Morphology and Distribution Patterns of the *Rhinogobius* Species Complexes (Gobiidae) in Taiwan

台灣產吻鰕虎屬魚類的形態與分布模式

Nico Jose Leander[1*], Wann-Nian Tzeng[1,2] and Ming-Fong Yeh[3*]

林德 [1*] 曾萬年 [1,2] 葉明峰 [3,*]

[1] Institute of Fisheries Science, College of Life Science, National Taiwan University, Taipei, Taiwan

[2] Department of Environmental Biology and Fisheries Science, National Taiwan Ocean University, Keelung, Taiwan

[3] Endemic Species Research Institute, Jiji, Nantou, Taiwan

[1]國立台灣大學漁業科學研究所 10617 台北市羅斯福路 4 段 1 號

[2]國立台灣海洋大學環境生物與漁業科學學系 20224 基隆市北寧路 2 號

[3]行政院農業委員會特有生物研究保育中心 55244 南投縣集集鎮民生東路 1 號

* Corresponding Author: d98b45005@ntu.edu.tw ; yeh@tesri.gov.tw

*通訊作者: d98b45005@ntu.edu.tw ; yeh@tesri.gov.tw

Abstract

The morphology and distribution patterns of the *Rhinogobius* species complexes (Gobiidae) in Taiwan were studied based on the specimens collected by Endemic Species Research Institute from various river systems around the island during the period from 1992 to 2005. Morphological examinations revealed ten valid nominal species which can be grouped into two species complexes, *R. giurinus* and *R. brunneus*. The former has only one species while the latter contains nine species namely, *R. candidianus*, *R. delicatus*, *R. gigas*, *R. henchuenensis*, *R. lanyuensis*, *R. maculafasciatus*, *R. nagoyae formosanus*, *R. nantaiensis* and *R. rubromaculatus*. These species can be distinguished from one another by a combination of morphometric measurements, coloration pattern and meristic counts that were slightly different between species and also by their geographical distributions. The shape of the fused pelvic fins that form the ventral adhesive apparatus was also different between the members of these two species complexes. Members of the *R. brunneus* complex have a round fleshy adhesive apparatus with frenum and connecting membrane while *R. giurinus* has a large, elliptical-shaped adhesive apparatus. In addition, three types of pre-dorsal fin scale pattern were found and can also be used for species identification. Further studies, particularly on habits, habitats, life histories, migratory patterns, and molecular phylogenetic relationships are needed for the conservation and management of this group of gobies.

摘　要

本研究使用行政院農業委員會特有生物研究保育中心於 1992-2005 年間採自全台不同河川之吻鰕虎屬(*Rhinogobius*)魚類樣本，分析其形態特徵與分布模式。在十個有效種樣本中，就其外部形態特徵可分爲極樂吻鰕虎種群 *R. giurinus* complex 與褐吻鰕虎種群 *R. brunneus* complex。極樂吻鰕虎種群在臺灣僅有極樂吻鰕虎(*R. giurinus*)一種，其餘九種均屬褐吻鰕虎種群，包括明潭吻鰕虎(*R. candidianus*)、細斑吻鰕虎(*R. delicatus*)、大吻鰕虎(*R. gigas*)、恆春吻鰕虎(*R. henchuenensis*)、蘭嶼吻鰕虎(*R. lanyuensis*)、斑帶吻鰕虎(*R. maculafasciatus*)、名古屋吻鰕虎(臺灣亞種) (*R. nagoyae formosanus*)、南臺吻鰕虎(*R. nantaiensis*)與短吻紅斑吻鰕虎(*R. rubromaculatus*)。上述物種可藉由測量形質、色斑特徵、計數形質與地理分布稍可辨別其種間差異。兩種群之左、右二枚腹鰭皆已癒合成吸盤狀，但其吸盤形狀在種群間則有不同，褐吻鰕虎種群腹部吸盤形狀呈圓形且有繫帶與連結膜，極樂吻鰕虎種群腹部吸盤較大且形狀呈橢圓形。另外，其背鰭前鱗模式可分爲三型，亦可作爲鑑種的依據。未來，將持續吻鰕虎種群的生態習性、棲地需求、生活史、洄游型態與分子親緣關係之研究，以提供物種保育與經營管理的參考。

Keywords: *Rhinogobius*, species complex, morphology, distribution, Taiwan

關鍵詞：吻鰕虎屬、相似種群、形態、分布、台灣

Received: December 17, 2013　　Accepted: March 21, 2014

收件日期：2013 年 12 月 19 日　　接受日期：2014 年 03 月 21 日

Introduction

Gobioidei is one of the largest vertebrate suborders (23% of the Perciformes) with approximately 2,211 extant species classified into 270 genera (Nelson 2006), making it one of the most speciose and morphologically diverse groups among teleost fishes (Thacker 2003). This group of fish is widely distributed throughout the tropical, subtropical and temperate regions of the world, in freshwater and near shore marine habitats. The high diversity, with small adult size of most goby species has hindered full understanding of their taxa and led to the confusion in their systematic relationship (Wang *et al.* 2001). Also, as compared to other Perciformes, gobies are often morphologically reduced with many species possessing simplifications and losses in various aspects of morphology (Thacker 2003). These factors, coupled with the generally cryptic nature of most goby species and the inherent difficulty to sample them hinder the study of their phylogeny and biology.

Among the Gobioidei, the Asiatic freshwater goby genus *Rhinogobius* Gill 1859, of the family Gobiidae, is of particular interest because of their wide distribution and great variation in coloration, morphology and ecological forms. *Rhinogobius* species are widely distributed on some islands of the West Pacific including Japan (Akihito *et al.* 1993, 2002), Taiwan (Chen and Shao 1996; Chen *et al.* 1998; Chen and Fang 1999), Hainan Province, China, (Chen *at al.* 2002), the Philippines (Herre 1927) as well as continental Asia in Russia, Korea, Vietnam, Laos, Cambodia and Thailand (Kottelat 1989, 2001a, 2001b; Chen and Miller 1998; Chen, Kottelat and Miller 1999; Chen, Wu and Shao 1999; Chen and Kottelat 2000, 2003). Studies on the life histories of this group of gobies indicated that the genus includes both diadromous and non-diadromous species (Mizuno 1960; Mizuno and Goto 1987; Kawanabe and Mizuno 1989; Iguchi and Mizuno 1991; Tzeng and Lin 1996; Akihito *et al.* 1993, 2002; Lee and Chang 1996; Shen *et al.* 1998; Chang *et al.* 2008; Tsunagawa and Arai 2008, 2009). Non-diadromous *Rhinogobius* are mainly landlocked continental species with limited distributions and are usually confined to the upper tributaries of the river systems (Chen and Miller 1998; Chen, Wu and Shao 1999b; Chen, Yang and Chen 1999), while the diadromous types are the migratory species mainly found in many islands with fast flowing rivers and streams.

