographed under a stereomicroscope (Nikon SMZ645). Electron micrographs were obtained using a scanning electron microscope (SEM) (ZEISS G300). Shell parameters were measured to 0.01 mm precision using digital calipers.

Phylogenetic analyses

Total genomic DNA was extracted from the tissue of each ethanol-preserved specimen using the Trelief™ Animal Genomic DNA Kit (Tsingke®). Partial sequences of COI, 16S, 18S, and 28S rDNA were amplified using the following primers: LCO1490 and HCO2198 for COI (Folmer et al. 1994), 16SH and 16SR for 16S (Simon et al. 1994), G01 and G07 for 18S (Saunders and Kraft 1994), and 28SD1 and 28ff for 28S (Hillis and Dixon 1991; Colgan et al. 2003). Each PCR reaction was performed in a total volume of 20 µl, including 9 µl of 2× Taq Plus Master Mix II (Vazyme Biotech Co., Ltd., Nanjing, China; Cat# P213-01), 8 µl of double-distilled water, 1 µl (10 µM) of each primer, and 1 µl of DNA template (50–100 ng). The PCR conditions were set as follows: initial denaturation at 95 °C for 3 min; 35 cycles of denaturation at 95 °C for 40 s, annealing at 55 °C for 16 s (52 °C for COI; 59 °C for 28S; 62 °C for 18S) for 30 s, and extension at 72 °C for 30 s; followed by a final extension at 72 °C for 7 min. Both strands were sequenced using Sanger sequencing on an Applied Biosystems 3730xl DNA Analyzer at Sangon Biotech Co., Ltd. (Shanghai, China). Sequences were aligned using MAFFT v. 7.505 based on the L-INS-i method (Kato and Toh 2008). The COI gene was codon-aligned using MUSCLE (Edgar 2004) in MEGA X (Kumar et al. 2018), and pairwise distances between species were subsequently calculated using the same software. Gblocks v. 0.91b (Castresana 2000) was used to exclude ambiguous regions from each gene alignment. Sequences were concatenated in PhyloSuite v. 2.3 (Zhang et al. 2020). All samples and GenBank accession numbers are shown in Table 1. Predefined data blocks for the partitioning scheme search were designated according to gene regions and codon positions (PCGs). Model selection and partitioning strategy were evaluated based on the corrected Akaike Information

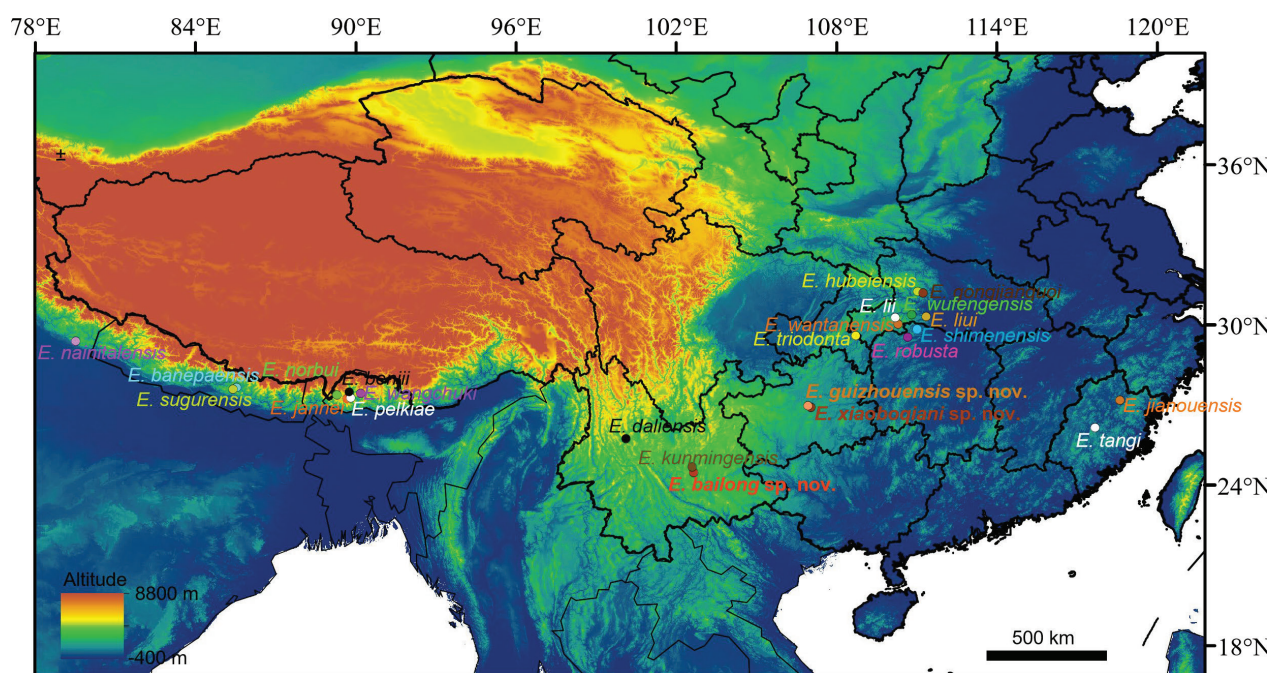


Figure 1. Distribution of *Erhaia* species across Asia.

