



## *Parapercis lutevittata*, a new cryptic species of *Parapercis* (Teleostei: Pinguipedidae), from the western Pacific based on morphological evidence and DNA barcoding

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### Abstract

*Parapercis lutevittata* **sp. nov.**, a new cryptic species closely related to *Parapercis sexfasciata* (Temminck & Schlegel, 1843), is described from the western Pacific Ocean off Japan and Taiwan based on morphological and molecular evidences. It differs from congeners by having four to five large V-shaped transverse dark-brown bands over the upper side of the body, dorsal fin between the spinous and soft-rayed portions without a prominent notch, a large dark-brown blotch on the pectoral fin base, a large black spot over the caudal fin base, and a dark vertical band below the eye. The new species differs from its sympatric species *P. sexfasciata* in having an additional numerous small black dots on the base of the pectoral fin (versus with only a single large dark blotch in *P. sexfasciata*), small black dots scattered on area between the V-shaped transverse bands, absence of black spots on the base of the dorsal fin ray membrane, and one longitudinal yellow stripe on body sides when in fresh. In addition, the 633 base pairs of the mitochondrial cytochrome *c* oxidase subunit I (CO I or COX I) gene in DNA barcoding showed a deep 7.9% genetic divergence between these two similar species. The Neighbor-joining algorithm also revealed that the specimens of these two species are clearly separated.

**Key words:** *Parapercis lutevittata* **sp. nov.**, CO I, COX I, DNA barcoding, Pinguipedidae, cryptic species

### Introduction

The perciform sandperch family Pinguipedidae was formally known as the Parapercidae or Mugiloididae (Rosa & Rosa, 1987; Randall, 2001, 2008). The family includes 79 species of 7 genera (Ho & Shao, 2010). *Parapercis* Bleeker, 1863, is the largest genus in the family, currently comprises 71 valid species (Johnson, 2006; Randall & Yamakawa, 2006; Randall, 2008; Randall *et al.* 2008; Ho & Shao, 2010). The early revision works on this genus have been done by researchers (Cantwell, 1964; Randall, 1984). Randall (2001) listed 22 species of *Parapercis* from the central and western Pacific. Shimada (2002) included 23 species, and recent new species brought to a total of 27 species in Japan (Randall & Yamakawa, 2006; Randall, 2008; Randall *et al.* 2008). Ho and Shao (2010) added one new species from Taiwan. The increasing number of new species of *Parapercis* indicates the potential for discovering new species (Randall *et al.* 2008).

*Parapercis* is characterized by ctenoid and cycloid scales on the head and abdomen, the upper and lower jaws with a row of curved canines, a band of villiform teeth in the front of the upper jaw, pelvic fins slightly in front of the pectoral fins, four or five dorsal spines and 19–25 soft rays, a truncate or emarginated caudal fin, and one spine on the opercle (Cantwell, 1964; Randall *et al.* 2008).

Within the genus, *Parapercis sexfasciata* (Temminck & Schlegel, 1843) can be distinguished from congeners by having the following characters: dorsal fin between the spinous and soft-rayed portion without a prominent notch, four to five large V-shaped dark-brown bands over the upper side of the body, a large deep-brown or black blotch on the pectoral fin base, one large black spot over the caudal fin base, and a dark vertical band below the eye (Kai *et al.* 2004). It inhabits the sublittoral zone on soft bottoms (Froese & Pauly, 2010) and is distributed from Japan to Taiwan (Shimada, 2002). It was also recorded in Indonesia (Gloerfelt-Tarp & Kailola, 1984). However,

Kai *et al.* (2004) mentioned two sympatric morphotypes of *P. sexfasciata* in Tosa Bay, southern Japan. Their analysis was based on the mitochondrial control region sequences which suggested two different species. Kuo (2007) also indicated the distinction between these two morphotypes from Taiwan in the phylogenetic study of the Pinguipedidae. These authors all suggested to treat these two morphotypes as different species, but none provided detailed descriptions of them or formally selected a name for the new species.

Recently, the DNA barcoding using the 5' region of the mitochondrial cytochrome *c* oxidase subunit I gene (CO I or COX I) as a molecular tool, was recommended by Hebert *et al.* (2003) to help identify uncertain species. Fish taxonomists are increasingly describing new species by combining DNA barcoding with morphological evidence (Victor, 2007, 2008, De Astarloa *et al.* 2008, Pyle *et al.* 2008). In this study, we describe a new species, *P. lutevittata* **sp. nov.**, from the western Pacific Ocean by using both the morphological data and DNA barcoding.

## Material and methods

The Taiwanese specimens examined are deposited in the Biodiversity Research Museum, Academia Sinica, Taipei (ASIZP) and United States National Museum of Natural History, Washington, DC (USNM). The Japanese specimens were loaned from the Laboratory of Marine Biology, Faculty of Science, Kochi University, Kochi, Japan (BSKU).

**Morphology.** The meristic and morphometric characters are listed in Table 1. The length of specimens is given as standard length (SL). Measurements followed Randall (2008) and were made with dial calipers to the nearest 0.1 mm. Proportional measurements were expressed as percent SL.

