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Metzia parva, a new cyprinid species (Teleostei: Cypriniformes) from south China

WEN LUO¹, JOHN P. SULLIVAN², HAI-TAO ZHAO^{1,3} & ZUO-GANG PENG¹

¹Key Laboratory of Freshwater Fish Reproduction and Development (Ministry of Education), Southwest University School of Life Science, Beibei, Chongqing 400715, China. E-mail: pengzuogang@gmail.com

²Cornell University Museum of Vertebrates, 159 Sapsucker Woods Road, Ithaca, New York 14850 USA.

E-mail: jpsullivan@cornell.edu

³School of Ecological Engineering, Guizhou University of Engineering Science, Bijie, Guizhou 551700, China.

Abstract

A new species of a small cyprinid fish, *Metzia parva* sp. nov., is described here based on specimens collected from a tributary of Hongshui-He River in the Pearl River basin at Anyang Town, Du'an County, Guangxi Province, south China. It differs from congeners in having a smaller body with a standard length of 48.3–57.7 mm (vs. 58.3–151.4 mm in other species); a complete lateral line (although some specimens show interruptions on the ventral margin above the anal-fin); 12–14 branched anal-fin rays (vs. 10–11 or 15–20); 10 branched pectoral-fin rays (vs. 11–16); 6 branched pelvic-fin rays (vs. 7–9); a longer caudal peduncle (17.8–21.7% vs. 14.8–17.4% SL); a shorter preanal length (60.9–66.0% vs. 69.0–73.0% SL) and an obviously larger interorbital width (28.4–33.0% vs. 20.2–24.7% of head length). While *Metzia parva* shares a lateral black stripe from the gill opening to the caudal-fin base with *M. formosae*, the new species can be distinguished from *M. formosae* by a deeper head (16.4–19.2% vs. 13.3–15.7% SL) and a longer anal fin (15.4–18.9% vs. 10.0–13.6% SL) in addition to the diagnostic characters above. Kimura's 2-parameter genetic distance between the two species is 6.6% for the barcoding region of the mitochondrial COI gene and 7.3% across the complete mitochondrial genome.

Key words: Cypriniformes, Cyprinidae, *Metzia parva*, new species, Guangxi Province, China

Introduction

Metzia, established by Jordan and Thompson (1914) with *Acheilognathus mesembrinum* Jordan & Evermann (1902) as type species, has frequently been confused with *Rasborinus* Oshima (1920) as diagnostic characters used to differentiate the two genera are poorly defined (i.e., Berg 1932; Myers 1934; Chen *et al.* 1998; Kottelat 2001; Chen & Fang 2002). Here we follow Kottelat (2001) and consider *Metzia* Jordan and Thompson (1914) as a senior synonym of *Rasborinus* Oshima (1920). Gan *et al.* (2009) and Shibukawa *et al.* (2012) revised this genus to comprise seven species: *M. mesembrinum* (Jordan & Evermann 1902), *M. lineata* (Pellegrin 1907), *M. formosae* (Oshima 1920), *M. alba* (Nguyen 1991), *M. hautus* (Nguyen 1991), *M. longinasus* (Gan *et al.* 2009) and *M. bounthobi* (Shibukawa *et al.* 2012). The principal diagnostic characteristics of *Metzia* include a compressed body, an abdomen with a sharp keel between the pelvic-fin insertion and the anus, soft dorsal-fin rays with 3 unbranched and 7 branched rays, and a bipartite gas bladder with a rounded posterior chamber (Chen *et al.* 1998). Here we determine that *Metzia* specimens collected from Anyang Town, Du'an County, Guangxi Province, south China represent a new species that we describe as *Metzia parva*. In addition to morphological evidence, we present genetic evidence for the distinctiveness of this new species from a newly obtained complete mitochondrial genome sequence.

Materials and methods

Specimens used for morphological examination were fixed in 10% formalin. Counts and measurements were taken on the left side of specimens, and techniques followed Xie *et al.* (2003) and Gan *et al.* (2009) with the exception of predorsal scales as these were too indistinct to count accurately in our specimens. Measurements were made with a dial caliper and recorded to a tenth of a millimeter. Fin-rays and scales were counted using a stereomicroscope. Measurements are given as percentage of standard length (SL), and some subunits of head are expressed in proportions of head length (HL). Measurements included standard length (SL), body depth, head length (HL), head depth, head width, dorsal-fin length, pectoral-fin length, pelvic-fin length, anal-fin length, caudal-peduncle length, caudal-peduncle depth, predorsal length, prepectoral length, prepelvic length, preanal length, snout length, eye diameter, interorbital width, dorsal-fin ray count, anal-fin ray count, pectoral-fin ray count, pelvic-fin ray count, lateral-line scales, scale rows above lateral line, scale rows below lateral line and circumpeduncular scales (Table 1). We also cleared and stained several specimens to observe osteological features of vertebrae, pharyngeal teeth, and infraorbital bones, as well as dorsal & anal fins with their pterygiophores. In the description, meristics of the holotype are noted with an asterisk, and the frequency of each count is given in parentheses.

TABLE 1. Morphometric data for *Metzia parva*, *M. formosae* and *M. longinasus*.

