

## Genetic Evidence to Clarify the Systematic Status of the Genera *Zacco* and *Candidia* (Cypriniformes: Cyprinidae)

Hung-Yi Wang<sup>1,2</sup>, Sin-Che Lee<sup>1,\*</sup> and Ming-Jenn Yu<sup>2</sup>

<sup>1</sup>Institute of Zoology, Academia Sinica, Taipei, Taiwan 115, R.O.C. E-mail: eleotris@sinica.edu.tw

<sup>2</sup>Department of Biology, Tunghai University, Taichung, Taiwan 400, R.O.C.

(Accepted February 20, 1997)

**Hung-Yi Wang, Sin-Che Lee and Ming-Jenn Yu (1997)** Genetic evidence to clarify the systematic status of the genera *Zacco* and *Candidia* (Cypriniformes: Cyprinidae). *Zoological Studies* 36(3): 170-177. Genetic relationships among species of the genera *Zacco* and *Candidia* were analyzed using allozyme data from sampled specimens collected from 6 rivers in Taiwan. A total of 78 alleles were resolved for 26 loci from 13 enzyme systems. Nei's genetic distance between 2 congeneric species (*Zacco pachycephalus* and *Z. platypus*) was 0.285, which is within the range for the same genus. A slightly larger mouth cleft, smaller lateral line scales, and fixed alleles at *mMDH\*100*, *ME-1\*100*, *PGI-B\*100*, *PGM-1\*100*, and *PGM-2\*100* in *Zacco pachycephalus* can be used to distinguish it from *Z. platypus*. Comparison with *Aphyocypris kikuchii*, *Candidia barbatus* showed more distant relationships with these 2 *Zacco* species, suggesting that *Zacco* and *Candidia* are 2 distinct genera. In addition, a barbel at mouth corner, and fixed alleles at *sAAT-1\*120*, *CK-A\*93*, *FH-1\*80*, *FH-2\*82*, *G<sub>6</sub>PDH-1\*80*, *IDHP-1\*113*, *IDHP-3\*120*, *ME-1\*103*, *ME-2\*50*, *PGM-1\*120*, and *PGM-2\*120* in *Candidia* can also be used to distinguish it from the genus *Zacco*. The colonization and speciation event of the genus *Zacco* in Taiwan was discussed in detail.

**Key words:** Allozyme comparisons, *Zacco* and *Candidia*, River habitats, Taiwan.

Species of the genera *Zacco* Jordan and Evermann 1902, and *Candidia* Jordan and Richardson 1909 (Cyprinidae: Rasborinae) are common minnows in western Taiwan rivers. Several species of the genus *Zacco* occur in Japan, Korea, China, and Taiwan (Banareescu 1968), while the genus *Candidia* containing only 1 species is unique to Taiwan. Some external features of these 2 genera are similar, such as in an elongated body, medium or small-sized scales, a lateral line profile running along the lower flank of the body, the origin of the dorsal fin inserted opposite to the base of the ventral fin, maxillae reaching or behind the front margin of the orbit, tubercles present on both sides of the snout, and elongated anal fin rays appearing only in mature males (Regan 1908, Banareescu 1968). However, the single species of the genus *Candidia* differs from species of the genus *Zacco* by having barbels at the mouth corner, and a longitudinal stripe on the body sides, and by the

anterior 4 branched anal rays not extending to the caudal base in sexually mature males.

According to recent studies, the genus *Zacco* in Taiwan contain 2 valid species, *Z. pachycephalus* and *Z. platypus* (Shen et al. 1993). *Zacco* species which appear in older literature, such as *Zacco evolans*, would be a junior synonym of *Z. pachycephalus* (Oshima 1919). The record of *Z. temmincki* in Taiwan by Oshima (1919) and the subsequent record by Chen and Yu (1986) were misidentifications of *Z. pachycephalus*. Actually, *Z. temmincki* (Temminck and Schlegel 1846) is only found in Korea, Japan, and Mainland China. The distributions of the 2 previously recognized *Zacco* species in Taiwan are different. *Z. platypus* is restricted to northern Taiwan, while *Z. pachycephalus* is distributed throughout Taiwan except on the eastern side. The recent occurrence on the latter species in eastern Taiwan is a result of artificial introduction from release of fish fry.