**Genetics.** Tissue samples of white muscle from caudal peduncle were cut and stored in 95% ethanol at 4 °C for the genetic analysis. Total DNA was extracted using the Genomic DNA Mini Kit (Geneaid, Taipei, Taiwan), then approximately 650 base pairs (bp) of the COX I gene was amplified using the primer pair FishF2 (5'TCGACTAATCATAAAGATATCGGCAC3') and FishR2 (5'ACTTCAGGGTGACCGAAGAATCAGAA3') (Ward *et al.* 2005), and other primers which amplified the mitochondrial control region, following Kai *et al.* (2004). A polymerase chain reaction (PCR) was carried out using a thermal cycler (BIO-RAD, Philadelphia, PA, USA) in 25- $\mu$ l reaction volumes containing 100 ng total DNA, 1  $\mu$ M of each primer, 0.4 mM dNTP, 1x reaction buffer, and 0.5 U of Taq polymerase (Genomics, Taipei, Taiwan) with denaturation at 94 °C for 4 min; this was followed by 35 cycles of denaturing at 94 °C for 30 s, annealing at 50 °C for 30 s, and extension at 72 °C for 50 s, with a final extension at 72 °C for 9 min. The PCR products were then sequenced bidirectionally and analyzed on an ABI3730XL model (Applied Biosystems, Foster City, CA, USA). The sequences were deposited in BOLD and GenBank under accession numbers FN677936-50.

All sequences were aligned and edited with CLUSTAL X vers. 1.81 (Thompson *et al.* 1997). A phylogenetic tree was constructed by the neighbor-joining (NJ) method and evaluated by 10,000 bootstrapping replications (Fleckenstein, 1985) using MEGA 3.1 (Kumar *et al.* 2004). Nucleotide genetic distances, the Kimura two-parameter distance (K2P), and between and within species comparisons were also calculated using MEGA 3.1.

## Results

### *Parapercis lutevittata* sp. nov.

New English name: Yellow-striped sandperch.

(Figs. 1, 2, 4A, Table 1)

*Parapercis sexfasciata* (not of Temminck & Schlegel, 1843) —Shen, 1984:114, pl. 114, fig. 371-1 (Taiwan); Shen, 1993:487, pl.164, fig. 9 (Taiwan); Kai *et al.*, 2004:381–385, fig. 1A (morphotype A) (Japan).

*Parapercis ommatura* (not of Jordan & Snyder, 1902)—Prokofiev, 2008:882–884, fig. 4b–d (Nha Trang Bay).

**Holotype.** ASIZP 0071627, 140.9 mm SL, male, Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, ca. 200 m depth, 6 June 2009.

**Paratypes.** 14 specimens from Taiwan: Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, no depth data: ASIZP 0071628, 4 specimens, 103.5–150.4 mm SL, 24 Apr. 2009; ASIZP 0071629, 7 specimens,

123.2–151.3 mm SL, 6 May 2009; ASIZP 0071630, 92.3 mm, 30 June 2009; USNM 398144, 2 specimens, 127.2–140.2 mm SL, 24 Apr. 2009. Another 10 specimens from Japan: BSKU 058458, 136.5 mm SL, 25 Apr. 2002; BSKU 064089, 148 mm SL, 16 Apr. 2003; BSKU 065030, 124 mm SL, 3 Apr. 2003; BSKU 066627, 96.5 mm SL, 23 Oct. 2003; BSKU 067610, 117.6 mm SL, 16 Apr. 2003; BSKU 070401, 118.7 mm SL, 3 Apr. 2004; BSKU 071738, 130.5 mm SL, 8 Mar. 2004; BSKU 074193, 135 mm SL, 13 Jan. 2005; BSKU 078374, 117 mm SL, 23 Apr. 2006, Tosa Bay, bottom trawl, no depth data; BSKU 075967, 101 mm SL, 33°20.6'N–33°19.2'N, 133°35.6'E–133°35.0'E otter trawl, R/V *Kotaka-maru*, St.1-1, 17 Jan. 2005.

Other specimens: ASIZP0054586, 2 specimens, 83–93 mm SL, 9 May, 1971, ASIZP 0060347, 2 specimens, 107–126 mm SL, 10 Jul. 1990, Tungkang, Pintung County, southwestern Taiwan, bottom trawl, no depth data; ASIZP 0055620, 3 specimens, 81–96 mm SL, Kaohsiung, southwestern Taiwan, bottom trawl, no depth data, 8 Aug. 1980. ASIZP 0062350, 3 specimens, 79–133 mm SL, off Xingda Harbor, Kaohsiung County, southwestern Taiwan, commercial bottom trawl, 100m depth, 1 Nov, 2001. ASIZP 0054778, 77 mm SL, Anpin, Tainan County, southwestern Taiwan, bottom trawl, no depth data, 1 Jan. 1976. ASIZP 0061025, 124 mm SL, off Jinshan, Taipei County, northern Taiwan, commercial bottom trawl, 23 Oct. 2000. ASIZP0061222, 2 specimens, 54–120 mm SL, off Jinshan, Taipei County, northern Taiwan, commercial bottom trawl, 100m depth, 23 Oct 2000. ASIZP 0058698, 101 mm SL, Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, no depth data, 27 Oct. 1997. ASIZP 0061101, 5 specimens, 66–109 mm SL, off Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, 100m depth, 1 Dec. 2000. ASIZP0061114, 4 specimens, 102–150 mm SL, off Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, 50 m depth, 1 Dec. 2000. ASIZP 0061526, 135 mm SL, off Tashi, Ilan County, northeastern Taiwan, 100 m depth, 1 Dec, 2000. ASIZP 0066583, 113 mm SL, Nanfangao, Ilan County, northeastern Taiwan, commercial bottom trawl, no depth data, 1 Oct. 2005.