At present, it is estimated that more than 80 species are known in East and Southeast Asia and some of them are still in need of formal description (Akihito *et al.* 2002; Chen and Kottelat 2003, 2005; Chen and Fang 2006). In Japan, most *Rhinogobius* species reported remain taxonomically uncertain, thus their scientific names has not yet been decided and only common names has been given on the basis of the color of macules and morphological features (Mizuno *et al.* 2001; Tsunagawa and Arai 2009). On the other hand, in Taiwan, two species complexes were recognized, *R. brunneus* and *R. giurinus* (Chen and Yu 1986; Tzeng 1986a). Collections and re-examinations of all *Rhinogobius* specimens from rivers in Taiwan during the last ten years revealed that *R. brunneus* species complex should include at least eight to nine species based on both morphological and molecular data (mtDNA sequences) as well as on some ecological considerations (Chen 1994; Chen and Shao 1996) while *R. giurinus* species has only a single species. It was reported in previous researches that the members of *R. brunneus* species complex are extremely variable in color and consist of many morphs (Akihito *et al.* 1984; Kawanabe and Mizuno 1989; Masuda *et al.* 1989; Katoh and Nishida 1994; Chen and Shao 1996; Kon and Yoshino 2003). Despite of these findings, however, the *Rhinogobius* species in Taiwan remain taxonomically uncertain and their biological cycle and the parameters leading to such extreme evolution in a small island remain poorly understood. Also, their phylogeny is difficult to resolve using morphological analyses alone because their meristic characters widely overlap, but the specific coloration patterns maybe useful in differentiating the members of the *R. brunneus* species complex (Mizuoka 1974; Masuda *et al.* 1984; Akihito *et al.* 1993; Chen *et al.* 1998).

In the present study, we examined the morphology and the geographical distributions of the members of *Rhinogobius* species complexes in Taiwan based on the fish collection done all over the island from 1992 to 2005. Also, diversity indices such as species richness (S), Margalef's and Menhinick's were calculated and compared between the different regions of Taiwan. S is the most common measurement of biodiversity used by scientists, conservationists and policy makers (Magurran 1988; Gray 2000; Wilsey *et al*., 2005; Flynn *et al*., 2009). It is also the simplest way to describe community and regional diversity. Diversity indices are a necessary tool to calculate and quantify diversity status (van Strien *et al*. 2012). The results obtained here will form the basis for future phylogenetic and ecological studies to help resolve their taxonomy and life histories in Taiwan. Understanding their evolution, distribution, dispersal and life histories is crucial for their management.

Materials and methods

Sample collection

All of the specimens of *Rhinogobius* examined in the present study were collected by Endemic Species Research Institute using electro-fishing from various rivers systems around the island from 1992 to 2005 (Fig. 1 and Table 1). The specimens were fixed with 15% formalin solution and then preserved in 75% ethyl alcohol. All specimens are deposited in the ichthyological collection of the Endemic Species Research Institute in Jiji, Nantou, Taiwan.

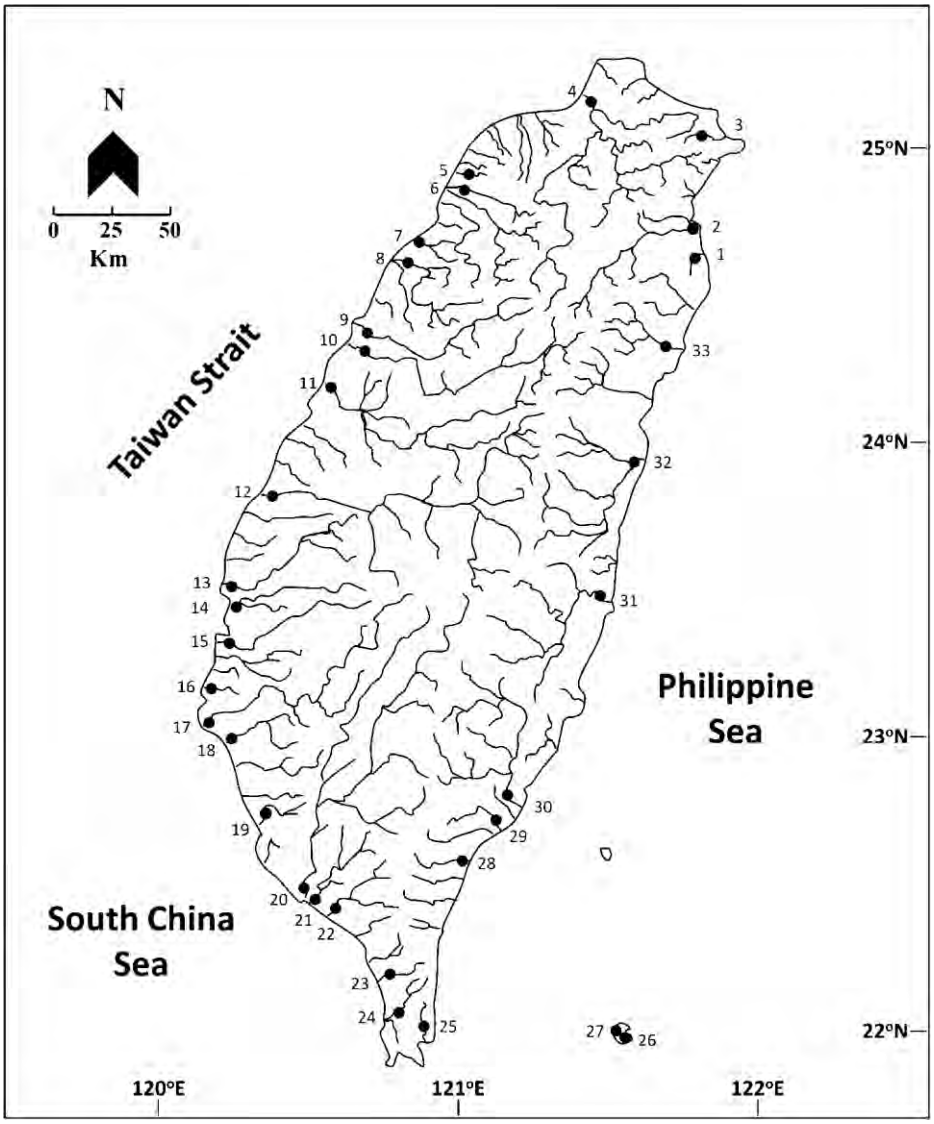

Fig. 1. Map showing the river systems and its tributaries (No. 1-33) around Taiwan where the Rhinogobius species were collected during the period from 1992 to2005. The names of the river systems and its tributaries are shown in Table 1.

Table 1. Data of the *Rhinogobius* species complexes samples collected in Taiwan

Region	No. of sampling location*	River system	Tributary/local branch	Sampling period	Sample size
Northern Taiwan	1	Dong'ao		2004	15
	2	Lan-yang		2003	2
			a. Songluo	2003	3
			b. Annong	2002-2003	25
			c. Cukeng	2002	1
			d. Paigu	2003	4
			e. Duowang	2004	1
			f. Xiao	2002	11
			g. Sichong	n/a	1
			h. Han	2003	6
			i. Malun	1999	106
	3	Shuangshi		2003	11
			a. Dingzailan	2002, 2004	15
			b. Hou Fanzaikeng	2002-2004	14
			c. Mudan Stream	2004	9
	4	Tanshui			
			a. Huiyao	2000	11
			b. Keelung	2000	17
			c. Dahan	1995, 2000, 2003	62
			d. Xindian	2002, 2004	42
	5	Fengshan		2000	17
	6	Touqian		2000	5
			a. Youluo	2000	10
Central Taiwan	7	Zhonggang		2000	4
			a. Dadong	2000	1
			b. Emei	2000	5
	8	Houlong		2000, 2005	54
			a. Wenshui	2000	6
	9	Da'an		2001	4
			a. Wushikeng	1997	1
	10	Dajia		1999, 2001, 2003	22
	11	Wu		2000, 2003-2005	250

