

## A New Goby, *Rhinogobius rubromaculatus* (Teleostei: Gobiidae), from Taiwan

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**Sin-Che Lee and Jung-Ti Chang (1996)** A new goby, *Rhinogobius rubromaculatus* (Teleostei: Gobiidae) from Taiwan. *Zoological Studies* 35(1): 30-35. A new species of gobiid fish, *Rhinogobius rubromaculatus* from the rivers of Taiwan is described. This species is distinguished from other members of *Rhinogobius* by the following criteria: a shorter snout, 27 vertebrae, and red spots on the body, including the fins, with those on the pectoral fin base in 2 transverse rows. This fluviatile species has the largest egg among the Taiwanese *Rhinogobius* members. A low degree of genetic similarity of 0.682 - 0.684 is estimated between the present species and the closely related *R. candidianus* within the species complex. The systematic relationships with other congeneric species are also discussed.

**Key words:** Species description, *Rhinogobius rubromaculatus* n. sp., Allozyme variation.

The genus *Rhinogobius* was first nominated in 1859 by Gill based on the monotypic *R. similis* collected from Japan by Dr. J. Morrow. Species of *Rhinogobius* are very common in Japan, Korea, China, Taiwan, and the Philippines. The name *R. similis* was used for many years until 1947, when Boeseman treated it as a synonym under *Rhinogobius brunneus* (Temminck and Schlegel 1845) after examination of the type specimen (Boeseman 1947). In Taiwan, an earlier account of this genus was given in 1919 by Oshima who recognized five species, *R. candidianus* (Regan 1908), *R. caninus*, *R. formosanus* (Oshima 1919), *R. giurinus* (Rutter), and *R. taiwanus* (Oshima 1919). Of these nominal species, *R. caninus* has been transferred to the genus *Yongeichthys* and *R. formosanus* is considered identical with *R. nagoyae* Jordan and Seale, 1906. The four existing taxa in Taiwan, *R. candidianus*, *R. giurinus*, *R. taiwanus*, and *R. nagoyae*, all with wide color pattern variations were previously placed under *R. similis* or the subsequently adopted name *R. brunneus*. The most recent revision by Aonuma (1992) confirmed that *R. candidianus*, *R. nagoyae*, and *R. taiwanus* are valid species and are in-

cluded in the so-called *R. brunneus* species complex. Beside these, he also mentioned four other undetermined species, namely *Rhinogobius* sp1, *R. sp2*, *R. sp3*, and *R. sp4*. *R. brunneus* has a wide range of color patterns and different ontogenical types which has resulted in a rather confusing taxonomic status. However, electrophoretic differences enabled researchers to subdivide them into several possible distinct species (Masuda et al. 1989). The presently described new species *R. rubromaculatus* fits well with 1 of these unnamed types, *R. sp2*. Unlike the amphidromous types, the presently described species is a fluviatile type whose larvae do not move to the sea but are confined to tributaries in the middle reaches of rivers. It also possesses the largest egg among the Taiwanese members of the complex. We suggest that the presently described taxon differs strikingly from other morphs within the complex by a combination of morphological, ecological, and genetic differences. As for the treatment of the other color types, their relationships and status will be clarified in a subsequent study by I. S. Chen. The purpose of the present study is to analyze both morphometric

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and allozyme electrophoretic variations among the relevant members of the complex and to elucidate the proper taxonomic status of this undescribed form.

## MATERIALS AND METHODS

Specimens for electrophoresis were based on the following materials: 10 *Rhinogobius rubromaculatus* from the Ta-an River, 28 *R. candidianus* from the Tachia and Shuili Rivers, and 44 *R. giurinus* from the Ta-an River. Procedures of electrophoresis followed those of Tsoi et al. (1987) and the enzymes scored, buffer systems and the sources of tissues used are tabulated in Table 1. An UPGMA phenogram was constructed using NTSYS-pc (Rohlf 1993) based on Nei's (1972) genetic distance (D). Specimens for morphometrics were chosen randomly from the above materials. Fin ray (except pectoral fin) counts and vertebral counts are based on radiography. Nomenclature of the lateral line canal pores followed the usage of Akihito (1984). Specimens are deposited in the Museum of the Institute of Zoology, Academia Sinica (ASIZP).