**FIGURE 1.** Holotype of *Parapercis lutevittata* sp. nov., ASIZP0071627, 135 mm SL, male, from Tashi, Ilan County, northeastern Taiwan. (A) Fresh condition; (B) preserved condition in alcohol.

**Diagnosis.** The new species of *Parapercis* with dorsal rays IV–VI (mostly V), 23–24; anal rays I, 19–21; pectoral rays 16–17; lateral-line scales 64–70; gill rakers 13–16. Greatest body depth 4.6–5.9 in SL; head length 3.5–3.9 in SL; orbit diameter 3.0–3.9 in head length; fifth dorsal spine longest, 3.0–3.8 in head length; posterior margin of caudal fin rounded; pectoral fins 4.2–5.2 in SL; pelvic fins just reaching anus, 4.2–5.6 in SL. Lower jaw projecting; palatine teeth present; vomerine teeth stout; scales on body, abdomen and cheek ctenoid; margin of opercle with a distinct sharp spinemostly single pore on lower margin of anterior preopercle.

With four to five large V-shaped dark-brown transverse bands over the upper side of the body; numerous black dots scattered on and between the V-shaped transverse bands, around pectoral fin, and at pectoral fin base; dorsal fin between the spinous and soft-rayed portion without a prominent notch, membrane between 1–4 spines with prominent black blotch; a dark vertical band below eye; a large deep-brown or black blotch on the pectoral fin base, and a large black spot over the caudal fin base; one irregular diffused longitudinal yellow stripe along the middle body when fresh.

**Description.** Measurements and counts are as shown in Table 1. Dorsal rays V, 24 (IV–VI, 23–24); anal rays I, 20 (I, 19–21); all dorsal and anal rays branched; pectoral rays 17 (16–17); pelvic fin rays I, 5; caudal rays 15 branched, additional unbranched rays on both upper and lower margin; lateral-line scales 66 (60–69) with 4 (3–6) additional scales on caudal fin base; scales above lateral line to middle of dorsal fin 9; scales below lateral line to origin of anal fin 19; median predorsal scales 9; circumpeduncular scales 26 (26–30); gill rakers 5+8=13 (5 or 6+8–10=14–16); pseudobranchial filaments 12 (12 or 13); branchiostegal rays 6; vertebrae 10+22 (rarely 21)=32.

**TABLE 1.** Meristic and morphometric data (in mm) of *Parapercis lutevittata* and *P. sexfasciata*.

	Holotype		Paratypes (n=24)		<i>P. sexfasciata</i> (nontype, n=27)		
	ASIZP 0071627		Mean	SD	Mean	SD	
SL (mm)	135	87.1–138.1			115–158.8		
Dorsal-fin rays	V, 23	IV–VI, 23–24			V, 22–23		
Anal-fin rays	I, 20	I, 19–21			I, 19–20		
Pectoral-fin rays	17	16–17			16–17		
Pelvic-fin rays	I, 5	I, 5			I, 5		
Gill rakers	5+8	13–16			14–16		
Lateral-line scales	66+4	64–69			64–70		
Vertebrae	10+21	10+21–22			10+22		
Head length	27.1	25.3–29.0	27.4	0.8	25.5–28.4	27.0	0.7
Snout length	8.0	7.3–10.3	8.7	0.6	7.5–9.5	8.6	0.6
Orbit diameter	8.0	7.0–9.3	7.9	0.6	6.3–8.1	7.3	0.4
Interorbital width	2.6	2.1–3.4	2.9	0.4	2.4–3.9	3.2	0.4
Cheek depth	4.2	3.7–5.3	4.5	0.4	3.5–4.8	4.4	0.3
Upper-jaw length	11.0	9.4–11.5	10.2	2.2	9.6–11.9	10.6	0.7
Greatest body depth	19.9	17.0–21.5	19.5	1.0	17.0–21.8	19.5	1.3
Body depth at anal fin origin	19.6	17.0–20.7	19.1	0.8	17.0–21.7	19.3	1.2
Body width	18.3	17.4–21.2	19.3	1.1	17.3–21.9	19.0	1.2
Caudal-peduncle depth	9.0	8.2–9.3	8.8	0.3	8.4–9.5	8.8	0.4
Caudal-peduncle length	8.5	7.8–9.4	8.9	0.4	8.4–10.1	9.3	0.5
Predorsal length	28.9	27.7–31.6	29.4	1.0	26.2–30.0	28.4	0.8
Preanal length	46.7	42.2–49.3	46.2	1.7	41.0–50.6	46.1	2.0
Prepectoral length	27.9	25.9–29.5	27.7	0.9	25.2–28.9	27.4	0.9
Prepelvic length	25.7	18.6–26.9	24.1	1.6	21.9–28.5	24.3	1.3

continued next page

TABLE 1. (continued)