\*To whom correspondence and reprint requests should be addressed.

The distribution pattern of *Candidia barbatus* is similar to that of *Z. pachycephalus*, also having the same problem of fry release in eastern Taiwan by the local government agents. Since *Z. pachycephalus* lives sympatrically with *C. barbatus* and have close resemblances of some external features as stated above, some authors have discussed placing *C. barbatus* under the genus *Zacco* (Banarescu 1968, Shen et al. 1993). Therefore, it is still unclear whether *C. barbatus* belongs with the *Zacco* species or it is in a separate genus. In this paper we use allozyme electrophoresis and choose *Aphyocypris kikuchii* as an outgroup to clarify the taxonomic status of the genera *Zacco* and *Candidia*.

## MATERIALS AND METHODS

A total of 66 *Zacco platypus* (56.9 to 89.6 mm in standard length, SL), 146 *Z. pachycephalus* (54.3 to 156.9 mm in SL), 87 *Candidia barbatus* (63.7 to 144.5 mm in SL), and 18 *Aphyocypris kikuchii* (38.9 to 58.6 mm in SL) were collected during 1991 to

1994 from 6 rivers: Hualien River, Nantzushian River, Peihsi River, Shuangshi River, Shuili River, and Tachia River (Fig. 1).

Tissues from eyes, heart, liver, and skeletal muscle were homogenized in 2-3 volumes of extraction buffer (0.1 M Tris-HCl, 1 mM EDTA (Na<sub>2</sub>), and 0.05 mM NADP<sup>+</sup>, pH 7.0; Shaklee and Keenan 1986). The homogenates were centrifuged at 17 000 g for 40 min, and the clear supernatants were stored at -70°C until electrophoresis.

The tissue extracts were then applied on a 12% starch gel for horizontal electrophoresis. The buffer solutions used were those of Sung et al. (1993). Staining methods and recipes were adopted from Shaklee and Keenan 1986, Pasteur et al. 1988, Murphy et al. 1990, and Sung et al. 1993. Locus nomenclature follows that of Shaklee et al. (1990). Alleles at any locus were given according to the proportion of their relative mobility to the most common allele which is designated as 100.

The BIOSYS-1 vers. 1.7 (Swofford and Selander 1989) computer program was used to estimate genetic variability (heterozygosity, and percent of polymorphic loci under the 0.95 criterion,  $P_{95}$ ), and Nei's (1972) and modified Roger's genetic distance (Wright 1978) between all pairwise combinations of taxa.

## RESULTS

Genetic data were obtained from electrophoresis on 26 loci with 78 alleles encoded for 13 enzymes from 4 species, among which, 19 loci showed clearly interspecific differences (Table 1). Genetic variabilities, expressed by mean heterozygosity ( $H$ ) and percentages of polymorphic loci ( $P_{95}$ ), of these species are  $H = 0.03$ ,  $P_{95} = 15.4\%$  in *Z. pachycephalus*;  $H = 0.024$ ,  $P_{95} = 11.5\%$  in *Z. platypus*;  $H = 0.021$ ,  $P_{95} = 8.0\%$  in *C. barbatus*; and  $H = 0.051$ ,  $P_{95} = 17.4\%$  in *A. kikuchii*. Some fixed allele frequency differences shown in Table 1 can be used to distinguish these species. First, at the generic level, genetic distances ( $D$ ) between *Candidia* and *Zacco* (0.951-1.115) as well as between *Zacco* and *Aphyocypris* (1.045 - 1.061) are almost the same (Table 2). An obviously complete substitution of alleles between *Zacco* and *Candidia* can also be well recognized from the following loci: *Candidia* has fixed alleles at *sAAT-1\*120*, *FH-1\*80*, *FH-2\*82*, *G<sub>6</sub>PDH\*80*, *IDHP-1\*113*, *IDHP-3\*120*, and *ME-2\*50*, while both *Zacco* species lack above alleles. Second, at the specific level within *Zacco* itself, Nei's genetic distance ( $D$ ) between