Table 1. GenBank accession numbers used in this study. Sequences obtained in the present study are marked with an asterisk (*).

Family	Speciecs	COI	16S	18S	28S
Anabathridae	<i>Anabathron contabulatum</i>	KC439793	KC109937	-	KC109989
Assimneidae	<i>Assiminea hiradoensis</i>	AB611807	AB611806	AB611804	AB611805
	<i>Paludinellassiminea japonica</i>	AB611811	AB611810	AB611808	AB611809
Bythinellidae	<i>Bythinella molcsany</i>	HM234195	FJ028876	JQ639804	FJ028894
	<i>Bythinella carinulata</i>	FJ029101	FJ028884	-	FJ028896
Bithyniidae	<i>Bithynia tentaculata</i>	JX970605	FJ160288	AF367675	FJ160289
Caecidae	<i>Caecum glabellum</i>	AB930481	LC598168	AB930393	AB930352
Calopiidae	<i>Calopia imitata</i>	KC439790	KC439912	-	KC439957
	<i>Calopia laseroni</i>	KC439792	KC439914	-	KC439959
Clenchiellidae	<i>Clenchiella iriomotensis</i>	LC598187	LC598173	LC598111	LC598127
Cochliopidae	<i>Semisalsa maltzani</i>	KM213742	-	KM213722	-
Elachisinidae	<i>Elachisinidae</i> sp.	-	LC598174	LC598112	-
Emmericidae	<i>Emmericia expansilabris</i>	KC810061	EU573985	EU573995	-
Erhaidae	<i>Akiyoshia kobayashii</i>	AB611823	AB611822	AB611820	AB611821
	<i>Erhaia jannei</i>	MT237716	MT239078	-	-
	<i>Erhaia benjii</i>	OQ221600	-	-	-
	<i>Erhaia norbui</i>	OM135616	OM135244	-	-
	<i>Erhaia wangchuki</i>	MT237715	KY798003	-	-
	<i>Erhaia jianouensis</i>	AF367652	EU573984	AF367688	-
	<i>Erhaia daliensis</i>	PV494970*	PV501083*	PV501075*	PV501091*
	<i>Erhaia daliensis</i>	PV494971*	PV501084*	PV501076*	PV501092*
	<i>Erhaia bailongensis</i> sp. nov.	PV494973*	PV501085*	PV501079**	PV501094*
	<i>Erhaia bailongensis</i> sp. nov.	PV494974*	PV501086*	PV501080*	PV501095*
	<i>Erhaia guizhouensis</i> sp. nov.	PV494968*	PV501081*	PV501073*	PV501089*
	<i>Erhaia guizhouensis</i> sp. nov.	PV494969*	PV501082*	PV501074*	PV501090*
	<i>Erhaia xiaoboqiani</i> sp. nov.	PV494972*	PV501087*	PV501077*	PV501093*
	<i>Erhaia xiaoboqiani</i> sp. nov.	PV494975*	PV501088*	PV501078*	PV501096*
Falsicingulidae	<i>Falsicingula mundana</i>	KC439798	KC109957	-	KC110009
	<i>Falsicingula mundana</i>	AB930492	AB930424	AB930398	AB930366
Fontigentidae	<i>Fontigens nickliniana</i>	JX970609	-	JX970573	-
Hydrobiidae	<i>Hydrobia acuta</i>	KC439801	KC109959	AF367680	KC110011
Hydrococcidae	<i>Hydrococcus brazieri</i>	-	KC109960	JX970579	KC110012
Iravadiidae	<i>Iravadia reflecta</i>	LC598188	LC598175	LC598116	LC598130
	<i>Fluviocingula resima</i>	KC439778	KC439900	-	KC439947
Lithoglyphidae	<i>Lithoglyphus naticoides</i>	AF367642	FJ160287	AF367674	FJ160290
Moitessieriidae	<i>Sardopaladilhia plagigeyera</i>	HQ623176	HQ623160	HQ623168	-
Pomatiopsidae	<i>Neotricula aperta</i>	AF531541	AF531556	AF531540	AY207034
	<i>Fukuia kurodai ooyagii</i>	AB611783	AB611782	AB611780	AB611781
	<i>Cecina manchurica</i>	AB611743	AB611742	AB611740	AB611741
Stenothyridae	<i>Stenothyra australis</i>	KC439692	KC439814	-	KC439915
Spirostyliferinidae	<i>Spirostyliferina lizardensis</i>	-	MN119719	MN119726	MN119727
Tateidae	<i>Tatea rufilabris</i>	KC439802	KC109980	-	KC110033
	<i>Potamolithus ribeirensis</i>	JX970618	JX970549	JX970591	-
Teinostomatidae	<i>Teinostoma lucidum</i>	-	LC598176	-	AB930343
	<i>Teinostoma</i> sp.	LC598189	LC598177	LC598117	LC598131
Tornidae	<i>Pseudoliotia micans</i>	KC439806	KC109971	-	KC110023
Tomichiidae	<i>Coxiella striata</i>	ON426688	OP863119	-	-
Truncatellidae	<i>Truncatella pfeifferi</i>	AB611819	AB611818	AB611816	AB611817
	<i>Truncatella subcylindrica</i>	KC439799	KC109982	-	KC110035
Vitrinellidae	<i>Vitrinella oldroydi</i>	-	LC598179	LC598119	LC598133
Epitoniidae	<i>Opalia gracilis</i>	AB930468	AB930412	AB930384	AB930334
	<i>Alexania inazawai</i>	AB930463	AB930407	AB930380	AB930329