	Holotype	Paratypes (n=24)			<i>P. sexfasciata</i> (nontype, n=27)		
	ASIZP 0071627		Mean	SD	Mean	SD	
Dorsal-fin base	67.1	59.0–69.1	66.7	5.6	60.2–69.1	65.2	2.1
First dorsal spine	2.7	2.8–5.2	3.8	0.6	2.6–4.4	3.4	0.4
Fourth dorsal spine	6.8	6.0–9.3	7.5	0.7	5.9–7.6	6.9	0.5
Fifth dorsal spine	7.7	7.5–9.3	7.9	1.7	6.9–8.5	7.6	0.5
Longest dorsal ray	14.3	12.7–17.3	15.2	1.3	12.6–16.5	14.3	1.0
Anal-fin base	45.9	41.5–47.8	46.3	1.7	42.7–50.2	46.8	1.8
Longest anal ray	11.9	9.9–15.0	13.1	1.2	11.2–14.6	12.5	0.9
Caudal-fin length	17.6	17.1–21.2	18.8	1.1	16.0–20.5	18.7	0.9
Pectoral-fin length	20.1	19.2–23.6	22.1	1.0	20.6–24.3	22.2	0.9
Pelvic-fin length	18.7	17.9–22.4	20.2	1.4	8.0–12.4	20.9	1.0
Pelvic-spine length	8.0	7.8–12.4	10.1	1.2	19.3–22.4	10.2	1.0

SD= standard deviation.

Greatest body depth 5.0 (4.6–5.9) in SL; body depth at origin of anal fin 5.1 (4.8–5.9) in SL; body nearly cylindrical anteriorly, width 5.5 (4.7–5.7) in SL; HL 3.7 (3.5–3.9) in SL; ventral part of head, chest, and abdomen slightly convex; snout length 3.4 (2.8–3.6) in HL; orbital diameter 3.4 (3.0–3.9) in HL; interorbital space slightly concave, least width 10.5 (7.7–13.1) in HL; caudal-peduncle depth 3.0 (3.0–3.4) in HL; caudal-peduncle length 3.2 (2.7–3.4) in HL.

Mouth large and oblique, maxilla nearly reaching vertical line from anterior edge of eye, upper-jaw length 2.5 (2.3–3.0) in HL, lower jaw protruding; anterior portion of upper jaw with a row of incurved canine teeth on each side, middle one largest, remaining teeth becoming progressively smaller; behind canines at front of upper jaw, a broad band of villiform teeth gradually narrowing posteriorly to a single row; front of lower jaw with 1–4 incurved canine teeth on each side, following a row of small canines posteriorly on side of lower jaw; a broad dense band of villiform teeth medial to anterior canines, narrowing and ending about 1/3 back in jaw; vomer with 2 or 3 rows of stout conical teeth; lips smooth; tongue with a rounded tip that nearly reaches median vomerine teeth.

Gill membranes free from isthmus with a broad, free fold across. Gill rakers short and spinous. Anterior nostril slightly more than 1/2 distance to edge of upper lip, with a long posterior flap; posterior nostril smaller and dorso-posterior to anterior one, aperture with a slight, nearly circular rim. Pores of cephalic sensory system mostly small, 10 in row from side of upper lip (including 1 large pore in front of anterior nostril), many tiny pores distributed from posterior nostril to entire occipital region and scaleless region in preopercle; from ventral view of head, a line of 10 apparent sensory pores on lower jaw; 11 pores counting from 1st serrated at edge of preopercle to front of chin (not including tiny pores associated with nodular serrated on preopercular margin); usually one 1st pore on end of preopercle from ventral view.