	<i>M. parva</i> sp. nov.		<i>M. formosae</i> *	<i>M. longinasus</i> *
	Holotype	Paratype (n=11)	(n = 9)	(n = 7)
SL(mm)	57.6	48.3–57.7 (52.3 ± 3.1)	58.3–79.2 (68.0 ± 7.6)	65.6–151.4 (100.6 ± 27.0)
In % of SL				
Body depth	26.7	24.4–29.5 (27.7 ± 1.3)	25.1–28.9 (27.0 ± 1.5)	23.7–26.8 (25.2 ± 1.2)
Head length	25.1	23.3–26.8 (25.4 ± 0.9)	24.1–26.5 (25.0 ± 0.7)	27.2–30.8 (29.3 ± 1.4)
Head depth	17.1	16.4–19.2 (17.6 ± 0.8)	13.3–15.7 (14.8 ± 0.8)	17.7–19.3 (18.4 ± 0.7)
Head width	11.7	10.3–12.6 (11.6 ± 0.7)	8.9–10.6 (9.6 ± 0.6)	12.2–13.8 (13.1 ± 0.6)
Dorsal-fin length	24.6	19.8–26.2 (22.9 ± 1.8)	18.5–22.6 (20.7 ± 1.6)	23.2–26.8 (25.6 ± 1.4)
Pectoral-fin length	16.0	15.7–19.6 (17.7 ± 1.1)	17.7–23.4 (21.2 ± 1.7)	19.6–22.8 (21.4 ± 1.1)
Pelvic-fin length	15.8	14.8–16.9 (15.9 ± 0.7)	13.8–16.8 (15.6 ± 1.0)	19.0–20.8 (19.7 ± 0.6)
Anal-fin length	17.4	15.4–18.9 (17.1 ± 0.9)	10.0–13.6 (12.1 ± 1.1)	15.6–19.4 (18.0 ± 1.3)
Caudal-peduncle length	19.0	17.8–21.7 (19.4 ± 1.1)	14.8–17.4 (16.1 ± 1.1)	15.0–17.4 (16.0 ± 0.9)
Caudal-peduncle depth	9.8	8.2–11.0 (9.7 ± 0.8)	8.8–10.9 (10.1 ± 0.7)	8.7–11.1 (9.6 ± 0.9)
Predorsal length	56.3	53.6–57.2 (55.5 ± 1.1)	53.1–55.4 (54.1 ± 1.0)	53.3–57.7 (55.4 ± 1.5)
Prepectoral length	25.2	23.2–26.8 (25.0 ± 1.1)	22.1–26.0 (24.1 ± 1.3)	26.4–31.6 (28.8 ± 1.8)
Prepelvic length	43.8	41.3–46.7 (44.5 ± 1.4)	45.1–48.5 (47.2 ± 1.2)	43.8–49.0 (46.5 ± 1.6)
Preanal length	64.2	60.9–66.0 (63.6 ± 1.6)	69.4–73.0 (71.2 ± 1.2)	69.0–70.8 (70.3 ± 0.6)
In % of HL				
Snout length	30.4	23.9–31.2 (27.2 ± 2.4)	26.8–30.8 (29.1 ± 1.6)	31.7–37.0 (34.3 ± 1.8)
Eye diameter	29.0	26.2–31.8 (29.3 ± 1.8)	26.0–30.6 (28.3 ± 1.6)	23.1–27.4 (25.0 ± 1.4)
Interorbital width	29.8	28.4–33.0 (31.0 ± 1.8)	20.2–24.7 (22.7 ± 2.1)	23.5–29.4 (27.0 ± 2.0)
Dorsal-fin rays	iii, 7	iii, 7	iii, 7	iii, 7–8
Anal-fin rays	iii, 12	iii, 12–14	iii, 17–18	iii, 10–11
Pectoral-fin rays	i, 10	i, 10	i, 13–14	i, 11–12
Pelvic-fin rays	i, 6	i, 6	i, 8	i, 8–9
Lateral-line scales	40	40–44	43–44	43–44
Scale rows above lateral line	10	9–10	9	8–9
Scale rows below lateral line	4	4	4–5	5
Circumpeduncular scales	14	14–15	14–15	17–18

Each character presented as: range (mean ± standard deviation).

*Data for *M. formosae* and *M. longinasus* were obtained from Gan *et al.* (2009).

The complete mitochondrial genome sequence of *M. parva* was obtained following methods in Peng *et al.* (2006) and has been deposited in GenBank with accession number KF955011 (Ma & Luo 2014). Kimura's 2-parameter distances (K2P; Kimura 1980) and neighbor-joining (NJ) trees were calculated and reconstructed by using MEGA6 (Tamura *et al.* 2013) for the mitochondrial COI gene barcoding region as well as for the complete

mitochondrial genome sequences of *M. parva* and its Chinese congeners *M. formosae* (GenBank accession No. KF246550, Lin *et al.* 2013), *M. lineata*, (HM224187, mitochondrial COI gene segment only, Tang *et al.* 2010), *M. mesembrinum*, (KJ585802, Jang-Liaw *et al.* 2014), and *M. longinasus* (unpublished). *Myxocyprinus asiaticus* was selected as the outgroup. Specimens were deposited at the Southwest University School of Life Science (SWU) in Beibei, Chongqing, China, and the Cornell University Museum of Vertebrates (CUMV) in Ithaca, New York, U.S.A.