### *Rhinogobius rubromaculatus* n. sp. (Fig. 1)

*Holotype*: ASIZP 056640, 1 female, 39.0 mm SL, collected on 30 November 1991, from the Tadu River, Taichung County, Taiwan.

*Paratypes*: ASIZP 057271, 7 specimens, 17.0-32.2 mm SL, collected on 14 April 1991, from the Tsoshui River, Nantou County, Taiwan.

*Diagnosis*: Snout short, measuring 20.8% – 27.7% (24.1%) SL, vertebrae 10 + 17 = 27; body including fins (except anal fin) with scattered red



Fig. 1. *Rhinogobius rubromaculatus*. Holotype, female, 39.0 mm SL, ASIZP 056640.

**Table 1.** Buffer systems and tissues used to resolve 22 presumptive enzyme loci in the *Rhinogobius* species

Enzyme or protein	E.C. number	Locus	Tissue	Buffer <sup>a</sup>
Aspartate aminotransferase	2.6.1.1.	AAT-A	Muscle	TVB
Creatine kinase	2.7.3.2.	CK-A	Muscle	LiOH
		CK-B	Eye	LiOH
Fumarase	4.2.1.2.	FUM-A	Eye	TC
Glyceraldehyde-3-phosphate dehydrogenase	1.2.1.12.	GAPDH	Eye	LiOH
Glucose-6-phosphate isomerase	5.3.1.9.	GPI-A	Muscle	LiOH
		GPI-B	Eye	LiOH
Isocitrate dehydrogenase	1.1.1.42.	IDH-A	Muscle	TC
		IDH-B	Liver	TC
L-Lactate dehydrogenase	1.1.1.27.	LDH-A	Muscle	TC
		LDH-B	Heart	TC
		LDH-C	Eye	TC
Malate dehydrogenase	1.1.1.37.	MDH-A	Muscle	TC
		MDH-B	Liver	TC
Malate dehydrogenase (NADP <sup>+</sup> )	1.1.1.40.	MDHP-A	Muscle	TVB
Mannose-6-phosphate isomerase	5.3.1.8.	MPI	Muscle	TVB
Phosphogluconate dehydrogenase	1.1.1.44.	6-PGDH	Eye	TC
Phosphoglucomutase	5.3.2.2.	PGM-A	Muscle	TVB
		PGM-B	Liver	TVB
Xanthine dehydrogenase	1.1.1.204.	XDH	Liver	TVB
Calcium-binding proteins		CBP-A	Muscle	TVB
		CBP-B		TVB

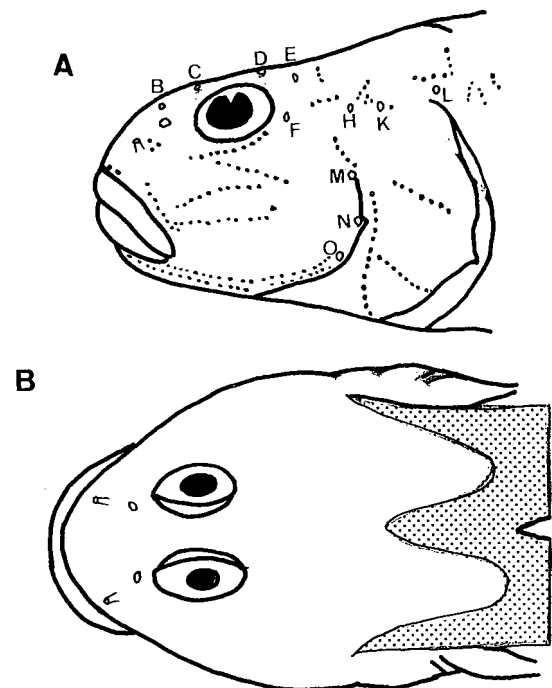
<sup>a</sup>TVB, Tris-versene-borate buffer (TVB) pH 8.0 and TC, Tris-citrate buffer (TC) pH 7.0 described by Siciliano and Shaw (1976); LiOH, Tris-citric-boric-LiOH buffer (Gel, pH 8.31) (Electrode, pH 8.26) described by Redfield and Salini (1980).