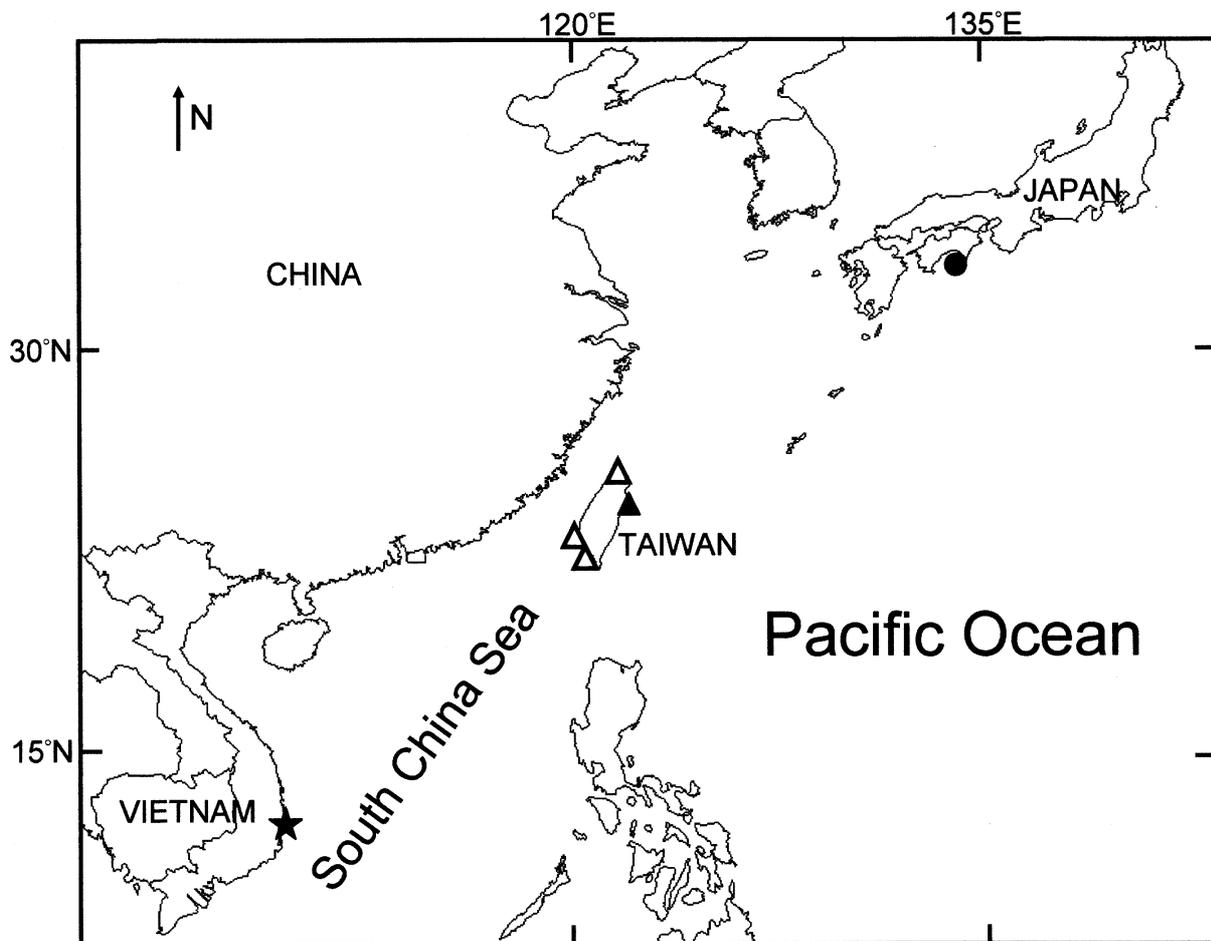
Opercle with a single sharp spine at level of lower margin of eye (when viewed from side); posterior-ventral margin of preopercle serrated, its free edge extending from center of eye to 1/2 distance of predorsal length.

Lateral line continuous, slightly arched over pectoral fin, then gradually declining to 1/2 of dorsal fin length and extending along middle of body to base of caudal fin. Scales ctenoid; body with rather large ctenoid scales; snout, interorbital and anterior predorsal region naked; no scales on dorsal, anal, or pelvic fins; 2 or 3 rows of smaller scales on base of pectoral fins; elongate progressively smaller ctenoid scales extending to 1/3 of caudal fin.

Predorsal length 3.6 (3.4–3.9) in SL; 1st dorsal spine short, 10.2 (5.2–9.5) in HL; 4th dorsal spine longest, 4.0 (3.3–4.1) in HL; 5th dorsal spine 3.5 (3.0–3.8) in HL; 19th and 20th dorsal soft rays longest, 1.9 (1.6–2.2) in HL; origin of anal fin below base of 5th dorsal soft ray, preanal length 2.1 (2.0–2.4) in SL; 1st anal spine 5.7 (3.4–6.4) in HL; 16th and 17th anal soft rays longest, 2.3 (1.8–2.7) in HL; caudal fin rounded, length 5.7 (4.7–5.8) in SL; pectoral fins rounded, 9th and 10th rays longest, 5.0 (4.2–5.2) in SL; prepelvic length 3.9 (3.7–4.6) in SL; pelvic fins just reaching anus, 4th soft pelvic ray longest, 5.4 (4.2–5.6) in SL; pelvic spine slender, 3.4 (2.3–3.6) in HL.

**Color when fresh based on holotype:** body reddish brown on upper part, lower half white with 4 prominent

V-shaped black transverse bands and one additional short transverse band under the lateral line on caudal peduncle, numerous black dots scattered on V-shaped transverse bands, between bands and around pectoral fin, and at pectoral fin base; one irregular diffused longitudinal yellow stripe along middle body, below the lateral line, extending from pectoral fin base to caudal fin base; head reddish brown, each side with two yellow strips, one extending from upper lip along nostril to anterior eye, another from middle of upper lip to suborbital eye on cheek, numerous yellow spots on opercle and preopercle, one indistinct vertical dark transverse band extending from suborbital to lower margin of preopercle; dorsal fin membrane transparent with numerous yellow spots, and one prominent black blotch between 1–4 spines, additional 8 dark spots on upper body corresponding to the V-shaped bands along the dorsal fin base; caudal fin with 5–6 vertical yellow stripes on upper 2/3 membrane, lower 1/3 black, one prominent black eye spot on upper caudal fin base; anal fin membrane transparent with numerous yellow stripes, outer margin blackish; pectoral fin transparent, reddish brown; pelvic fin membrane gray to blackish (Fig. 1).