			a. Fazi	2001-2002, 2005, 2007	85
			b. Mei	2004	41
			c. Maopukeng	2004	16
			d. Toubiankeng	2004-2005	7
			e. Dongbiankeng	2004	10
			f. Caohu	2005	1
			g. Cukeng	2005	4
			h. Zhangping	2005	31
			i. Wupengkeng	2005	6
			j. Maoluo	2005	47
			k. Dali	2005	32
			l. Pinglin	2005	38
			m. Nangang	2004	70
			n. Sanguang	2004	7
			o. Meiyuan	2005	3
			p. Beikeng	2004	17
			q. Gan	2005	6
			r. Shigang	2004	6
	12	Zhuoshui		2001	12
			a. Qingshui	2001, 2003	50
			b. Dongpurui	2003	15
			c. Pinglai	2004	3
	13	Beigang		2004-2005	59
			a. Huaxing	2001	2
Southern Taiwan	14	Puzi		2001	8
			a. Shitou	2001	1
	15	Bazhang		2002	14
			a. Chilan	2000-2002	30
	16	Jishui		2002	1
			a. Baishui	2002	9
	17	Zengwen		2002-2004	30
			a. Houjue	2002-2003	46
			b. Cailiao	2003	12
			c. Cao	2002-2003	106
	18	Yanshui	a. Xu	2002	4
			b. Wukan	2002	5

	19	Angongdian		2002	1
	20	Kaoping		2000-2003	70
			a. Qishan	2002-2004	29
			b. Laonong	2002, 2004	8
			c. Qingshui	2002-2003	95
			d. Koushe	2002	15
	21	Donggang		2000-2003	7
	22	Linbian		2002	4
			a. Walusi	2002	2
	23	Fenggang		2004	3
			a. Shuangliu	2002-2004	18
			b. Daren	2004	8
	24	Sichong		2002	39
			a. Damei	2002	4
			b. Mudan Stream	2002	38
	25	Gangkou		2004	8
			a. Jiadoulu	2004	3
	26	Dongqing		2004	1
	27	Yeyou		2004	1
Eastern Taiwan	28	Nantaimali		2000	4
	29	Zhiben		2004	52
	30	Beinan			
			a. Luye	2000	3
	31	Hsiukuluan		2002-2003, 2005	41
			a. Hongye	1992, 2003-2004	18
			b. Lehe	2003	6
			c. Fuyuan	2003	2
			d. Amei	2003	8
	32	Hualien			
			a. Lao Stream	2001-2004	36
			b. Bai-bao Stream	2002-2004	65
			c. Matai'an	2001-2002	4
	33	Heping		2003	26
Total					2188

*No. of sampling location refer to Fig.1

Morphometric measurements and species identification

After initial species identification, 20 individuals (when applicable) were chosen from each species for morphometric measurements and meristic counts following the methods of Akihito *et al.* 1984, Chen and Shao 1996 and Lee and Chang 1996. All measurements and counts were made from preserved specimens. Morphometric measurements include total length, standard length, head length (HL), body depth (BD) and width (BW), pre-dorsal fin (PDL) and pre-anal fin (PAL) lengths, caudal peduncle length (CPL) and depth (CPD) and 1st dorsal fin (D1bl), 2nd dorsal fin (D2bl) and anal fin (Abl) base lengths. Meristic counts on the other hand, include 1st dorsal fin (D1), 2nd dorsal fin (D2), pectoral fin (P1) and anal fin (A) ray counts.

Species diversity index calculation

The species diversity per geographic region was calculated using different species diversity indices (Equations 1-2):

(1) Margalef's species diversity index,

$$D = \frac{(S-1)}{\ln N}$$

(2) Menhinick's species diversity index,

$$D = \frac{S}{\sqrt{N}}$$

where *D* is the number of species for a given number of individuals, *S* is the number of species recorded (species richness) and *N* is the number of individuals (Jennings *et al*. 2001). The higher the index, the greater the diversity.

Results and discussions

Species Composition

A total of 2,188 individuals were collected from 33 river systems around Taiwan during the period from 1992 to 2005, and out of these, ten species were identified (Fig. 2) and assigned into two species complexes, *R. giurinus* and *R. brunneus*. *Rhinogobius giurinus* complex has only one species under it, *R. giurinus* (Fig. 2d), while *R. brunneus* complex contains the remaining nine species namely *R. candidianus* (Fig. 2a), *R. delicatus* (Fig. 2b), *R. gigas* (Fig. 2c), *R. henchuenensis* (Fig. 2e), *R. lanyuensis* (Fig. 2f), *R. maculafasciatus* (Fig. 2g), *R. nagoyae formosanus* (Fig. 2h), *R. nantaiensis* (Fig. 2i) and *R. rubromaculatus* (Fig. 2j). About 95.34% of the specimens examined were adults while the rest of the collection was composed of juveniles (4.43%) and larvae (0.23%) (Table 2).

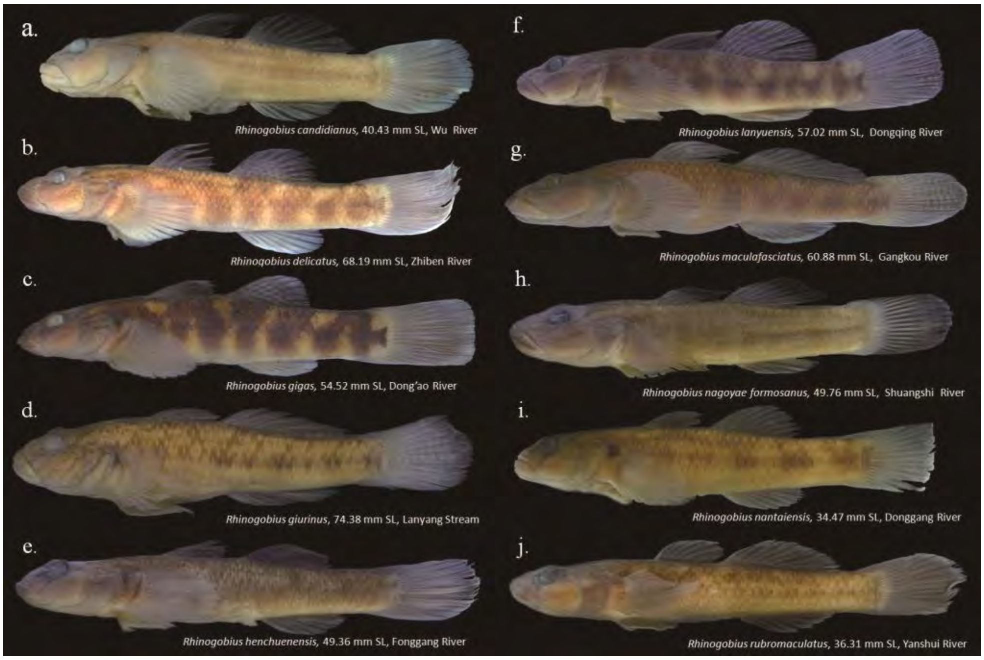

Fig. 2. External features of the 10 *Rhinogobius* species found in Taiwan.