Criterion (AICc). Partition schemes and substitution models were selected using PartitionFinder 2 (Lanfear et al. 2017) under a greedy search algorithm with unlinked branch lengths. The best-fit models for each partition were determined as follows: GTR+I+G for COI_codon1, COI_codon2,

18S, and 28S; HKY+G for COI_codon3; and GTR+I+G for 16S. Maximum likelihood phylogenies were inferred using IQ-TREE under the Edge-unlinked partition model (Nguyen et al. 2015), with branch support assessed with 10,000 ultra-fast bootstraps (Minh et al. 2013). Bayesian inference phy-

logenies were constructed using MrBayes 3.2.7 (Ronquist et al. 2012). Four independent Markov chain Monte Carlo (MCMC) runs were conducted. After 10 million MCMC generations, the standard deviation of split frequencies of the two runs was less than 0.01, and the potential scale reduction factor (PSRF) was 1. This indicates convergence, and 25% of sampled trees were discarded as burn-in.

Results

Phylogenetic analyses

Phylogenetic analyses reveal a paraphyletic arrangement of *Erhaia*, with *E. jianouensis* (Fujian) forming a strongly supported clade with Japanese *Akiyoshia kobayashii* (BS = 100, BPP = 1) rather than with congeneric species in both BI and ML trees (Figs 2, 3). The Bhutanese radiation (*E. benji*,

E. jannei, *E. wangchuki*, and *E. norbui*) constitutes a robust monophyletic group (BS = 100, BPP = 1), although its phylogenetic context differs between analyses (Figs 2, 3). In the BI reconstruction, this Bhutanese clade shows a sister relationship with *E. daliensis* (Yunnan), forming a polytomy with both the Guizhou lineage (*E. guizhouensis* sp. nov. + *E. xiaoboqiani* sp. nov.) and *E. bailong* sp. nov. (Yunnan), all with high nodal support (Fig. 2). The ML topology alternatively resolves the Bhutanese taxa as sister to a Yunnan subclade (*E. daliensis* + *E. bailong*; BS = 78), with the Guizhou endemics subsequently sister to this larger assemblage (BS = 100) (Fig. 3). The three newly discovered lineages—*E. guizhouensis* sp. nov., *E. xiaoboqiani* sp. nov. (both from Guizhou), and *E. bailong* sp. nov. (Yunnan)—exhibit distinct phylogenetic positions and substantial molecular differentiation from congeners, with mean uncorrected p-distances of 11.7% (range 8–15%) for COI sequences. Specifically, *E. guizhouensis* sp. nov. shows 12% divergence