**FIGURE 2.** Distribution map of *Parapercis lutevittata* based on specimens from Japan (solid circles) and Taiwan, including holotype and paratype (solid triangles); and other specimens (open triangles). One additional record from Nha Trang, Vietnam (solid star, data from Prokofiev, 2008).

**Color in alcohol based on holotype:** Head and body mostly grayish-brown. Head with one unclear vertical dark transverse band extending from suborbital to lower margin of preopercle. Four prominent V-shaped black transverse bands and one additional short transverse band under the lateral line on caudal peduncle; numerous black dots scattered on the V-shaped transverse bands and between bands, around pectoral fin and at pectoral fin base; dorsal fin membrane transparent with numerous yellow spots, with one prominent black blotch between 1–4 spines; additional 8 dark mark on upper body sites corresponding to the V-shaped bands along the dorsal fin base;

caudal fin with 5–6 vertical gray stripes on upper 2/3 membrane, lower 1/3 black, one prominent black spot on upper caudal fin base; outer margin of anal fin membrane blackish; pelvic fin membrane gray to blackish (Fig. 1).

**Etymology.** *Lute* for yellow and *vitta* for stripe from Latin, in reference to the longitudinal yellow stripe extending from the pectoral fin base to the caudal fin base on the body of this species.

**Distribution.** Known from Tosa Bay, southern Japan, and northern and southern Taiwan. It could be also distributed to Vietnam (Prokofiev, 2008) (Fig. 2). Depth range is from 50 to 100 meters.

**Barcode sequence.** The 633-bp sequences of the mitochondrial cytochrome *c* oxidase subunit I (CO I or COX I) gene were bidirectionally sequenced for the holotype (ASIZP 071627, GenBank accession no. FN677936) and 14 paratypes (USNM 398144 and ASIZP 071628-71630, GenBank accession no. FN677937-677938, and FN677939-950, respectively). The 15 sequences were closely matched with 0.1% K2P genetic divergence.

## Discussion

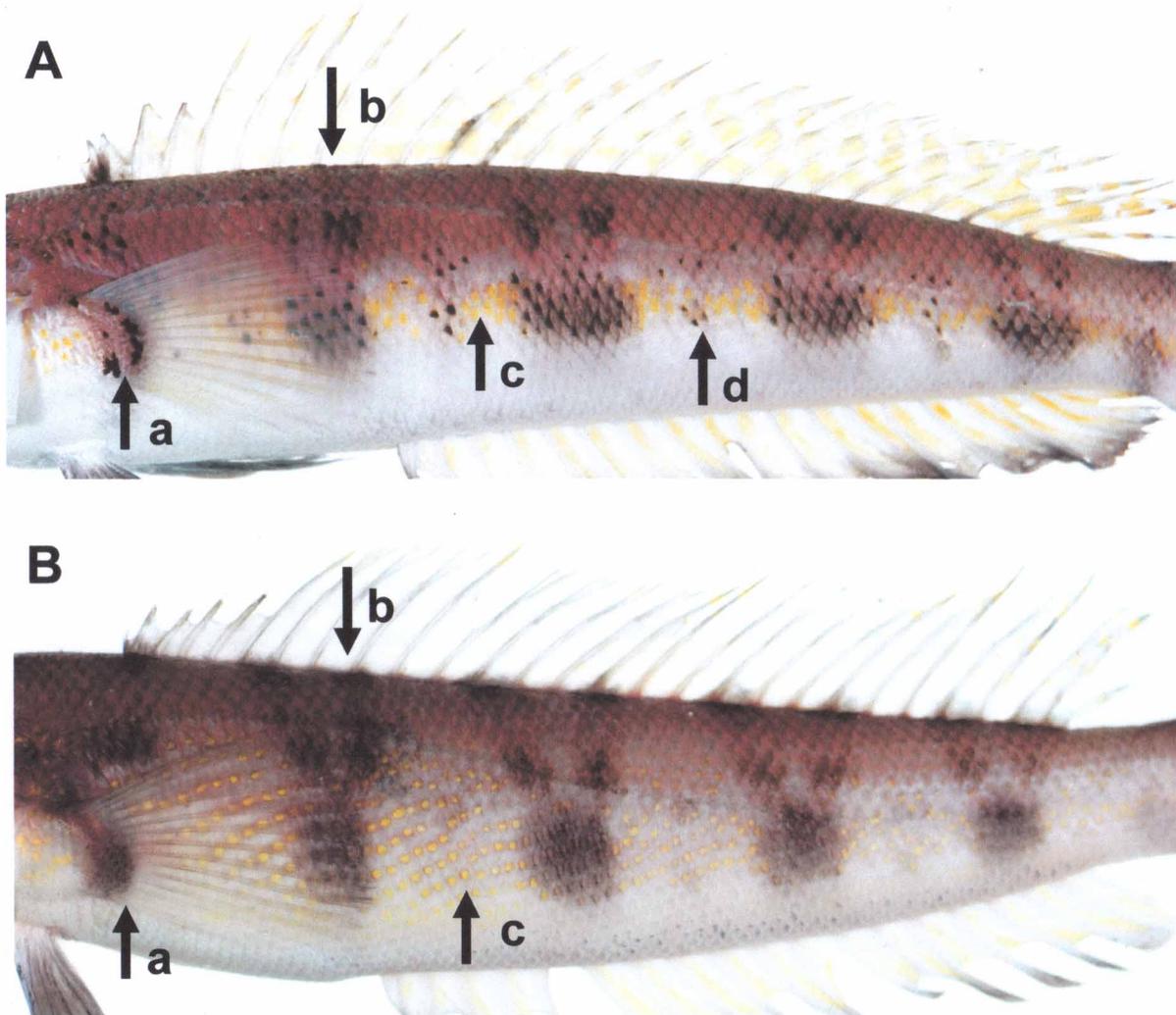
When *P. lutevittata* is compared with the lectotype of *P. sexfasciata*, RMNH 746 (160 mm SL), it is difficult to distinguish them because of the poor quality of the stuffed type specimen. However, the original description of RMNH 746 “...Les pectorales sont jaunatres, les ventrales d’un brun-rougeatre.” in Temminck and Schlegel (1843) indicated that the pectoral fin was yellow, the ventral with a brown-reddish, viz. its distinct color markings on the base of pectoral fin. Boeseman (1947) mentioned that Von Siebold’s another specimen in spirits, RMNH 415 (142 mm SL), fitted the descriptions of coloration better and was the only specimen labeled “*Percis japonica* v. Siebold, F. jap., Japon;” even though the less convincing specimen, RMNH 746, was chosen as type. Since the paralectotype specimen RMNH 415 not only has representative coloration but also is in good quality, we recommend it as the representative type specimen of *Parapercis sexfasciata* (Fig. 3).