Table 2. Composition of developmental stages and comparison of the 3 morphological characteristics (Pre-dorsal fin scale pattern, and ventral adhesive apparatus and scale types) of the 10 *Rhinogobius* species collected in Taiwan

Species	Stage composition			Total	Pre-dorsal fin scale pattern[1]	Ventral adhesive apparatus type[2]	Scale type
	Larva	Juvenile	Adult				
R. candidianus	5	62	1126	1193	Type 2	Type 2	ctenoid (flank) and cycloid (predorsal area)
R. delicatus	0	1	94	95	Type 3	Type 2	
R. gigas	0	0	183	183	Type 3	Type 2	
R. giurinus	0	9	68	77	Type 1	Type 1	ctenoid (flank and predorsal)
R. henchuenensis	0	2	112	114	Type 1	Type 2	ctenoid (flank) and cycloid (predorsal area)
R. lanyuensis	0	0	2	2	Type 3	Type 2	
R. maculafasciatus	0	3	311	314	Type 2	Type 2	
R. nagoyae formosanus	0	0	6	6	Type 3	Type 2	
R. nantaiensis	0	0	34	34	Type 2	Type 2	
R. rubromaculatus	0	20	150	170	Type 3	Type 2	
Total	5	97	2,086	2,188			

[1]Predorsal fin scale pattern refer to Fig. 3; [2]Ventral adhesive apparatus type refer to Fig. 5

Morphological Features

Ventral adhesive apparatus

The shape of the fused pelvic fins that forms the ventral adhesive apparatus was different between the members of these two *Rhinogobius* species complexes (Fig. 3 and Table 2). *Rhinogobius giurinus* has a large, elliptical-shaped adhesive apparatus (Type 1) while the members of the *R. brunneus* species complex have a round adhesive apparatus with frenum and connecting membrane (Type 2). Also the distance of the tip (posterior part) of the ventral adhesive apparatus in relation to the anus and genital pore was different between the members of these two species complexes. When adpress the posterior of part of the Type 1 ventral adhesive apparatus is closer to the anal pore as compared to that of Type 2.

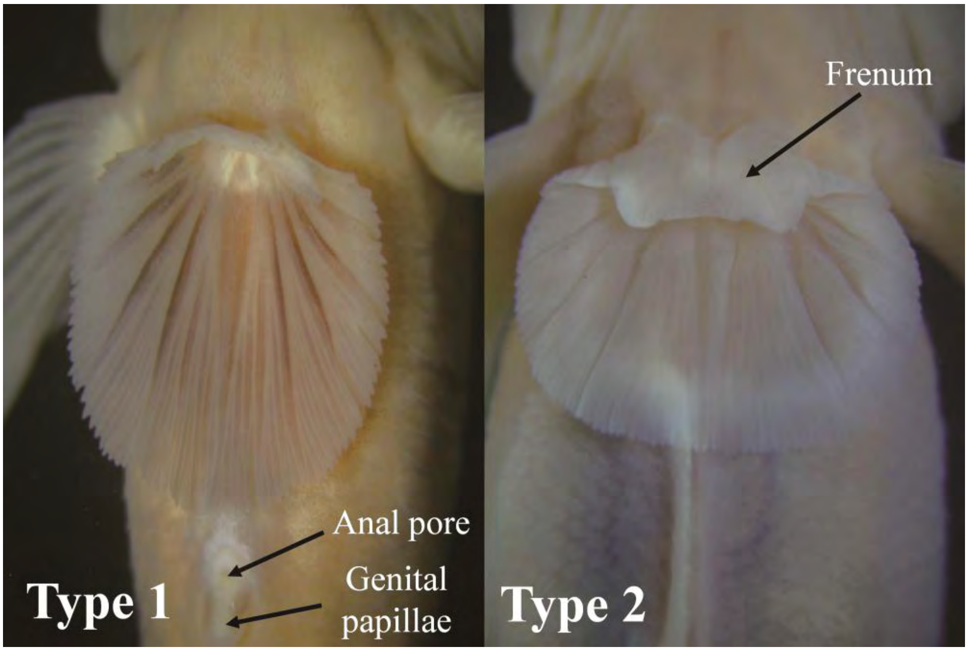

Fig. 3. Two types of fused pelvic fins that form the ventral adhesive apparatus in *Rhinogobius* spp. Type 1: *R. giurinus* complex; Type 2: *R. brunneus* complex.

Body scale type

Scales were collected along the flank, head and caudal regions of each species and examined under the microscope. The scales of the *Rhinogobius* species examined were classified as ctenoid (Fig. 4) and cycloid. Ctenoid was the only type of scale observed in the different body regions of *R. giurinus*. On the other hand, all the members of the *R. brunneus* complex have two types of scales: ctenoid on the flank region and small cycloid scales on the predorsal fin area. Ctenoid scale can be divided into two fields, the anterior field and the posterior field. The anterior field is the part of the scale that is buried (embedded) in the fish skin. Prominent vertical grooves that begin outward until the scale margin can be observed in the anterior field, and these are called secondary radii (Fig. 4b). In between these secondary radii (inter-radial area) and also in the lateral field of the scale were elevated ridges called circuli that usually appear as lines that more or less follow the outline of the scale (Fig. 4b). The posterior field of the scale, on the other hand, is the exposed part and it contains pigment cells (chromatophores) (Fig. 4c); and the tiny, comb-like projections on the margin called ctenii (Fig. 4d).

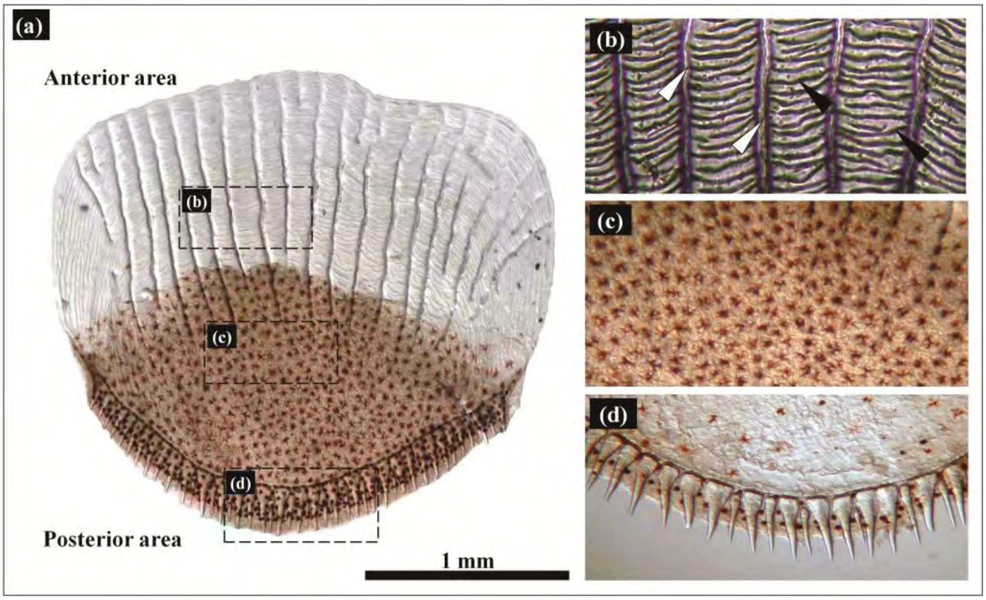

Fig. 4. Microstructures of the scale of *Rhinogobius*. (b-d) is partially magnified from the scale (a): (b) circuli (black arrow) and radii (white arrow), (c) pigment cells (chromatophores) and (d) ctenii.