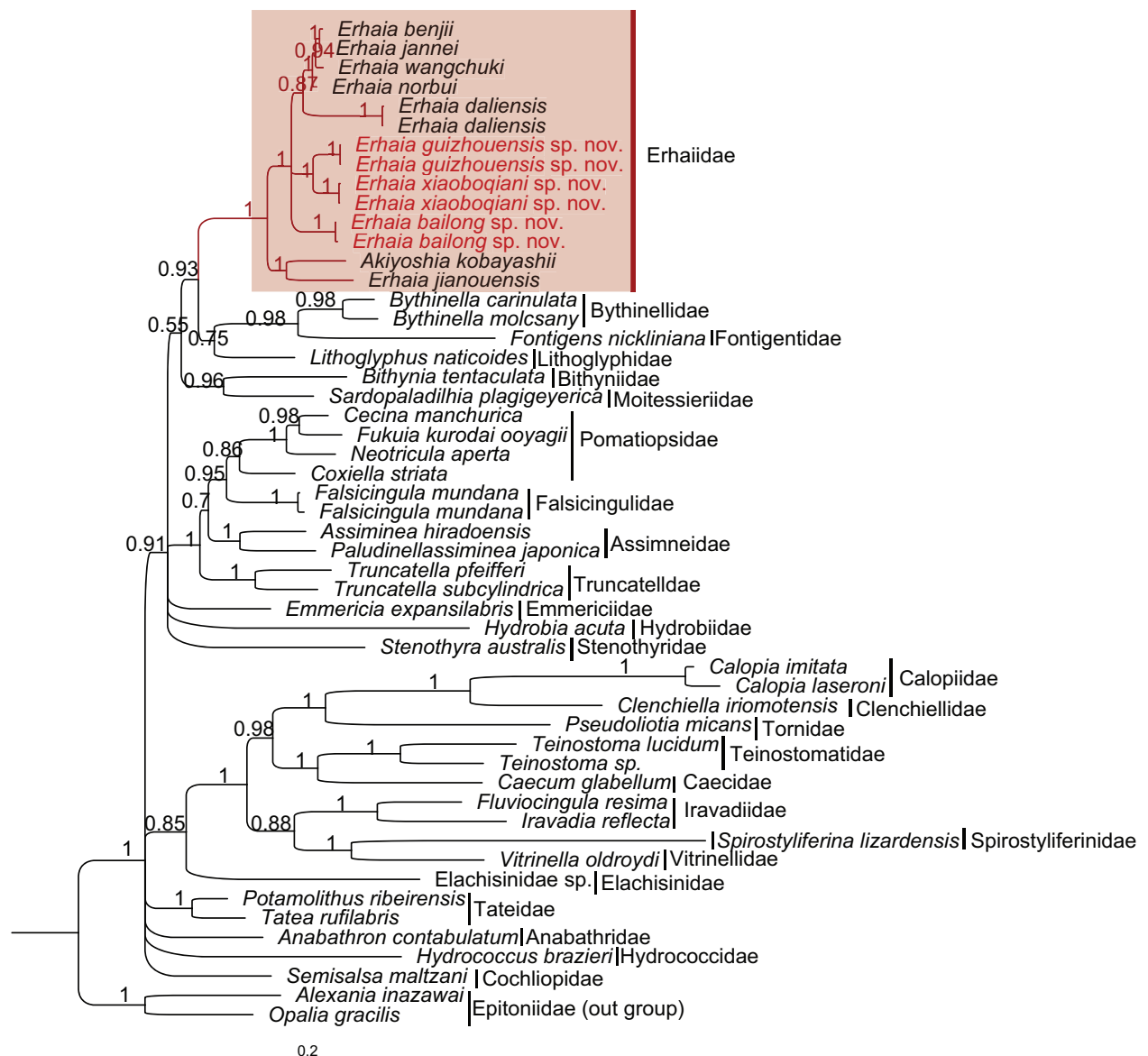


Figure 2. Bayesian inference (BI) tree for the new species and other freshwater snails based on a multilocus dataset (COI, 16S, 18S, and 28S). Values at nodes represent Bayesian posterior probabilities (BPP). Red indicates new species.