**FIGURE 3.** *Parapercis sexfasciata*, paralectotype, RMNH 415, 142 mm SL. (photo by R. Ruiter).

Most specimens of *P. lutevittata* in Taiwan were previously misidentified as *P. sexfasciata* due to their morphological similarity (Shen, 1984, 1993). Nevertheless, it can be separated from *P. sexfasciata* by coloration when

fresh. Its morphological characters include: one large dark-brown blotch and several black dots on the base of the pectoral fin (vs. one big deep-brown or black blotch in *P. sexfasciata*), absence of dark spots on the base of the dorsal fin ray membrane (vs. 8 dark spots on the membrane), a continuously irregular pattern of a yellow stripe along middle side of the body (vs. 14 or 15 yellow lines on the body), 1 anterior sensory pore along the lower margin of preopercle (vs. usually 2), and numerous small black dots scattered on and between the transverse V-shaped bands (vs. absent). The preserved specimens can also be clearly distinguished by the black spots on the body and pectoral fin base, absence of dark spots on the base of the dorsal fin ray membrane (Fig. 4).

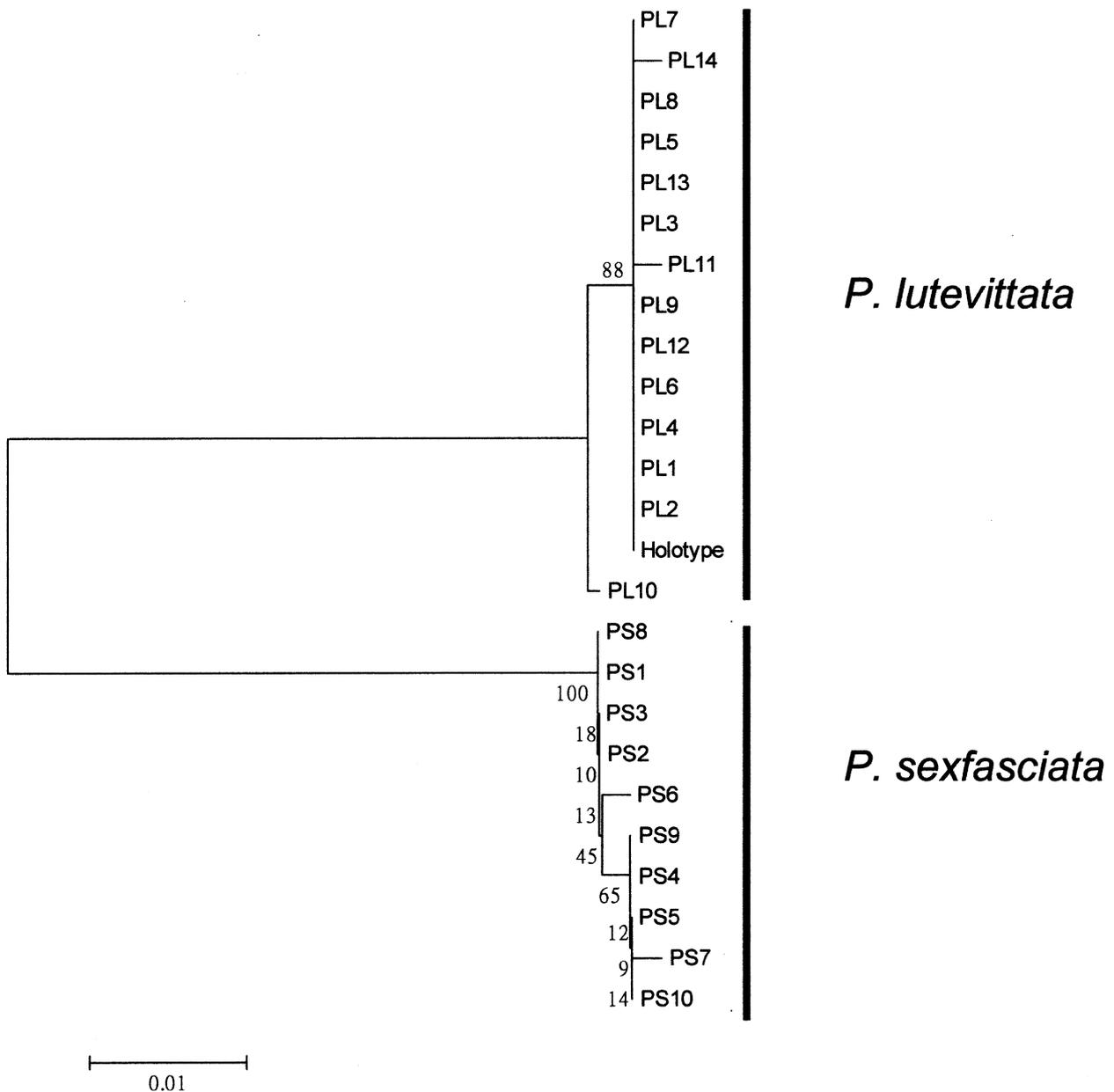


**FIGURE 4.** Comparisons of coloration between (A) *Parapercis lutevittata*, ASIZP0071627, holotype, 135 mm SL and (B) *P. sexfasciata*, ASIZP0071631, 142.7 mm SL. a- a large dark-brown blotch and several small black dots vs. a big deep-brown or black blotch on base of pectoral fin; b- absence vs. presence of black spots on base of dorsal fin ray membrane; c- yellow dotted strip midlaterally on body vs. yellow dotted lines from lower left running obliquely to upper right; d- presence vs. absence of scattered black dots on and between V-shaped transverse bands along sides of body.

The 633 bp of the COX I sequence data showed 7.9% sequence divergence in K2P distance between these two species, and 0.2% and 0.1% within species of *P. sexfasciata* and *P. lutevittata*, respectively. In addition, the average K2P distance of all the specimens of these two species was 4.0%, much higher when compared to 0.35% (Ward, 2009) and 0.39% (Ward, 2005) within species. The NJ algorithm also showed that the specimens of these two species clearly separated into two clades (Fig. 5). Furthermore, the data (not shown) of analyzing the anterior part