Pre-dorsal fin scale pattern

Three distinct types of pre-dorsal fin scale pattern were found in the ten *Rhinogobius* species examined (Fig. 5). In first type of pre-dorsal fin scale pattern, the scaled area extends almost to the posterior margin of the eyes (Fig. 5a). *Rhinogobius giurinus* and *R. henchuenensis* exhibited this type of pattern (Table 2). On the other hand, in the second and the third type of pre-dorsal fin scale patterns, the scaled area does not extend beyond the posterior margin of the preoperculum with the third type noticeably shorter in coverage (Fig. 5c) than the second type (Fig. 5b). *Rhinogobius candidianus, R. maculafasciatus* and *R. nantaiensis* exhibited the second type pattern while *R. delicatus, R. gigas, R. lanyuensis, R. nagoyae formosanus* and *R. rubromaculatus* exhibited the third type.

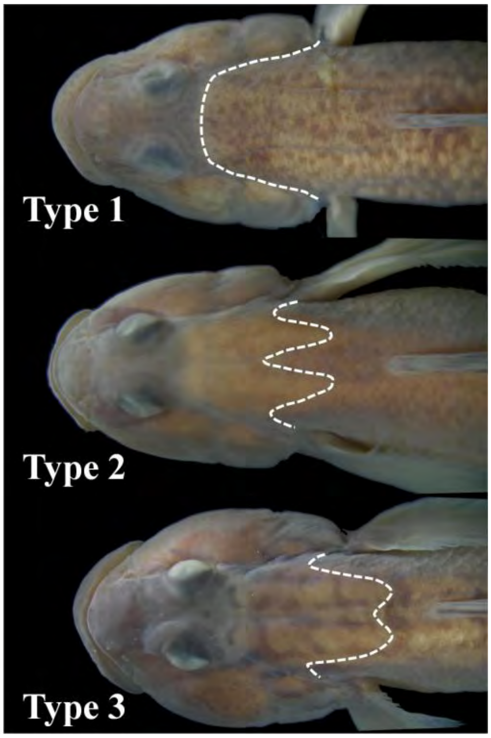

Fig. 5. Types of pre-dorsal fin scale patterns found among different *Rhinogobius* species from Taiwan.

Morphological measurements and fin ray counts

Morphometric measurement data and meristic counts are listed in Table 3. *Rhinogobius lanyuensis* has the shallowest BD (15.12±1.29 mm) while *R. maculafasciatus* has the deepest (23.89±2.17 mm). In terms of BW, *R. gigas* has the narrowest body (15.88±1.89 mm) while *R. maculafasciatus* has the widest (20.33±2.12 mm). PDL ranged from 39.58±1.74 mm in *R. rubromaculatus* to 42.90±1.51 mm in *R. lanyuensis* while PAL ranged from 62.57±1.26 mm in *R. giurinus* to 67.32±1.73 mm in *R. nagoyae formosanus*. CPL ranged 16.22±2.30 mm in *R. rubromaculatus* to 19.77±0.84 mm in *R. lanyuensis*. CPD on the other hand, ranged from 12.39±0.96 mm in *R. giurinus* to 14.75±1.49 mm in *R. henchuenensis*. D1bl ranged from 15.83±1.64 in *R. henchuenensis* to 18.30±1.33 mm in *R. candidianus* while D2bl ranged from 16.34±1.39 mm in *R. gigas* to 20.80±1.64 mm in *R. rubromaculatus*. Abl ranged from 12.80±1.33 in *R. delicatus* to 16.20±1.17 mm in *R. rubromaculatus*. *Rhinogobius maculafasciatus* has the longest head length (34.06±1.87 mm) while *R. nantaiensis* had the shortest head (30.50±2.15 mm). The D1 of the specimens examined ranged from 5 to 6 while D2 from 7 to 10. A on the other hand ranged from 7 to 10 while P1 ranged from 15 to 22.

The members of the *Rhinogobius* species complex of Taiwan have only very few distinguishable morphological differences except probably for their color patterns. Chen and Shao (1996) also indicated that the *R. brunneus* species complex in Taiwan has radiated into many distinct morphological species with a high degree of local endemism. But previous researches have indicated that these species exhibit distinct segregation in terms of the ecological niche they occupy such as preference for fast or slow water current, upstream or downstream areas, deep or shallow waters, migratory habit and egg size diversity (Chen and Shao 1996, Lee and Chang 1996, Shen *et al*. 1998, Cheng *et al*. 2005a). Therefore, it is important to use a combination of morphological characters and ecological considerations in identifying the different *Rhinogobius* species in Taiwan.

Table 3. Comparison of meristic counts and morphometric measurements (mean ± S.D.) among 10 different *Rhinogobius* species in Taiwan. All values shown except for the meristic counts are percentages (%) as ratio with standard length

	R. candidianus	***R. delicatus***	***R. gigas***	***R. giurinus***	***R. henchuenensis***	***R. lanyuensis***	***R. maculafasciatus***	***R. nagoyae formosanus***	***R. nantaiensis***	***R. rubromaculatus***
Sample size	20	20	20	20	20	2	20	6	20	20
Morphometric										
BD	20.69±2.47	20.33±3.52	17.19±1.78	20.38±2.83	21.90±3.13	15.12±1.29	23.89±2.17	19.19±1.55	20.94±3.49	19.94±2.89
BW	19.21±2.40	18.37±2.52	15.88±1.89	17.23±1.85	18.81±1.66	16.44±3.57	20.33±2.12	17.02±2.68	18.67±2.77	18.09±2.36
PDL	40.93±2.19	41.92±1.64	41.38±1.99	40.21±1.12	42.77±1.31	42.90±1.51	41.75±4.74	42.06±1.53	42.28±4.21	39.58±1.74
PAL	64.17±2.33	65.84±2.30	66.90±3.78	62.57±1.26	66.92±1.82	65.34±2.11	64.53±1.58	67.32±1.73	63.01±2.17	63.81±1.43
CPL	18.68±1.79	18.70±1.93	19.42±1.55	19.35±1.31	17.32±1.77	19.77±0.84	18.67±1.52	17.80±0.83	19.36±2.18	16.22±2.30
CPD	14.36±0.80	13.76±1.41	13.02±0.83	12.39±0.96	14.75±1.49	14.35±0.42	13.19±0.67	13.33±0.51	13.76±0.80	13.60±0.78
D1bl	18.30±1.33	17.54±1.41	16.82±1.17	18.02±1.66	15.83±1.64	16.58±0.62	18.22±1.98	16.01±0.75	15.93±2.31	18.04±1.86
D2bl	18.58±1.02	16.38±1.67	16.34±1.39	19.07±1.14	17.56±0.85	16.92±0.56	17.06±0.99	16.45±1.34	17.81±1.08	20.80±1.64
Abl	14.07±1.40	12.80±1.33	13.09±1.40	15.90±0.86	14.23±1.40	13.01±0.16	13.30±1.02	13.84±1.40	13.33±0.93	16.20±1.17
HL	30.88±3.40	31.02±1.91	31.56±3.09	32.53±1.24	33.72±2.15	33.98±0.72	34.06±1.87	34.71±3.34	30.50±2.15	31.57±1.42
Meristic										
D1	5-6	6	6	6	6	6	6	6	6	6
D2	7-10	5-6	8-10	10	9-10	9-10	9-10	8-9	10	9-10
A	7-10	9-10	8-10	10	9-10	10	9-10	8-9	10	8-10
P1	15-18	20-22	21-22	20	18-21	20	18-21	17-18	19-20	15-18