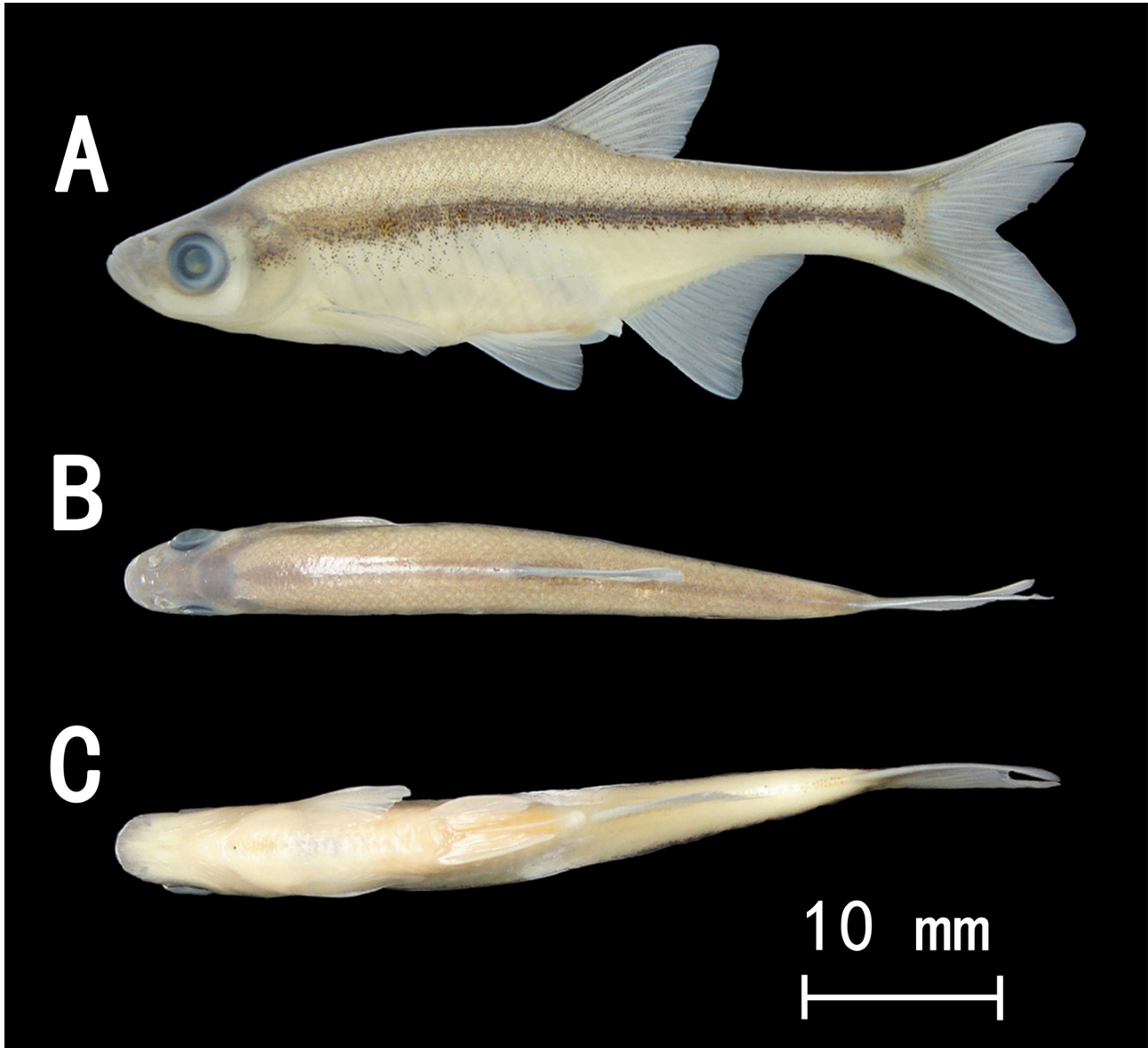


FIGURE 1. *Metzia parva* preserved in formalin (holotype, 57.6 mm SL, SWU 20140620012, Hongshui-He River of the Pearl River basin, Guangxi Province, south China). (A) Lateral, (B) dorsal, and (C) ventral views.

***Metzia parva*, new species (Fig. 1; Table 1)**

Holotype. SWU 20140620012, 57.6 mm SL, the Cheng-jiang River, a tributary flowing into Hongshui-He River of the Pearl River basin at Anyang Town, Du'an County, Guangxi Province, south China (23°93' N, 108°10' E), collected by J.H. Lan, November 2012.

Paratypes. (11) SWU 20140620005–20140620011, 48.3–54.2 mm SL, same data as holotype; CUMV 98211-98214, 51.1–57.7 mm SL, same data as holotype.

Diagnosis. The following characters distinguish *Metzia parva* from congeners: smaller body size with standard

length between 48.3–57.7 mm (vs. 58.3–151.4 mm); lateral line complete, but interrupted in some specimens along ventral margin above anal-fin; 12–14 branched anal-fin rays (vs. 10–11 or 15–20); 10 branched pectoral-fin rays (vs. 11–16); 6 branched pelvic-fin rays (vs. 7–9); longer caudal peduncle (17.8–21.7% vs. 14.8–17.4% SL); shorter preanal length (60.9–66.0% vs. 69.0–73.0% SL); interorbital width distinctly larger (28.4–33.0% vs. 20.2–24.7% HL).

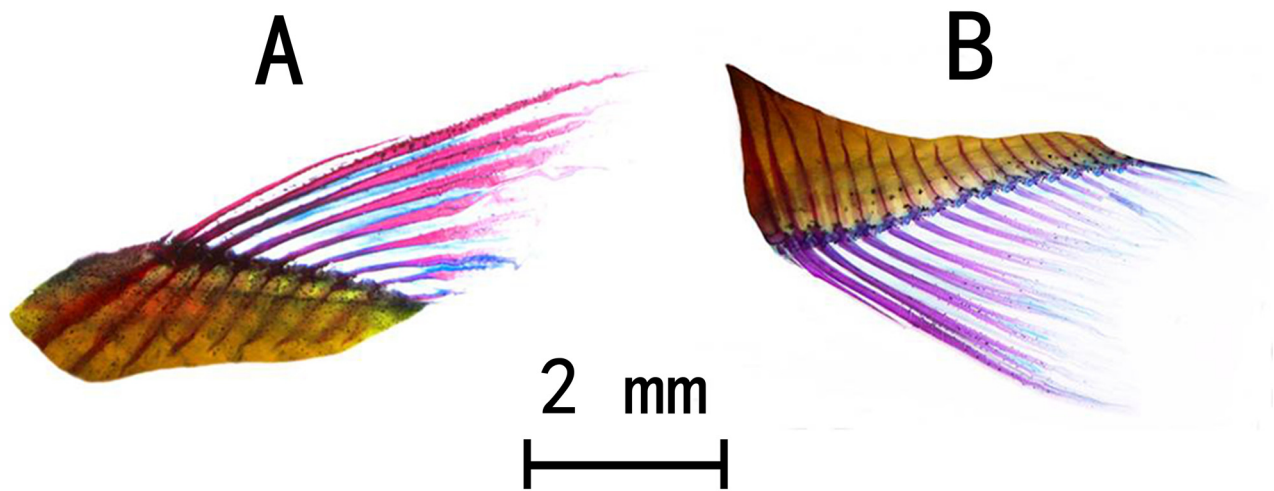


FIGURE 2. (A) Dorsal fin with pterygiophores and (B) anal fin with pterygiophores of *Metzia parva*.