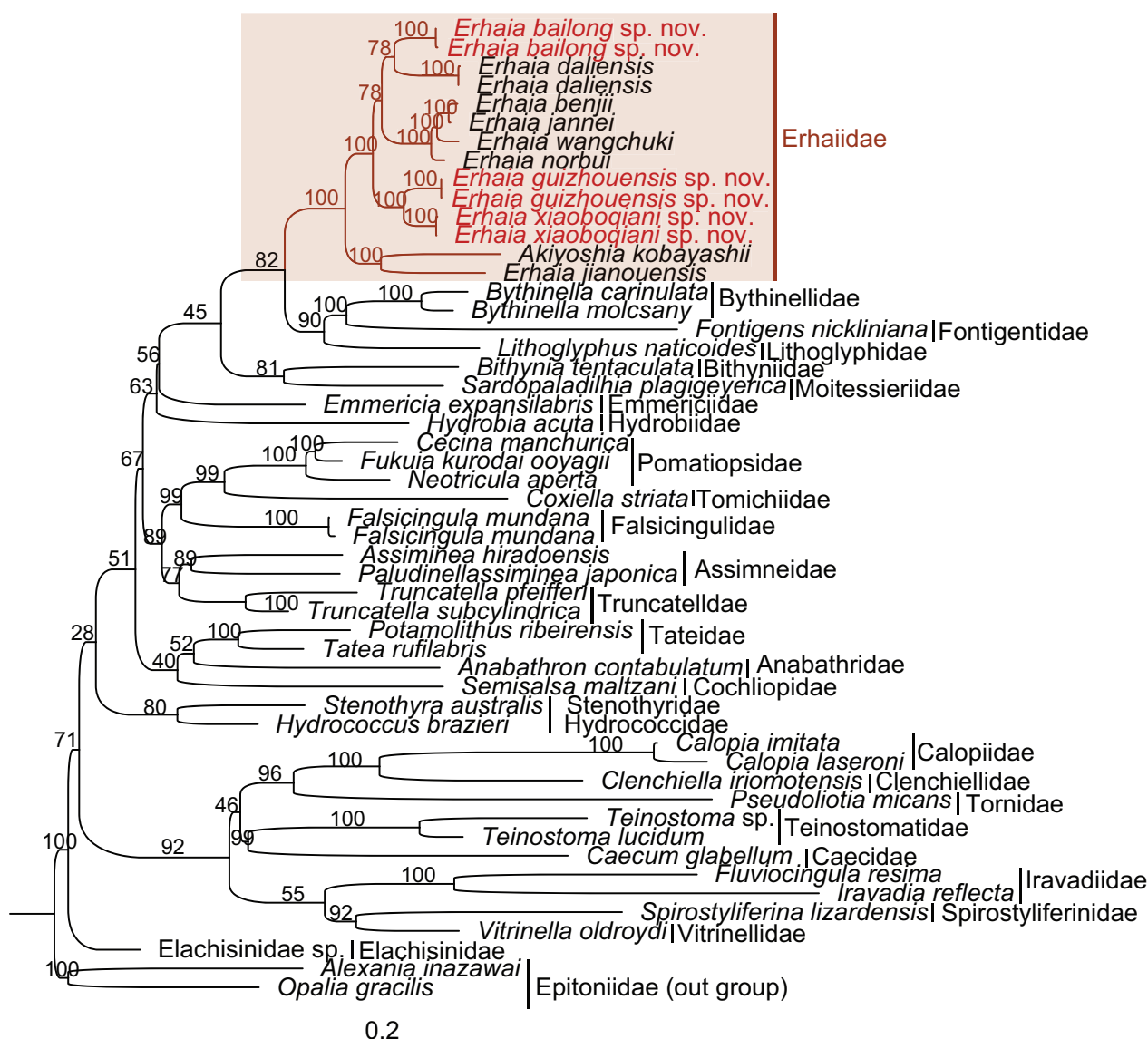


Figure 3. Maximum likelihood (ML) tree for the new species and other freshwater snails based on a multilocus dataset (COI, 16S, 18S, and 28S). Values at nodes represent bootstrap support (BS). Red indicates new species.

from its closest relative, *E. xiaoboqiani* sp. nov., while *E. bailong* sp. nov. differs by 12% from sympatric *E. daliensis* (Table 2). Given their consistent molecular divergence and diagnostic morphological differentiation, we formally describe these lineages as new species herein.

Systematics

Family Erhaiidae Davis & Kuo, 1985

Genus *Erhaia* Davis & Kuo, 1985

Figs 4A, B, 5A

Pseudobythinella Y.-Y. Liu & W.-Z. Zhang, 1979 (invalid, junior homonym of *Pseudobythinella* Melville, 1956; see Gittenberger et al. 2022).

Type species. *Erhaia daliensis* Davis & Kuo, 1985: by original designation.

***Erhaia bailong* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, sp. nov.**

<https://zoobank.org/25E6965F-98C2-472B-952A-AB193C0727CD>

Figs 4C, D, 5B

Material examined. Holotype: • NCUEB250101, shell height 2.11 mm (Fig. 4C), Bailongtan, Hongtaia District, Yuxi City, Yunnan Province, China, 24.3958°N, 102.6000°E (Fig. 1).

Paratypes: • 20 specimens, NCUEH250102–21, August 2023, shell height 1.75–2.14 mm, collected by Hong Quan Xiang and Yue Ming He, locality and habitat same as holotype.

Diagnosis. Shell small, pale greyish, ovoid in shape. Aperture relatively large, sub-ovate, featuring a thick tooth on the columella.

Description. Shell small, pale greyish, ovoid, consisting of six convex whorls separated by a deep suture. Shell surface exhibits fine irregular growth lines and occasional

Table 2. Genetic distances of COI sequences.

	<i>A. kobayashii</i>	<i>E. jannei</i>	<i>E. norbui</i>	<i>E. wangchuki</i>	<i>E. daliensis</i>	<i>E. bailong</i>	<i>E. guizhouensis</i>	<i>E. xiaoboqiani</i>
<i>E. jannei</i>	0.14							
<i>E. norbui</i>	0.13	0.04						
<i>E. wangchuki</i>	0.15	0.05	0.05					
<i>E. daliensis</i>	0.16	0.12	0.11	0.13				
<i>E. bailong</i>	0.13	0.09	0.08	0.10	0.12			
<i>E. guizhouensis</i>	0.16	0.13	0.13	0.13	0.15	0.12		
<i>E. xiaoboqiani</i>	0.17	0.11	0.11	0.12	0.14	0.11	0.12	
<i>E. jianouensis</i>	0.15	0.15	0.13	0.15	0.15	0.14	0.16	0.15

periostracal ridges. Peristome is continuous and thickened. Without umbilical chink. Apex is typically eroded and obtuse (Fig. 4C, D). Aperture is relatively large and sub-ovate, featuring a thick tooth on the columella that extends around the entire body whorl (Fig. 5B).

Etymology. The specific epithet “bailong” (from Chinese 白龙, ‘white dragon’) is treated as a noun in apposition, alluding to a local legend of a white loong (Chinese dragon) inhabiting this spring. The suggested Chinese common name is “白龙洱海螺” (Báilóng Ērhǎi Luó).

Biology. This species inhabits mountain springs and streams, often attaching to fallen leaves on the riverbed, where it occurs in high densities. It avoids deep water and is typically found in slow-moving water at depths of 0–20 cm. Its distribution is recorded at elevations of around 1,800 m.

Remarks. This species possesses a thickened columellar tooth and is morphologically similar to *E. liui* (Kang, 1983), *E. shimenensis* (Liu, Zhang & Chen, 1982), *E. tangi* (Cheng et al., 2007), and *E. jianouensis* (Liu & Zhang, 1979). The present species can be distinguished by its unique combination of a thickened peristome and sub-ovate aperture morphology (Fig. 4C, D).