Geographical Distribution

Thirteen years of intensive collections from various river systems and its drainages around Taiwan revealed that the different *Rhinogobius* species examined exhibited species-specific distribution patterns (Fig.6). Some species have a very narrow geographic distribution while the others are distributed widely. Among all the species examined, *R. candidianus* and *R. giurinus* can be found in the majority of the river systems in Taiwan (Fig. 6a and 6d). *Rhinogobius delicatus*, on the other hand, can only be found in rivers along the northern, eastern and southern Taiwan (Fig. 6b). *Rhinogobius henchuenensis* and *R. maculafasciatus* can only be found in the rivers in southern Taiwan (Fig. 6e and 6g), while *R. lanyuensis* seems to be restricted only in Orchid Island (Lanyu), a 42 km^2 volcanic island off the southern coast of Taiwan (Fig. 6f). *Rhinogobius nagoyae formosanus* is only restricted in northern Taiwan (Fig. 6h) and *R. nantaiensis* can only be found in the rivers in central and southern Taiwan (Fig. 6i). *Rhinogobius rubromaculatus* is found in northern, central and southern Taiwan (Fig. 6j). In addition, population genetic studies on some of the species such as *R. maculafasciatus* and *R. rubromaculatus* showed that there is little genetic differences among their respective populations in Taiwan (Cheng *et al*. 2005a,b), indicating contemporary gene flow among its populations through oceanic larval dispersal. Unfortunately, the population genetic structures of the other *Rhinogobius* species in Taiwan have not yet been investigated. On the other hand, the geographic distribution pattern of the different *Rhinogobius* species in Taiwan might be affected by a number of factors such as temperature preference, river topology, inter-specific competition and habits of different goby species. The dominance of one or more species in a certain region might restrict the ability of the other species to colonize that area. Species that prefers warmer water temperature might not be able to colonize the colder northern region of Taiwan. But some researchers have suggested that the occurrence of freshwater fish species of marine origin (like amphidromous gobies) in northern Taiwan is probably because of the strong Kuroshio Current that flows from south to north (Chen and Fang 1999). Diadromous types usually have wider geographic distribution since their oceanic larval duration allows them to be transported in areas not reached by non-diadromous types. Non-diadromous types also have limited opportunities for gene flow (Tzeng *et al*. 2006). Also, since each region in Taiwan offer different types of habitat, it is expected that the *Rhinogobius* species in the island will have a variety of ecological forms according to the niche they occupy. Species that prefers muddy or sandy river substrate with slow river flow were often found in western Taiwan while those that preferred rocky substrate, steep river topology and swift river current were found in eastern Taiwan.

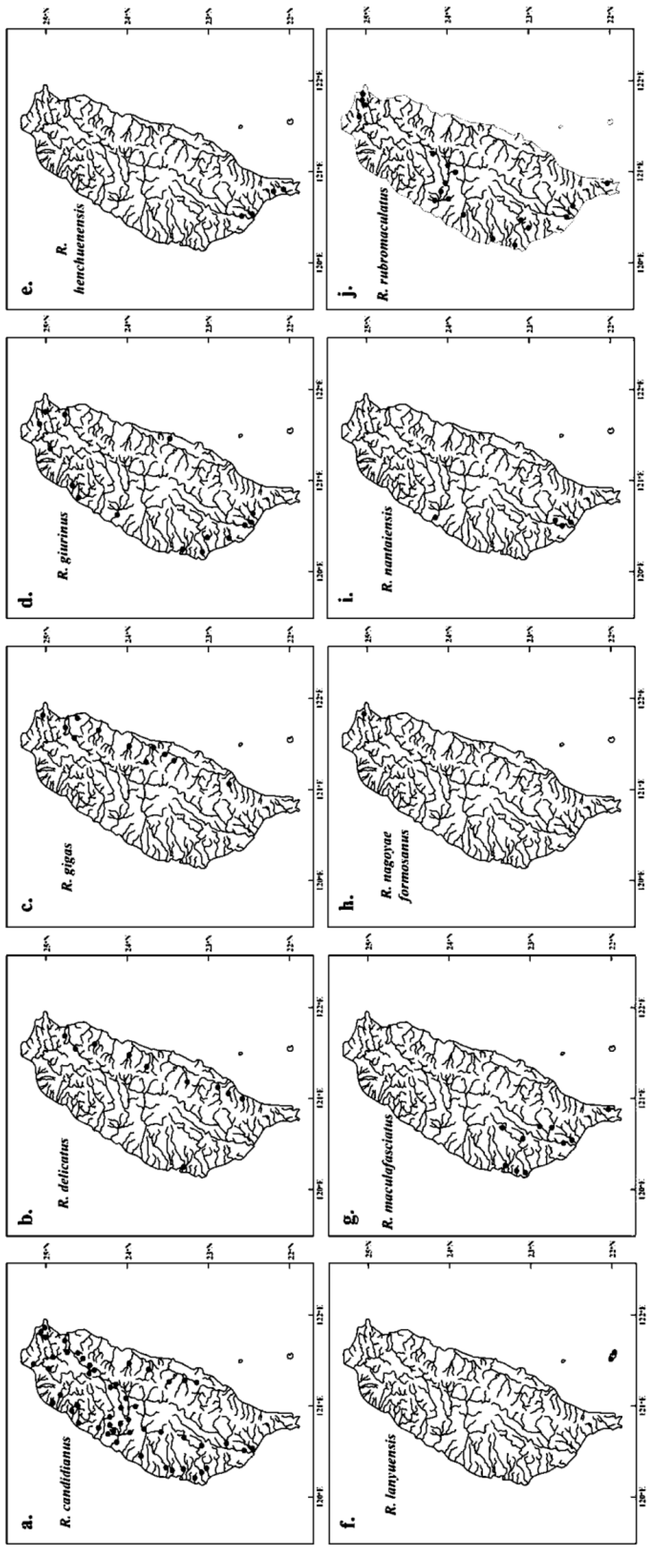

Fig. 6. Different distribution patterns of the 10 *Rhinogobius* species in Taiwan.