Description. Morphological characteristics of the genus *Metzia* were presented by Chen *et al.* (1998) and Gan *et al.* (2009) and are not repeated herein. Morphometric data of the twelve type specimens are shown in Table 1. Dorsal-fin rays soft with 3 unbranched, 7* (12) branched rays (Fig. 2A), final ray split to base, fin slightly shorter than head length, origin located behind pelvic-fin insertion, nearer to caudal-fin base than to tip of snout, and nearer to vertical through anal-fin origin than to pelvic-fin origin; distal margin straight. Anal-fin with 3 unbranched, 12* (2) or 14 (10) branched rays (Fig. 2B), outer margin concave, nearer to pectoral-fin insertion than to caudal-fin base, origin opposite terminus of dorsal-fin base, distal margin slightly concave, anal-fin base 1.5–2.1 times greater than dorsal-fin base. Pectoral-fin arc-shaped, with 1 unbranched and 10* (12) branched rays, shorter than HL, tip not extending beyond pelvic-fin origin. Pelvic-fin with 1 unbranched and 6* (12) branched rays, its origin nearer to snout tip than to caudal-fin base, length approximately equal to pectoral fin and nearly reaching anus when depressed. Caudal-fin deeply bifurcated with 10 + 9* (2), or 9 + 8 (10) branched rays, tip of each lobe sharply rounded. Lateral line complete and difficult to observe, sharply deflected ventrally anterior to pelvic-fin origin, then running parallel with ventral profile and ending midlaterally below caudal-fin origin (however, 8 specimens of type series show interruptions on ventral margin above anal-fin). Lateral-line scales 40* (8), 43 (3), or 44 (1) with 2 or 3 scales basally at midlateral point of caudal-fin; scale rows above and below lateral line 10* (9) or 9 (3) and 4* (12), respectively. Circumpeduncular scales 14* (7) or 15 (5). Gill rakers on outer surface of first gill arch 14–16.

A small fish with standard length up to 57.7 mm. Body fusiform, compressed and moderately deep. Dorsal profile of head slightly concave, predorsal profile strongly convex/arched. Abdominal keel between pelvic-fin insertion and anus. Caudal-peduncle depth 46.1%–50.7% SL. Head short, compressed, length shorter than body depth. Snout rounded, short, size similar to eye diameter. Mouth sub-superior, oblique, lower jaw projecting beyond upper, corner of upper jaw extending beyond nostril, but not to anterior margin of eye. Eye large, positioned laterodorsally in anterior half of head, diameter slightly less than interorbital width, distance from posterior margin of eye to tip of snout greater than to posterior of operculum. Interorbital width broad, approximately 1.1 times eye diameter. Scales cycloid, scales on formalin-fixed specimens inconspicuous and difficult to count.

Five infraorbital bones with fifth fairly small, almost invisible (Fig. 3A). Pharyngeal teeth in three rows: 5, 3, 2 - 2, 3, 5 (Fig. 3B). Air bladder bipartite, posterior chamber 1.5 times longer than anterior chamber with rounded posterior end (Fig. 4A). Vertebrae 4 + 32.

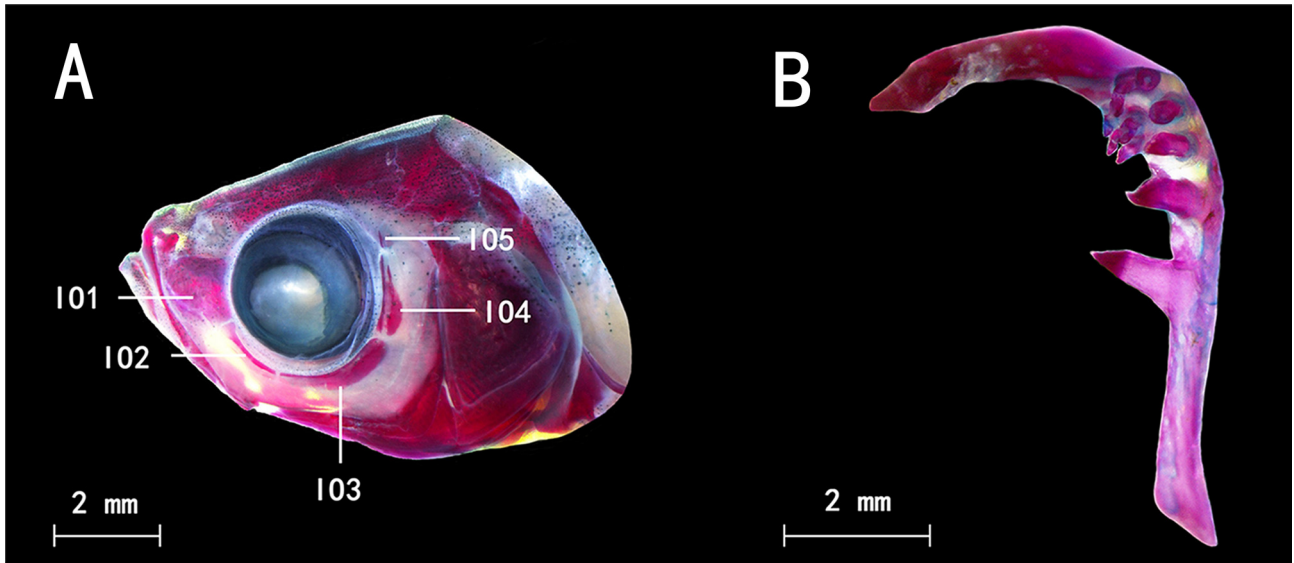


FIGURE 3. (A) Lateral view of infraorbital bones and (B) mesial view of pharyngeal tooth of *Metzia parva*. Abbreviation: IO, infraorbital.