***Erhaia guizhouensis* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, sp. nov.**

<https://zoobank.org/CC298968-123C-408A-A269-2DFB5F36DD92>

Figs 4E, F, 5C

Material examined. Holotype: • NCUEG250201, shell height 2.06 mm (Fig. 5E), Lengshuihe River, Guiyang City, Guizhou Province, China, 26.9011°N, 106.8728°E (Fig. 1).

Paratypes: • 26 specimens, NCUEG250202–27, August 2023, shell height 1.68–2.13 mm, collected by Xiao Bo Qian, locality and habitat same as holotype.

Diagnosis. Shell small, white, ovoid in shape. Aperture nearly circular, with a thick tooth on the columella.

Description. Shell small, white, ovoid; five convex whorls separated by a deep suture. Surface with fine, irregular growth lines. Peristome continuous and thickened. Without umbilical chink. Apex usually eroded and obtuse (Fig. 4E, F). Aperture relatively large, nearly circular, with a thick tooth on the columella, tooth surrounding the entire body whorl of the columella (Fig. 5C).

Etymology. The species name “guizhouensis” refers to Guizhou Province, where the species was discovered. The Chinese name is “贵州洱海螺” (Guizhōu Ērhǎi Luó).

Biology. This species inhabits mountain springs and streams, often attaching to stone on the riverbed, where it occurs in high densities. It avoids deep water and is typically found in slow-moving water at depths of 0–30 cm. Its distribution is recorded at elevations of around 1,200 m.

Remarks. *E. guizhouensis* sp. nov. differs from *E. bailong* sp. nov., *E. liui*, *E. shimenensis*, and *E. tangi* in having fewer whorls, a nearly circular aperture, and lacking periostracal ridges on the shell surface.

***Erhaia xiaoboqiani* H. Chen, Y.-M. He, H.-Q. Xiang & X.-P. Wu, sp. nov.**

<https://zoobank.org/4BE51D3D-231D-4632-8B5C-CB42B160735A>

Figs 4G, H, 5D

Material examined. Holotype: • NCUEX250301, shell height 1.82 mm (Fig. 4G), Zijiangdifeng, Guiyang City, Guizhou Province, China, 26.9078°N, 107.0533°E (Fig. 1).

Paratypes: • 16 specimens, NCUEX250302–17, August 2023, shell height 1.68–1.94 mm, collected by Xiao Bo Qian, locality and habitat same as holotype.

Diagnosis. Shell small, greyish-white, conical in shape. Aperture nearly circular, featuring a triangle, thick tooth on the columella.

Description. Shell small, white, ovoid, consisting of six convex whorls separated by a deep suture. Shell surface exhibits fine irregular growth lines and periostracal ridges. Apex usually eroded and obtuse. Peristome continuous and thickened. Without umbilical chink (Fig. 4G, H). Aperture nearly circular, featuring a triangle, thickened tooth on the columella that extends around the entire body whorl (Fig. 5D).

Etymology. The species name “xiaoboqiani” is derived from the name of “Qianxiaobo,” the discoverer of the species. The suggested Chinese common name is “钱氏洱海螺” (Qiánsǐ Ērhǎi Luó).

Biology. This species inhabits mountain springs and streams, often attaching to stones on the riverbed, with a lower density. It does not prefer deep water and is typically found in slow-moving water at depths of 0–30 cm. Its distribution is recorded at elevations of around 1,100 m.

Remarks. *E. xiaoboqiani* sp. nov. differs from *E. bailong* sp. nov., *E. guizhouensis* sp. nov., *E. liui*, *E. shimenensis*, and *E. tangi* in having a more slender shell (W/H = 0.41, Table 3) and a triangular, thickened columellar tooth (Fig. 5D).