**Table 2.** Comparisons of some selected body measurements and meristic counts among three *Rhinogobius* species with the means (measurements) and modes (meristics) in parentheses

Character	<i>R. giurinus</i>	<i>R. rubromaculatus</i> n. sp.			<i>R. candidianus</i>
	<i>n</i> = 20	Holotype <i>n</i> = 1	Paratypes <i>n</i> = 7	Dissected specimens <i>n</i> = 8	<i>n</i> = 10
Standard length (mm SL)	37.8-56.5	39.0	17.0-32.2	29.0-46.5	48.5-66.4
% of SL					
Head	29.1%-32.7% (30.7%)	29.0%	29.6%-34.3% (31.1%)	26.2%-33.1% (29.3%)	24.6%-30.2% (27.6%)
Body depth	14.5%-20.0% (17.2%)	20.5%	17.7%-22.9% (21.6%)	16.3%-24.3% (18.7%)	16.9%-20.4% (19.1%)
% of HL					
Snout	26.9%-33.6% (29.8%)	24.8%	20.8%-25.1% (23.5%)	21.4%-27.7% (24.1%)	31.7%-35.7% (33.3%)
Orbit	22.5%-29.6% (26.2%)	20.4%	19.1%-26.9% (23.3%)	20.7%-27.6% (22.5%)	20.8%-26.0% (24.5%)
Fin ray formulae					
Second dorsal	I, 8	I, 9	I, 7-10 (10)	I, 9-10 (9)	I, 8-10 (9)
Pectoral	19-20 (20)		15-17 (16)	16-18 (17)	17-19 (18)
Anal	I, 8	I, 8	I, 7-9 (8)	I, 8	I, 8-10 (9)
Branched caudal	14-16 (15)	15	14-15 (15)	14-16 (14)	14-16 (15)
Vertebrae	26	27	27-28 (27)	27	25-26 (26)

spots that are usually in two transverse series on pectoral fin base; fluviatile type, with largest egg size among *Rhinogobius brunneus* complex in Taiwan.

**Descriptions:** The critical body measurements and meristic counts of this new species are summarized in Table 2. Body moderately elongated and compressed, head slightly depressed anteriorly. Ctenoid scales on body except nape, opercle, cheek, and snout; the predorsal scales extending to posterior margin of opercle with edge of squamosus area W shaped (Fig. 2B) when viewed dorsally on head. Snout shorter than in other species; interorbital space narrower than eye. Anterior nasal pore in short tube, posterior in pore-like structure. Mouth oblique, with 3-4 series of canine teeth on each jaw, the outermost row largest, vomer and palatines toothless. Lateral line canal on head. Eleven canal pores on head when viewed laterally: 1 (B) medial to posterior nostril, 2 (C, D) above orbit on interorbital space, 2 (E, F) behind orbit, 3 (M, N, O) along posterior margin of preopercle, 2 (H, K) at the straight uppermost part and 1 (L) at upper corner of opercle. Sensory papillae numerous with patterns resembling those of most species of complex (Fig. 2A). Cheek



**Fig. 2.** Lateral line canal pores and sensory papillae (A), and cephalic squamous areas (B) of *Rhinogobius rubromaculatus*. English letters from B to O on the side of the head indicate canal pores.

with 4 horizontal rows of papillae below orbit, additional short rows behind head. Opercle with 1 transverse and 2 oblique rows, the lowermost closely contacting transverse one. Suborbital papillae rows horizontal (Fig. 2A). First dorsal fin commencing at anterior third of pectoral fin, moderately high with 6 spines; 2nd dorsal fin inserted exactly opposite to anus, with 1 spine and 9-10 (typically 10) rays; anal fin with 1 spine and 7-9 rays; pectoral fin with 16-18 (typically 17) rays; ventral fin in disc with frenum concave posteriorly in the middle and with 1 spine and 5 rays; caudal fin rounded with 14-16 (typically 14) branched rays;

vertebrae including urostyle  $10 + 17 = 27$ ; epural plate 1.

*Live coloration:* Generally pale brownish with dusky transverse bands, numerous red spots scattered over entire body except anal fin which is uniformly dark brownish; vertical fins with pale margins; red spots on pectoral fin base in 2 transverse series; anterodorsal and ventral margins of orbit with dark brownish lines.