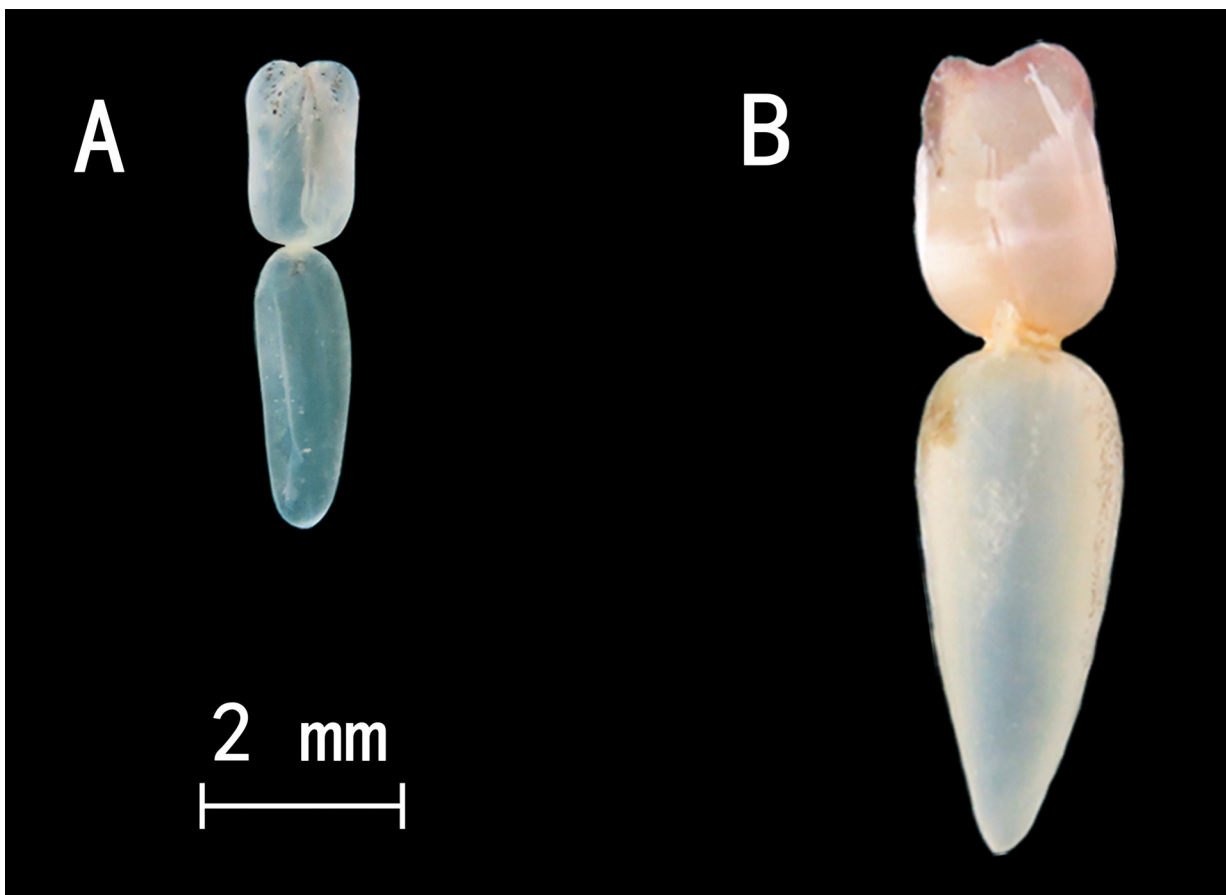


FIGURE 4. Gas bladder in ventral view of (A) *Metzia parva*, and (B) *M. longinasus* (SWU 20140325001, 74.1 mm SL).

Coloration in formalin. The preserved holotype specimen is shown in Fig. 1. Body pale-yellowish, darker above. All fins semi-translucent with fine black spots on fin spine. Black longitudinal stripe extends along side of body from posterior of operculum to caudal-fin base.

Distribution. Known from the Cheng-jiang River, a tributary flowing into Hongshui-He River of the Pearl River basin at Anyang Town, Du'an County, Guangxi Province, south China (23°92'N, 108°10'E, 161 meters altitude above sea-level, Fig. 5).

Reproduction. Females contained a large number of eggs. Reproductive system of males not examined closely, and no data are available on reproductive behavior.

Etymology. *Metzia parva* was named for its small body size with the Latin word *parva* (gender feminine) meaning small or little.

Comparative material. *Metzia longinasus*: SWU 20140325001–10, 10 type specimens, 74.10–128.50 mm SL, Hongshui-He River of the Pearl River, Guangxi Province, south China.