Species diversity

In terms of the number of species observed, southern Taiwan is the most speciose region in the island with seven out of ten *Rhinogobius* species found, followed by northern Taiwan with six species (Table 4). Central and eastern Taiwan has similar number of species, four each. The other indices of species diversity showed different pattern. Margalef's diversity index indicated that southern Taiwan was the most speciose region while central Taiwan was the least. Menhinick's on the other hand, indicated that northern region of Taiwan was the most speciose while its central region was the least. High species diversity is also expected in southern Taiwan since it is a subtropical region and productivity is high. On the other hand, the restriction of some freshwater fish species to the western or eastern part of Taiwan was thought to be highly correlated with the topographical isolation due to the rise of the Central Mountain Range about one million years ago (Lin 1966; Tzeng 1986b; Wang *et al*. 1999, 2000). Taiwan is an isolated island located between East and Northeast China and South China Sea in the southwest and is under the influence of subtropical weather regimes. The waters on its western slope are shallow while very deep (up to 1,000-2,000 m) on the eastern slope (Wu *et al*. 2007). On the other hand, the majority of the river systems on the island mainly flows to the western and eastern coasts and is well separated by the Central Mountain Ridge (Page and Suppe 1981; Wu *et al*. 2007). These features resulted in a unique freshwater fish fauna on the island. Therefore the study of freshwater fishes in Taiwan is extremely important because it confirms the relationship between the island and its adjacent areas. Tzeng *et al*. (2006) also stressed that the use of freshwater species for biogeography studies are very appropriate primarily because of their restricted distribution and strong association between evolutionary history and geological events.

Table 4. Comparison of species diversity indices of *Rhinogobius* species among different regions of Taiwan

Region	No. of specimen collected	Species diversity indices		
		Species richness	Margalef's	Menhinick's
North	388	6	0.84	0.30
Central	915	4	0.44	0.13
South	620	7	0.93	0.28
East	265	4	0.54	0.25

Conclusion and perspectives

The *Rhinogobius* species in Taiwan exhibits great variations in coloration, morphology and ecological forms and such variations resulted in confused and problematic taxonomy. A reliable phylogeny for the group would help in setting evolutionary hypothesis that resulted in their extreme diversity in such a small island like Taiwan. Also, determining their phylogeny would establish their exact relationship and would help establish a timeline for their speciation. This would present a more detailed evolutionary history of the diverse *Rhinogobius* species in the island. It is also interesting to explore the effect of different barriers to dispersal such as mountain ranges and oceanographic current systems on the distribution pattern of the different *Rhinogobius* species. Understanding this information is essential for their conservation and management and also will present an important contribution to the understanding of the historical biogeography of freshwater fishes of East Asia.

Acknowledgements

The authors are grateful to the former students of the Fisheries Biology Laboratory, Institute of Fisheries Science, National Taiwan University (Taipei, Taiwan) and to Dr. Rung-Tsung Chen, Prof. Chu-Fa Tsai and the staff of the Division of Habitats and Ecosystems, Endemic Species Research Institute (Jiji, Taiwan) for their assistance in both the field work and specimen collections.

Literatures cited

Akihito, M. Hayashi and T. Yoshino. 1984. Suborder Gobioidei. pp. 228-289. *In*: H. Masuda, K. Amaoka, C. Araga, T. Uyeno and T. Yoshino (eds.). The fishes of the Japanese Archipelago. Tokai University Press, Tokyo, Japan.

Akihito, A. Iwata, Y. Ikeda and K. Sakamoto. 1993. Suborder gobioidei. pp. 997-1116. *In*: T. Nakabo (ed.). Fishes of Japan with Pictorial Keys to the Species. Tokai University Press, Tokyo, Japan.

Akihito, K. Sakamoto, Y. Ikeda and K. Sugiyama. 2002. Gobioidei. pp. 1139-1310. *In*: T Nakabo (ed.). Fishes of Japan with Pictorial Keys to the Species. Tokai University Press, Tokyo, Japan.

Chang, M. Y., W. N. Tzeng, C. H. Wang and C. F. You. 2008. Differences in otolith elemental composition of the larval *Rhinogobius giurinus* (Perciformes Gobiidae) among estuaries of Taiwan: Implications for larval dispersal and connectance among metapopulation. Zoological Studies 47: 676-684.

Chen, I. S. 1994. The systematic studies of *Rhinogobius brunneus* complex from Taiwan. Master’s Thesis, National Sun Yat-Sen University, Kaoshiung, Taiwan.

Chen, I. S., C. H. Hsu, C. F. Hui, K. T. Shao, P. J. Miller and L. S. Fang. 1998. Sequence length and variation in the mitochondrial control region of two freshwater gobiid fishes belonging to *Rhinogobius* (Teleostei: Gobioidei). Journal of Fish Biology 53: 179-191.

Chen, I. S. and K. T Shao. 1996. A taxonomic review of gobiid fish genus *Rhinogobius* Gill, 1859, from Taiwan, with descriptions of three new species. Zoological Studies 35: 200-214.

Chen, I. S., H. L. Wu and K. T. Shao. 1999. A new species of *Rhinogobius* (Teleostei: Gobiidae) from Fujian Province, China. Ichthyological Research 46: 171-178.

Chen, I. S., J. X. Yang and Y. R. Chen. 1999. A new species of *Rhinogobius* (Teleostei: Gobiidae) from the Honghe basin, Yunnan Province. Acta Zoologica Taiwanica 10: 45-52.

Chen, I. S. and L. S. Fang. 1999. Freshwater and estuarine fishes of Taiwan. National Museum of Marine Biology and Aquarium, Pingtung, Taiwan.

Chen, I. S. and L. S. Fang. 2006. A new species of *Rhinogobius* (Teleostei: Gobiidae) from the Hanjiang basin in Guangdong Province, China. Ichthyological Research 53: 247-253.

Chen, I. S. and M. Kottelat. 2000. *Rhinogobius maculicervix*, a new species of goby from the Mekong basin in northern Laos. Ichthyological Explorations of Freshwater 11: 81-87.

Chen, I. S. and M. Kottelat. 2003. Three new freshwater gobies of the genus, *Rhinogobius* (Teleostei: Gobiidae) from northeastern Laos. Raffles Bulletin of Zoology 51: 87-95.

Chen, I. S. and M. Kottelat. 2005. Four new freshwater gobies of the genus *Rhinogobius* (Teleostei: Gobiidae) from northern Vietnam. Journal of Natural History 39: 1407-1429.

Chen, I. S., M. Kottelat and P. J. Miller. 1999. Freshwater gobies of the genus *Rhinogobius* from the Mekong basin in Thailand and Laos, with descriptions of three new species. Zoological Studies 38: 19-32.

Chen, J. T. F and M. J. Yu. 1986. A synopsis of vertebrates of Taiwan, Vol. II. pp. 442. Commercial Books Co., Taipei, Taiwan.

Chen, I. S. and P. J. Miller. 1998. Rediscription of *Gobius davidi* (Teleostei: Gobiidae) and comparison with *Rhinogobius lentiginis*. Cybium 22: 211-221.

Chen, I. S., P. J. Miller, H. L. Wu and L. S. Fang. 2002. Taxonomy and mitochondrial sequence evolution in non-diadromous species of *Rhinogobius* (Teleostei: Gobiidae) of Hainan Island, southern China. Marine and Freshwater Research 53: 259-273.

Cheng, H. L., S. Huang and S. C. Lee. 2005a. Phylogeography of the endemic goby, *Rhinogobius maculafasciatus* (Pisces: Gobiidae), in Taiwan. Zoological Studies 44: 329-336.

Cheng, H. L., S. Huang and S. C. Lee. 2005b. Morphological and molecular variation in *Rhinogobius rubromaculatus* (Pisces: Gobiidae) in Taiwan. Zoological Studies 44: 119-129.

Flynn, D. F. B., M. Gogol-Prokurat, T. Nogeire, N. Molinari, B. T. Richers, B. B. Lin, N. Simpson, M. M. Mayfield and F. DeClerck. 2009. Loss of functional diversity under land use intensification across multiple taxa. Ecology Letters 12: 22-33.