*Genetic differences:* As stated in Table 3, several fixed allelic differences were observed at *CK-A*<sup>113</sup>, *CK-A*<sup>100</sup>, *LDH-A*<sup>115</sup>, *LDH-A*<sup>100</sup>, *LDH-B*<sup>130</sup>, *LDH-B*<sup>100</sup>, *MDHP-A*<sup>96</sup>, *XDH*<sup>100</sup>, and *XDH*<sup>89</sup> between

**Table 3.** Allele frequencies of 13 loci scored from 4 populations of 3 *Rhinogobius* species. The following 9 monomorphic loci, *CK-B*, *FUM-A*, *GAPDH*, *LDH-C*, *MDH-A*, *MDH-B*, *PGM-A*, *CBP-A*, and *CBP-B*, are excluded from this list

Locus	Allele	Species and localities sampled			
		<i>R. giurinus</i> Ta-an River (n = 44)	<i>R. rubromaculatus</i> Shihkeng River (n = 10)	<i>R. candidianus</i> Shihkeng R. (n = 11)	Shuili R. (n = 17)
AAT-A	116	0.000	0.300	0.000	0.000
	111	0.023	0.300	1.000	0.000
	100	0.773	0.400	1.000	1.000
	86	0.204	0.000	0.000	0.000
CK-A	113	0.000	1.000	0.000	0.000
	100	1.000	0.000	1.000	1.000
GPI-A	225	0.114	0.200	1.000	1.000
	-100	0.886	0.800	0.000	0.000
GPI-B	115	0.000	0.000	0.136	0.000
	100	1.000	0.700	0.864	0.941
	84	0.000	0.300	0.000	0.000
	64	0.000	0.000	0.000	0.059
IDH-A	130	0.986	0.000	0.000	0.000
	100	0.014	1.000	1.000	1.000
IDH-B	114	0.391	0.000	0.000	0.000
	107	0.078	0.000	0.000	0.000
	100	0.531	1.000	1.000	1.000
	115	0.000	1.000	0.000	0.000
LDH-A	100	1.000	0.000	1.000	1.000
	130	0.000	1.000	0.000	0.000
	113	1.000	0.000	0.000	0.000
	100	0.000	0.000	1.000	1.000
MDHP-A	109	0.000	0.000	1.000	1.000
	100	1.000	0.000	0.000	0.000
	96	0.000	1.000	0.000	0.000
	127	0.635	0.000	0.000	0.000
MPI	118	0.365	0.000	0.000	0.000
	107	0.000	0.167	1.000	0.969
	100	0.000	0.833	0.000	0.000
	95	0.000	0.000	0.000	0.031
6-PGDH	108	0.000	1.000	1.000	1.000
	100	1.000	0.000	0.000	0.000
PGM-B	120	0.000	0.000	0.045	0.000
	100	1.000	1.000	0.955	1.000
XDH	100	1.000	1.000	0.000	0.000
	89	0.000	0.000	1.000	1.000

the new species and *R. candidianus*. Using the data in Table 3 to calculate Nei's (1972) genetic identity, indicates a rather high similarity between two lots of *R. candidianus* (0.999) though these were collected from different locations, while those between the new species and any lots of *R. candidianus* samples and the outgroup, *R. giurinus*, show much lower levels of similarity (0.682, 0.684, and 0.653, respectively). It is clear from the genetic identity level and its derived UPGMA clusterogram (Fig. 3), that the new species is sufficiently distinct from the others to be considered a valid species.

**Etymology:** The species name is given based on the red spots scattered over the body.

**Ecological note:** This species mainly inhabits shallower small brooks or rivers and pools with low water velocity. The substratum of the preferred habitat is composed of rocks or small pebbles. When compared with other species of the *Rhinogobius brunneus* complex, this new species prefers habitat in smaller branches of the middle reaches of rivers.