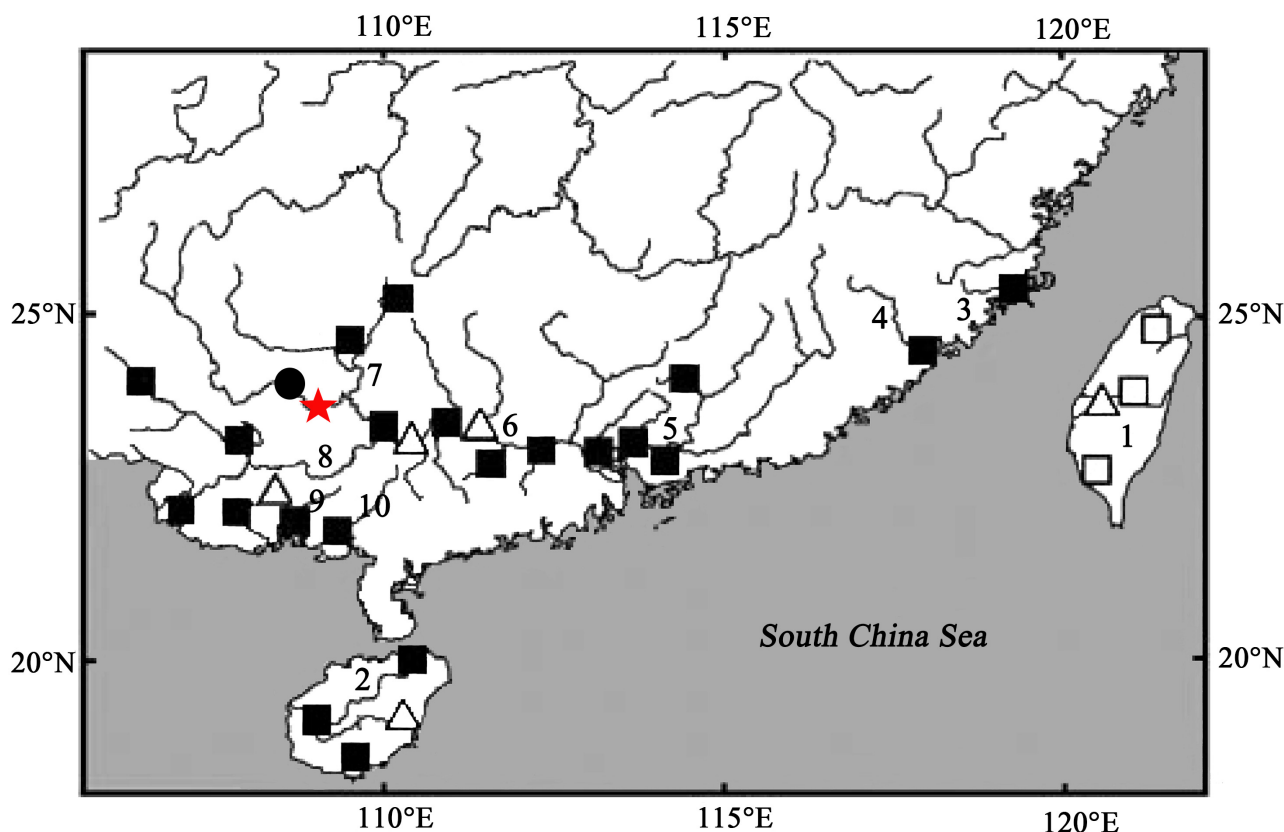


FIGURE 5. Distributions of *Metzia parva* (red star) and other Chinese species of *Metzia*: *M. longinasus* (filled circle), *M. formosae* (open triangle), *M. lineata* (filled square), and *M. mesembrinum* (open square). 1 Taiwan Island, 2 Hainan Island, 3 Jin-Jiang River, 4 Jiulong-Jiang River, 5 Dong-Jiang River, 6 Xi-Jiang River, 7 Liu-Jiang River, 8 Rong-Jiang River, 9 Qing-Jiang River, 10 Nanliu-Jiang River.

Discussion

Metzia parva was diagnosed and classified in the genus *Metzia* principally by means of the following generic characters: body compressed, abdomen with a sharp keel between the pelvic-fin insertion and anus, dorsal-fin rays soft and with 3 unbranched and 7 branched rays, gas bladder bipartite and the posterior chamber rounded (Chen *et al.* 1998), making it the fifth species of *Metzia* distributed in China. The other four are *M. mesembrinum*, *M. lineata*, *M. formosae* and *M. longinasus*. Two species, *M. alba* and *M. hautus*, are found in Vietnam, and *M. bounthobi* is found in Laos. *M. mesembrinum* is endemic to Taiwan and has recently been designated as endangered (Chen *et al.* 2013). Chen and Fang (2002) distinguished *M. mesembrinum* from *M. lineata* and considered it as endemic to Taiwan. After reviewing descriptions of the widely distributed *M. lineata* in the literature (Pellegrin 1907, Chu and Chen 1989, Nguyen and Ngo 2001) and examining specimens, Gan *et al.* (2009) thought this species should be split into two; for the time being its status remains unclear. There is less doubt about *M. formosae* and two other newly described species: *M. longinasus* (Gan *et al.* 2009) and *M. bounthobi*

(Shibukawa *et al.* 2012). While their descriptions were not available to us, *M. alba* and *M. hautus* from northern Vietnam were regarded as valid by Gan *et al.* (2009) who compared these two species with *M. lineata* and *M. longinasus* using characters described in Nguyen (1991), Nguyen and Ngo (2001) and Kottelat (2001).

TABLE 2. The K2P genetic distances between species of *Metzia* based on sequences of the mitochondrial COI gene barcoding region.

	<i>Metzia parva</i>	<i>M. formosae</i>	<i>M. longinasus</i>	<i>M. mesembrinum</i>
<i>Metzia parva</i>				
<i>M. formosae</i>	0.066			
<i>M. longinasus</i>	0.082	0.107		
<i>M. mesembrinum</i>	0.112	0.119	0.112	
<i>M. lineata</i>	0.107	0.119	0.105	0.023