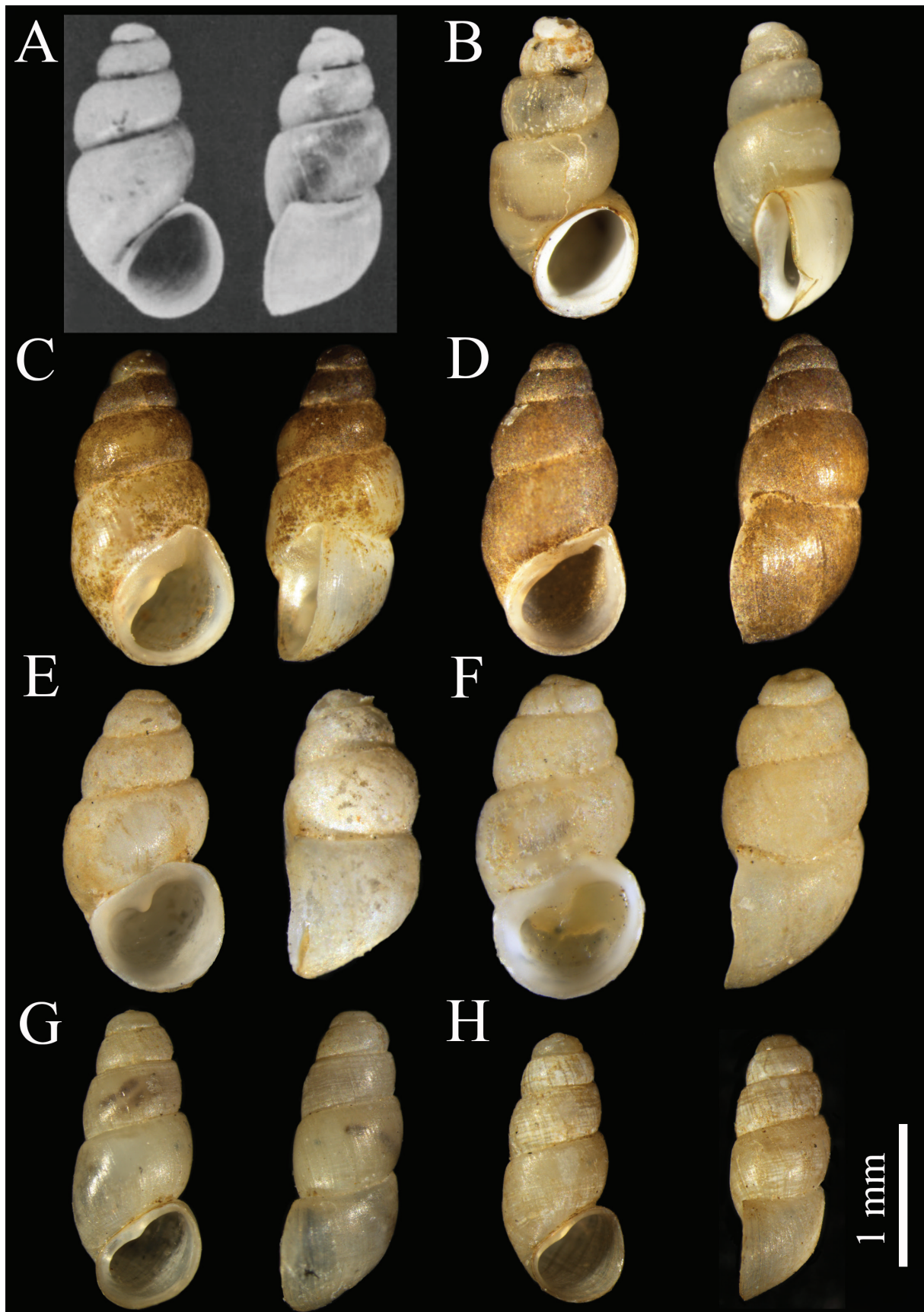


Figure 4. Species of *Erhaia*. **A.** Original figure of *E. daliensis* Davis & Kuo, 1985; **B.** *E. daliensis* NCUED250101; **C.** *E. bailong* sp. nov. holotype, NCUEB250101; **D.** *E. bailong* sp. nov. paratype, NCUEB250102; **E.** *E. guizhouensis* sp. nov. holotype, NCUEG250201; **F.** *E. guizhouensis* sp. nov. paratype, NCUEG250202; **G.** *E. xiaoboqiani* sp. nov. holotype, NCUEx250301; **H.** *E. xiaoboqiani* sp. nov. paratype, NCUEx250302.