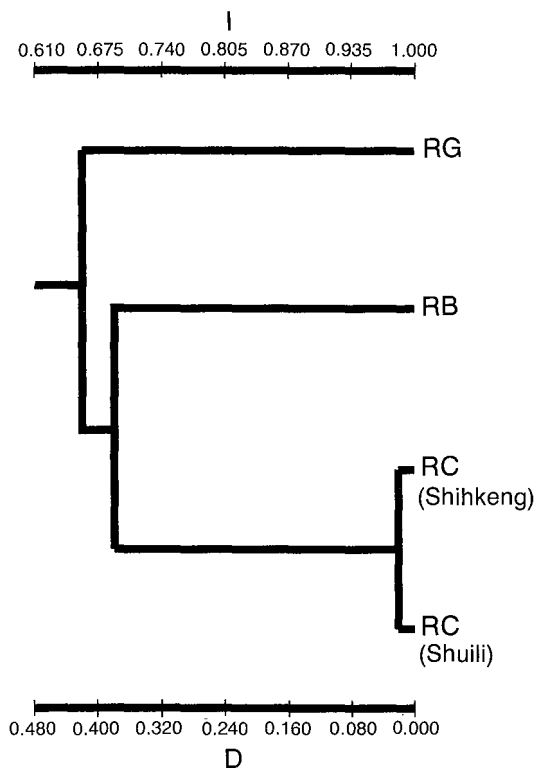


Fig. 3. UPGMA phenogram based on Nei's D value showing the relationships among three Taiwan *Rhinogobius* species. RB, *Rhinogobius rubromaculatus*; RC, *R. candidianus*; RG, *R. giurinus*.

## DISCUSSION

In Taiwan, a systematic revision of *Rhinogobius* species other than *R. giurinus* is needed. Unlike the *Rhinogobius brunneus* complex, *R. giurinus* is more constant in morphological characters. It is likely to be distinct from species in the *R. brunneus* complex based on the transverse series of sensory papillae on its cheek and more extensive nape squamation which nearly reaches the posterior margin of the eye. The morphological distinction of *R. giurinus* from the members of the *R. brunneus* complex is in agreement with the high degree of genetic differences observed.

As for the *R. brunneus* complex itself in Taiwan, the species name was first given in 1845 by Temminck and Schlegel, and several species once considered to be synonyms are now resurrected (Aonuma 1992 unpublished thesis). Various color types described in Japan also have been suggested as valid species as a result of electrophoretic studies (Masuda et al. 1989, Katoh and Nishida 1994). Several *R. brunneus* color morphs (Aonuma 1992, Chen 1994, both unpublished) are also recognized as valid species in Taiwan though they have not been named. Among them, the presently described species is the only one distinguished by a high genetic distance from other members of the complex. Validity of this species is supported by the following evidence: 27 vertebrae compared with 26 or fewer in other species; non-amphidromous habitat preference with large-sized eggs (large larvae remaining in the middle reaches of rivers); and complete allelic substitution found between *R. rubromaculatus* and *R. candidianus* at loci *CK-A*, *LDH-A*, *LDH-B*, *MDHP-A*, and *XDH*. The concordant morphological, genetic and ecological distinctions presented here strongly support the recognition of this new species. *R. brunneus* and *R. flumineus* which is endemic to Japan resemble each other in their higher vertebral counts, large-sized egg and fluviatile style of life. However, there are several points which well distinguish these two species according to the species diagnosis of *R. flumineus* described by Mizuno (1960), Masuda et al. (1984), and Akihito et. al. (1993). *R. rubromaculatus* has red spots scattered over the body but that is not so in *R. flumineus*; the pectoral fin base has 2 transverse series of red spots in *R. rubromaculatus* as compared with 2 transverse dark brown stripes in *R. flumineus*; there are 10 abdominal vertebrae in *R. rubromaculatus* compared with 11 in *R. flumineus*. We believe they are 2 valid species.

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## 記臺灣之一新種短吻紅斑吻鰕虎

李信徹<sup>1</sup> 張戎悌<sup>1</sup>

本文記載一種採自臺灣大肚溪之新種短吻紅斑吻鰕虎。本種與同屬他種鰕虎魚間之最大差異在於本種脊椎骨數稍多[27]，全身佈滿紅斑，其在胸鰭基部者排成二斑點列；為固棲河川不洄游外海產卵者，卵粒頗大，為臺灣產同屬鰕虎魚中卵徑最大者。與近緣種 *R. candidianus* 間之遺傳相似度頗低[0.682-0.684]，足證本種應為合理之一個獨立種。至於與同屬其他種鰕虎魚間之系統分類關係，文中亦一併加以討論。

關鍵詞：川鰕虎屬，分類，短吻紅斑吻鰕虎新種，異構酶變異。

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