Metzia parva can be easily distinguished from its congeners by its small size and several other characters (Table 1). Fig. 4 shows a comparison of the gas bladders of *M. parva* and *M. longinasus*. Besides the difference in their sizes, the bladder of *M. parva* has a rounded distal end (Fig. 4A) while that of *Mt. longinasus* is pointed (Fig. 4B). *Metzia parva* is morphologically similar to *M. formosae* in having a lateral black stripe extending from the gill opening to the caudal-fin base. However, *M. parva* has a greater head depth (16.4–19.2% vs. 13.3–15.7% SL) and a longer anal-fin length (15.4–18.9% vs. 10.0–13.6% SL). When compared with *M. mesembrinum*, *M. parva* has fewer pectoral-fin rays (10 vs. 14–15), more lateral-line scales (40–44 vs. 35–39) and a subsuperior (vs. terminal) mouth. Fin-ray counts distinguish *M. parva* from *M. lineata* and *M. bounthobi*: anal-fin rays 12–14 (vs. 15–20), pectoral-fin rays 10 (vs. 12–16) and pelvic-fin rays 6 (vs. 7–8). Although there is little information available for *M. alba* and *M. hautus*, based on their descriptions in Kottelat (2001) *M. parva* can be distinguished from these two species by more numerous lateral-line scales (40–44 vs. 35–37) and a snout close in length to its eye diameter (vs. snout longer than eye diameter). COI K2P genetic distances (Table 2) show less differentiation between *M. parva* and *M. formosae* (6.6%) than between *M. parva* and its other Chinese congeners: *M. longinasus* (8.2%), *M. mesembrinum* (11.2%) and *M. lineata* (10.7%). Across the entire mitochondrial genome, *M. parva* differs from *M. formosae* by 7.3% K2P distance vs. 8.8% from *M. longinasus* and 9.4% from *M. mesembrinum* (Table 3). Neighbor-joining (NJ) trees with these data also place *M. parva* and *M. formosae* together with respect to the other Chinese species of *Metzia* with moderate to high bootstrap values: 79% for the mitochondrial COI gene barcoding region (Fig. 6A) and 100% for the complete mitochondrial genome sequences (Fig. 6B).

TABLE 3. The K2P genetic distances between species of *Metzia* based on complete mitochondrial genome sequences.

	<i>Metzia parva</i>	<i>M. formosae</i>	<i>M. longinasus</i>
<i>Metzia parva</i>			
<i>M. formosae</i>	0.073		
<i>M. longinasus</i>	0.088	0.093	
<i>M. mesembrinum</i>	0.094	0.102	0.102

The species in genus *Metzia* were divided into two subgroups by Gan *et al.* (2009). The *mesembrinum*-like group included *M. mesembrinum*, *M. lineata*, *M. alba* and *M. hautus*, and the *formosae*-like group included *M. formosae* and *M. longinasus*. Members of the former group have 35–39 lateral-line scales and a terminal mouth while the latter have 43–48 lateral-line scales and a superior mouth. However, the recently discovered *M. bounthobi* (Shibukawa *et al.* 2012) has 49–55 lateral-line scales with a terminal mouth, and *M. parva* has 40–44 lateral-line scales with a superior mouth. Clearly, the divisions by Gan *et al.* (2009) require reassessment, and further work is needed to explore the monophyly and phylogeny of this group of fishes (Wang *et al.* 2007; Tang *et al.* 2010, 2013).

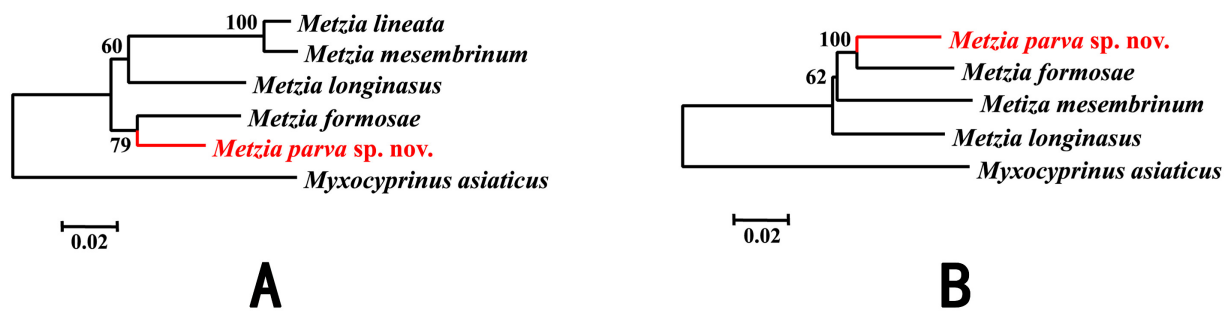


FIGURE 6. Neighbor-joining (NJ) trees of species of *Metzia* based on (A) the mitochondrial COI gene barcoding region, and (B) complete mitochondrial genome sequences. Bootstrap values are shown at the nodes.