Gill, T.N. 1859. Notes on a collection of Japanese fishes by Dr. J. Morrow. Proceedings of the Academy of Natural Sciences of Philadelphia 1859: 144-149.

Gray, J. S. 2000. The measurement of marine species diversity, with an application to the benthic fauna of the Norwegian continental shelf. Journal of Experimental Marine Biology and Ecology 250: 23-49.

Here, A. W. 1927. Gobies of the Philippines and China Sea. Monograph of the Bureau of Science Manila 23: 1-352.

Iguchi K. and N. Mizuno. 1991. Mechanism of embryonic drift in the amphidromous goby, *Rhinogobius brunneus*. Environmental Biology of Fishes 31: 295-300.

Jennings, S., M. J. Kaiser and J. D. Reynolds. 2001. Marine Fisheries Ecology. pp. 245-250. Blackwell Science, Oxford, London.

Kawanabe, H. and N. Mizuno. 1989. Freshwater fishes in Japan. pp. 600-603. Yama-Kei Publications, Tokyo, Japan.

Katoh, M. and M. Nishida. 1994. Biochemical and egg size evolution of freshwater fishes in the *Rhinogobius brunneus* complex (Pisces: Gobiidae) in Okinawa, Japan. Biological Journal of the Linnaean Society 51: 325-335.

Kon, T. and T. Yoshino. 2003. Coloration and ontogenetic features of fluviatile species of *Rhinogobius* (Gobioidei: Gobiidae) in Amami-oshima Island, Ryukyu Islands, Japan. Ichthyological Research 50: 109-116.

Kottelat, M. 1989. Zoogeography of the fishes from Indo-Chinese inland waters with an annotated check-list. Bulletin of the Zoological Museum of the University of Amsterdam 12: 1-55.

Kottelat, M. 2001a. Freshwater fishes of northern Vietnam. pp. 140. World Bank, Washington, District of Colombia, USA.

Kottelat, M. 2001b. Fishes of Laos. pp. 198. Wildlife Trust Heritage Publications, Colombo, Sri Lanka.

Lee, S. C. and J. T. Chang. 1996. A new goby, *Rhinogobius rubromaculatus* (Teleost: Gobiidae) from Taiwan. Zoological Studies 35: 30-35.

Lin, C. C. 1966. An outline of Taiwan's quaternary geohistory with a special discussion on the relation between natural history and cultural history in Taiwan. Bulletin of the Department of Archaeology and Anthropology 28: 7-44.

Magurran, A. E. 1988. Ecological diversity and its measurement. Princeton University Press, New Jersey, United States of America.

Masuda, H., K. Amaoka, C. Araga, T. Uyeno and T. Yoshino. 1984. pp. 433. The fishes of Japanese Archipelago. Tokai University Press, Tokyo, Japan.

Masuda, Y., T. Ozawa and S. Enami. 1989. Genetic differentiation among eight color types of freshwater goby, *Rhinogobius brunneus*, from western Japan. Japanese Journal of Ichthyology 36: 30-41.

Mizuno, N. 1960. Description of a new freshwater goby from Japan. Memoirs of the College of Sciences, University of Kyoto Series B 27: 97-119.

Mizuno, N. and A. Goto. 1987. pp. 244. Japanese freshwater fishes and their distribution, variation and speciation. Tokai University Press, Tokyo, Japan.

Mizuno, N., K. Tsuji, T. Suzuki, T. Koshikawa and A. Iwata. 2001. *Rhinogobius* spp. pp. 584-603. *In*: H. Kawanabe, N. Mizuno and K. Hosoya (eds.). Freshwater fishes of Japan. Yamatokeikokusha, Tokyo, Japan.

Mizuoka, S. 1974. Studies on the variation of *Rhinogobius brunneus* (Temminck et Schlegel) III. On the six types of body color and color pattern in the Sanin district, the Hokuriku district, Sanyo district and the Goto Islands. Bulletin of the Faculty of Education, Hiroshima University 23: 31-40.

Nelson, J. S. 2006. Fishes of the world, 4th edition. pp. 419-424. John Wiley and Sons, New York, USA.

Page, B.M. and J. Suppe. 1981. The Pliocene Lichi mélange of Taiwan: its plate-tectonic and olistostromal origin. American Journal of Science 281: 193-227.

Shen, K. N., Y. C. Lee and W. N. Tzeng. 1998. Use of otolith microchemistry to investigate the life history pattern of gobies in a Taiwanese stream. Zoological Studies 37: 322-329.

Thacker, C. E. 2003. Molecular phylogeny of the gobioid fishes (Teleost: Perciformes: Gobioidei). Molecular Phylogenetics and Evolution 26: 354-368.

Tsunagawa, T. and T. Arai. 2008. Flexible migration of Japanese freshwater gobies *Rhinogobius* spp. as revealed by otolith Sr:Ca ratios. Journal of Fish Biology 73: 2421-2433.

Tsunagawa, T. and T. Arai. 2009. Migration diversity of the freshwater goby *Rhinogobius* sp. BI, as revealed by otolith Sr:Ca ratios. Aquatic Biology 5: 187-194.

Tzeng, C. S. 1986a. Freshwater fishes of Taiwan. pp. 197. Taiwan Province Education Department Press, Taipei, Taiwan.

Tzeng, C. S. 1986b. Distribution of freshwater fishes of Taiwan. Journal of Taiwan Museum 39: 127-164.

Tzeng, C. S. and Y. S. Lin. 1996. Phylogenetic relationship of *Rhinogobius giurinus* of Taiwan and mainland China based on the mitochondrial DNA sequence analysis. Chinese Bioscience 39:66.

Tzeng, C. S., Y. S. Lin, S. M. Lin, T. Y. Wang and F. Y. Wang. 2006. The Phylogeography and population demographics of selected freshwater fishes in Taiwan. Zoological Studies 45: 285-297.

van Strien, A. J., L. L Soldaat and R. D. Gregory. 2012. Desirable mathematical properties of indicators for biodiversity change. Ecological Indicators 14: 202-208.

Wang, H. Y., M. P. Tsai, M. J. Yu and S. C. Lee 1999. Influence of glaciations on divergence patterns of the endemic minnow, *Zacco pachycephalus*, in Taiwan. Molecular Ecology 8: 1879-1888.

Wang, H. Y. 2001. Molecular phylogeny of gobioid fishes (Perciformes: Gobioidei) based on mitochondrial 12s rRNA sequences. Molecular Phylogenetics and Evolution 20: 390-408.

Wang, J. P., K. C. Hsu and T. Y Chiang. 2000. Mitochondrial DNA phylogeography of *Acrossocheilus paradoxus* (Cyprinidae) in Taiwan. Molecular Ecology 9: 1483- 1494.

Wilsey, B. J., D. R. Chalcraft, C. M. Bowles and M. R. Willig. 2005. Relationship among indices suggest that richness is an incomplete surrogate for grassland biodiversity. Ecology 86: 1178-1184.

Wu, J. H., C. H. Hsu, L. S. Fang and I. S. Chen. 2007. The molecular Phylogeography of *Candidia barbata* species complex (Teleostei: Cyprinidae) from Taiwan. The Raffles Bulletin of Zoology 14: 61-67.