of the mitochondrial control region revealed complete congruence with the results in Kai *et al.* (2004). Our result based on the neighbor-joining algorithm indicated that *Parapercis lutivittata* has less haplotypic variation than that of *P. sexfasciata*, congruent with Kai *et al.* (2004). Moreover, Kai *et al.* (2004) stated that *P. sexfasciata* comprises historically larger and older population than this sympatric cryptic species (*viz.* *P. lutivittata*).

DNA barcoding can be useful for flagging cryptic or new species in taxonomic research when deep intraspecific divergences are exhibited, e.g., the longnose skate in Argentina (De Astarloa *et al.* 2009), larval goby from the western Caribbean (Victor, 2007), damselfishes from deep coral reefs in the western Pacific (Pyle *et al.* 2008), and a possible new Asian sea bass (Ward, 2008). Our results on both the molecular evidence and morphological differences confirmed that *Parapercis lutevittata* is a new species.



**FIGURE 5.** Neighbour-joining tree of mitochondrial cytochrome *c* oxidase subunit I (COI or COX I) sequences of *Parapercis lutevittata* and *P. sexfasciata*. 10,000 bootstrap replications.

**Comparative materials:** *P. sexfasciata*: the lectotype and paralectotypes were compared by specimen photos from the National Museum of Natural History, Leiden, the Netherlands (RMNH) for RMNH 746, lectotype, 160 mm SL; paralectotype: RMNH 415, 142 mm SL, RMNH 747, 145 mm SL, and RMNH 4836 (not *P. sexfasciata*)

from Japan. Other specimens from Taiwan: ASIZP 0071631, 10 specimens, 112.8–160.5 mm SL, Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, no depth data, 24 Apr. 2009. ASIZP0061169, 4 specimens, 133.2–145 mm SL, off Aodi, Taipei County, northeastern Taiwan, commercial bottom trawl, 200m in depth, 15 Nov. 2000; ASIZP0060959, 139 mm SL, off Jinshan, Taipei County, northern Taiwan, commercial bottom trawl, no depth data, 23 Oct. 2000; ASIZP0066555, 158.8 mm SL, Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, 600 m in depth; ASIZP0066626; 124 mm SL, Tashi, Ilan County, northeastern Taiwan, commercial bottom trawl, 600 m in depth; specimens from Tosa Bay of Japan: BSKU 029998, 130 mm SL; BSKU 038893, 140 mm SL; BSKU 039581, 137. mm SL; BSKU 054353, 131 mm SL; BSKU 065315, 150 mm SL; BSKU 057923, 125.5 mm SL; BSKU 059670, 145 mm SL; BSKU 082820, 115 mm SL; BSKU 088192, 115 mm SL; BSKU 089047, 118.5 mm SL.

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