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References

- Berg, L.S. (1932) Note on the genera *Metzia* and *Rasborinus*. *Copeia*, 1932, 156.
<http://dx.doi.org/10.2307/1436076>
- Chen, I.S. & Fang, L.S. (2002) Redefinition of a doubtful cyprinid, *Acheilognathus mesembrinum* Jordan and Evermann, 1902, with replacement in the valid genus, *Metzia* Jordan and Richardson, 1914, a senior synonym of the genus *Rasborinus* Oshima, 1920. *Journal of the Fisheries Society of Taiwan*, 29, 73–78.
- Chen, I.S., Weng, C.J., Chen, Y.R., Huang, S.P., Wen, Z.H., Jang-Liaw, N.H. & Tsai, T.H. (2013) The checklist of inland-water and mangrove fish fauna of Kinmen Island, Fujian Province, Taiwan with comments on ecological conservation of native fishes. *Journal of Marine Science and Technology*, 21, 316–319.
- Chen, Y.Y., Chu, X.L., Luo, Y.L., Chen Y.R., Liu, H.Z., He, M.C., Chen, W., Yue, P.Q., He, S.P. & Lin, R.R. (1998) *Fauna Sinica. Osteichthyes. Cypriniformes II*. Science Press, Beijing, 118 pp.
- Chu, X.L. & Chen, Y.R. (1989) *The fishes of Yunnan, China. Part I. Cyprinidae*. Science Press, Beijing, 377 pp.
- Gan, X., Lan, J.H. & Zhang, E. (2009) *Metzia longinasus*, a new cyprinid species (Teleostei: Cypriniformes) from the Pearl River drainage in Guangxi Province, South China. *Ichthyological Research*, 56, 55–61.
<http://dx.doi.org/10.1007/s10228-008-0085-7>
- Jang-Liaw, N.H., Wen, Z.H. & Chen, I.S. (2014) The complete mitochondrial genome of the Kinmen's population of endangered minnow *Metzia mesembrinum* (Cypriniformes, Cyprinidae) from Taiwan. *Mitochondrial DNA*. [published online]
<http://dx.doi.org/10.3109/19401736.2014.908374>
- Jordan, D.S. & Evermann, B.W. (1902) Notes on a collection of fishes from the island of Formosa. *Proceedings of the United States National Museum*, 25, 315–368.
<http://dx.doi.org/10.5479/si.00963801.25-1289.315>
- Jordan, D.S. & Thompson, W.F. (1914) Record of the fishes obtained in Japan in 1911. *Memoirs of the Carnegie Museum*, 6, 205–313.
- Kimura, M. (1980) A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution*, 16, 111–120.
<http://dx.doi.org/10.1007/BF01731581>
- Kottelat, M. (2001) *Freshwater fishes of northern Vietnam. A preliminary check-list of the fishes known or expected to occur in northern Vietnam with comments on systematics and nomenclature*. Environment and Social Development Unit, East Asia and Pacific Region, The World Bank, Washington, D.C., iii + 123 + 18 pp., 15 pls.
- Lin, H.D., Lin, F.J., Chiang, T.Y. & Lee, T.W. (2015) The complete mitochondrial genome sequence of *Metzia formosae* (Cypriniformes, Cyprinidae). *Mitochondrial DNA*, 26 (2), 257–258.

- <http://dx.doi.org/10.3109/19401736.2013.823187>
- Ma, Q.Q., & Luo, W. (2014) The complete mitochondrial genome of a cyprinid fish; *Metzia longinasus* (Teleostei, Cypriniformes). *Mitochondrial DNA*. [published online]
<http://dx.doi.org/10.3109/19401736.2013.879652>
- Myers, G.S. (1934) Corrections of the type localities of *Metzia mesembrina*, a Formosan cyprinid, and of *Othonocheirodus eigenmanni*, a Peruvian Characin. *Copeia*, 1934, 43.
<http://dx.doi.org/10.2307/1436438>
- Nguyen V.H. & Ngo S.V. (2001) *Cá'u'ò'c ngot Việt Nam. Tập I. Ho cá chép (Freshwater fishes of Vietnam. Vol. I. Family Cyprinidae)*. Agriculture Publish House, Hanoi, 622 pp.
- Nguyen, T.T. (1991) Giông *Rasborinus* Oshima 1920 (Pisces: Cyprinidae) (New members of the genus *Rasborinus* Oshima, 1920 in the Lam River). *Tap Chi Thuy San*, 1991, 32–36.
- Oshima, M. (1920) Notes on freshwater fishes of Formosa, with descriptions of new genera and species. *Proceedings of the Academy of Natural Sciences of Philadelphia*, 72, 120–135.
- Pellegrin, J. (1907) Missions permanente Française en Indo-Chine Poissons du Tonkin. *Bulletin du Musee d'Histoire Naturelle de Paris*, 13, 499–503.
- Peng, Z.G., Wang, J. & He, S.P. (2006) The complete mitochondrial genome of the helmet catfish *Cranoglanis boudierius* (Siluriformes: Cranoglanididae) and the phylogeny of otophysan fishes. *Gene*, 376, 290–297.
<http://dx.doi.org/10.1016/j.gene.2006.04.014>
- Shibukawa, K., Phousavanh, P., Phongsa, K. & Iwata, A. (2012). A new species of *Metzia* (Cypriniformes: Cyprinidae) from Northern Laos. *Zootaxa*, 3586, 264–271.
- Tamura, K., Stecher, G., Peterson, D., Filipiński, A. & Kumar, S. (2013) MEGA6: molecular evolutionary genetics analysis version 6.0. *Molecular Biology and Evolution*, 30, 2725–2729.
<http://dx.doi.org/10.1093/molbev/mst197>
- Tang, K.L., Agnew, M.K., Hirt, M.V., Sado, T., Schneider, L.M., Freyhof, J., Sulaiman, Z., Swartz, E.R., Vidthayanon, C., Miya, M., Saitoh, K., Simons, A.M., Wood, R.M. & Mayden, R.L. (2010) Systematics of the subfamily Danioninae (Teleostei: Cypriniformes: Cyprinidae). *Molecular Phylogenetics and Evolution*, 57, 189–214.
<http://dx.doi.org/10.1016/j.ympev.2010.05.021>
- Tang, K.L., Lumbantobing, D.N. & Mayden, R.L. (2013) The phylogenetic placement of *Oxygastervan* Hasselt 1823 (Teleostei: Cypriniformes: Cyprinidae) and the taxonomic status of the family-group name *Oxygastrinae* Bleeker 1860. *Copeia*, 2013, 13–22.
<http://dx.doi.org/10.1643/CG-10-121>
- Wang, X.Z., Li, J.B. & He, S.P. (2007) Molecular evidence for the monophyly of East Asian groups of Cyprinidae (Teleostei: Cypriniformes) derived from the nuclear recombination activating gene 2 sequences. *Molecular Phylogenetics and Evolution*, 42, 157–170.
<http://dx.doi.org/10.1016/j.ympev.2006.06.014>
- Xie, Z.G., Xie, C.X. & Zhang, E. (2003) *Sinibrama longianalis*, a new cyprinid species (Pisces: Teleostei) from the upper Yangtze River basin in Guizhou, China. *Raffles Bulletin of Zoology*, 51, 403–411.