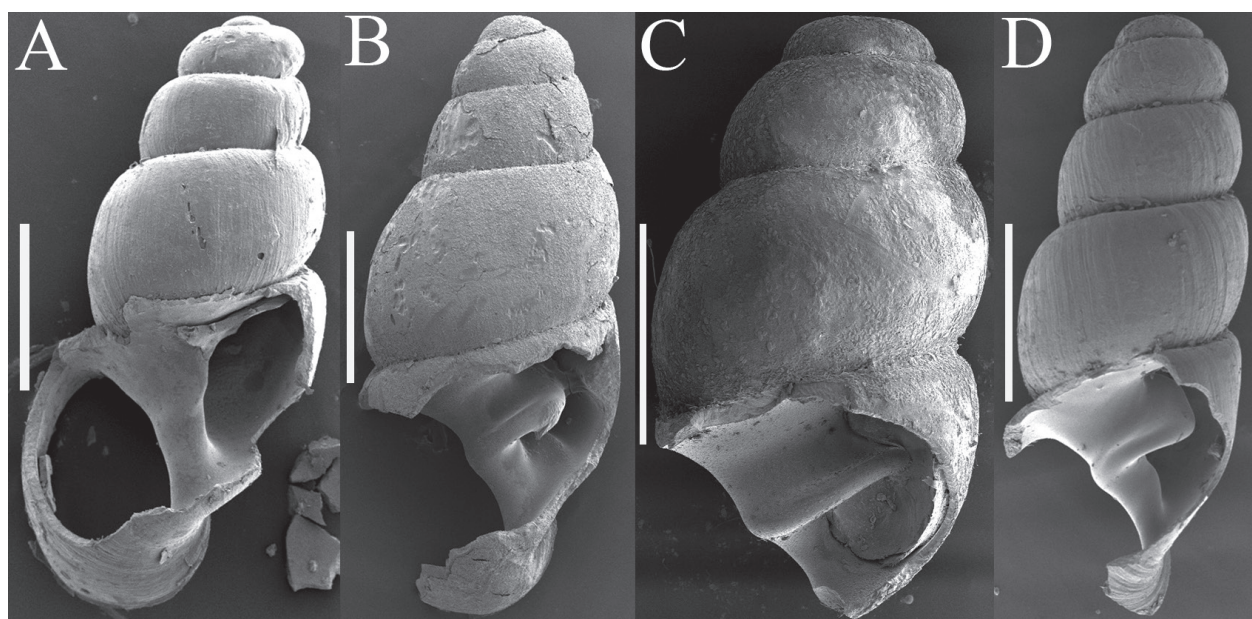


Figure 5. SEM photo of the *Erhaia* species with artificial breakage at the body whorl to expose columella teeth. **A.** *E. daliensis*; **B.** *E. bailong* sp. nov.; **C.** *E. guizhouensis* sp. nov.; **D.** *E. xiaoboqiani* sp. nov. Scale bars: 0.5 mm (A–D).

Table 3. Shell measurements. Values given are averages (minimum–maximum) of height (H) and width (W) of shell for N measured specimens.

	N	H (mm)	W (mm)	W/H
<i>E. bailong</i>	21	1.98 (1.75–2.14)	0.94 (0.85–1.02)	0.47 (0.41–0.55)
<i>E. guiyangensis</i>	27	1.84 (1.68–2.13)	0.94 (0.84–1.11)	0.51 (0.47–0.57)
<i>E. xiaoboqiani</i>	17	1.76 (1.68–1.94)	0.73 (0.63–0.88)	0.41 (0.37–0.52)

Discussion

The disjunct montane distribution of *Erhaia* species may reflect a freshwater “sky island” biogeographic pattern, in which high-elevation stream habitats function as isolated patches separated by uninhabitable lowland barriers. Species of this genus exhibit strict habitat specificity, occurring exclusively in mountain streams while being conspicuously absent from connected rivers at lower elevations. This pronounced habitat specificity, likely facilitated by the continued uplift of the Himalayas (Tada et al. 2016), appears to promote geographic isolation among *Erhaia* populations. The Wuyi Mountains, straddling the Jiangxi–Fujian border, constitute one of southeastern China’s most significant biogeographic barriers. Often referred to as the “Roof of Eastern China,” this mountain range exerts particularly strong isolating effects on freshwater species dispersal and diversification (Shih et al. 2011; Gao et al. 2019; Zhou et al. 2023). The uplift of the Wuyi Mountains (Zhou et al. 2006; Ni et al. 2021) played a pivotal role in driving the divergence of the two major clades within Erhaiidae. Notably, our current support for the sky island model derives primarily from the distributional concordance between *Erhaia*’s exclusive mountain stream occupancy and the physical isolation of these habitats by uninhabitable lowlands. Future studies incorporating broader sampling and more comprehensive analyses will be essential to substantiate these findings.

The taxonomy of *Erhaia* species presents dual challenges due to highly conserved shell morphology with limited diagnostic characters and a critical lack of molecular data for key taxa. This morphological uniformity has contributed to persistent uncertainties regarding the genus’ monophyly, which remains unresolved despite recent taxonomic revisions. Multiple molecular phylogenetic studies have consistently demonstrated that *Erhaia* does not form a monophyletic group, with *E. jianouensis* showing closer affinity to *Akiyoshia kobayashii* than to other *Erhaia* congeners (Gittenberger et al. 2017; Gittenberger et al. 2020; Gittenberger et al. 2022). These results fundamentally challenge the genus-level classification and necessitate a re-evaluation of diagnostic characters in light of molecular evidence. Notably, on the phylogenetic tree, *Erhaia* species with a columellar tooth do not form a distinct cluster. Compounding these taxonomic difficulties is the critical lack of available nucleotide sequences for several nominal species, leaving their true phylogenetic positions and taxonomic validity impossible to properly assess. Future studies should prioritize comprehensive sampling, multi-locus molecular data, and comparative microanatomical investigations to resolve these taxonomic uncertainties.

Despite their fascinating distribution patterns and morphological adaptations, *Erhaia* species face significant conservation challenges. In this study, some *Erhaia* species were found living under unfavorable conditions.

For example, during the search for *E. kunmingensis* Davis & Kuo, 1985, in Kunming, Yunnan Province, China, the streams and springs recorded in the literature had either dried completely or been converted into artificial ornamental fish ponds. No specimens were found, underscoring the urgent need for further research to identify potential distribution areas and reassess its conservation status. As specialized inhabitants of montane stream ecosystems, these snails are particularly vulnerable to environmental disturbances due to their strict habitat requirements and naturally fragmented distributions. Our discovery of three new *Erhaia* species on the Yunnan–Guizhou Plateau highlights the region’s remarkable yet threatened freshwater gastropod diversity. *Erhaia* may be among the first casualties of climate change and anthropogenic impacts in these fragile sky-island habitats. Our findings provide a critical foundation for understanding and conserving these ecologically vulnerable yet often overlooked freshwater microgastropods.

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