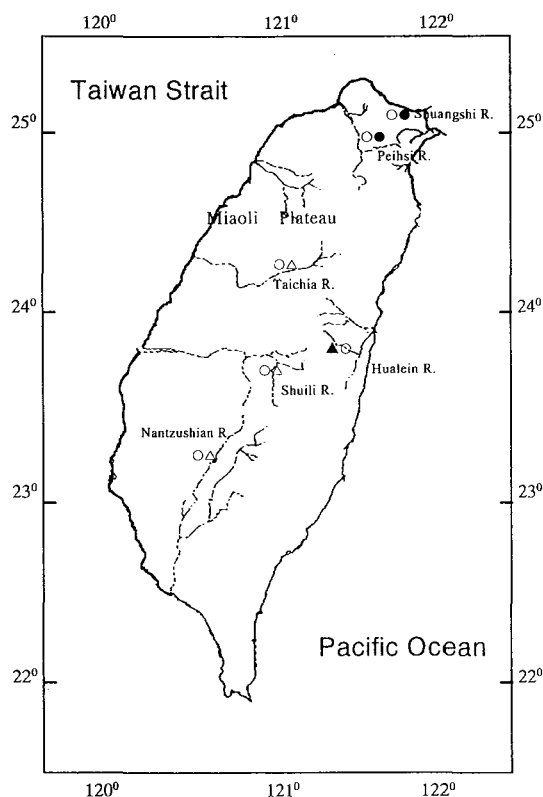


Fig. 1. Map of Taiwan showing the location of sampling sites. *Zacco pachycephalus* (○), *Z. platypus* (●), *Candidia barbatus* (△), and *Aphyocypris kikuchii* (▲).

**Table 1.** Allelic frequency of 23 comparable loci among 4 species, *Zacco pachycephalus*, *Z. platypus*, *Candidia barbatus*, and *Aphyocypris kikuchii*. Six monomorphic loci, including *CK-B*, *LDH-B*, *LDH-C*, and *XDH*, are excluded from this table

Locus	allele	<i>Z. pachycephalus</i>	<i>Z. platypus</i>	<i>C. barbatus</i>	<i>A. kikuchii</i>
sAAT-1	100	0.975	0.923	0.000	0.000
	113	0.025	0.077	0.000	0.000
	120	0.000	0.000	1.000	0.000
	142	0.000	0.000	0.000	1.000
sAAT-2	-20	0.000	0.000	0.000	0.167
	-100	1.000	1.000	1.000	0.833
CK-A	75	0.000	1.000	0.000	0.000
	93	0.000	0.000	1.000	0.000
	100	0.993	0.000	0.000	0.000
	112	0.000	0.000	0.000	1.000
	120	0.007	0.000	0.000	0.000
CK-C	97	0.152	0.000	1.000	0.000
	100	0.848	1.000	0.000	1.000
FH-1	80	0.000	0.000	1.000	ns
	100	1.000	1.000	0.000	ns
FH-2	82	0.000	0.000	1.000	ns
	100	1.000	1.000	0.000	ns
G <sub>6</sub> PDH	80	0.000	0.000	1.000	0.000
	100	1.000	1.000	0.000	1.000
IDHP-1	68	0.000	0.000	0.000	0.028
	87	0.000	0.000	0.000	0.972
	100	1.000	0.985	0.000	0.000
	113	0.000	0.000	1.000	0.000
	120	0.000	0.015	0.000	0.000
IDHP-2	75	0.000	0.000	0.176	ns
	100	1.000	1.000	0.000	ns
	115	0.000	0.000	0.824	ns
IDHP-3	86	0.000	0.000	0.000	0.278
	98	0.000	0.000	0.000	0.722
	100	1.000	1.000	0.000	0.000
	120	0.000	0.000	1.000	0.000
LDH-A	100	1.000	1.000	1.000	0.000
	110	0.000	0.000	0.000	1.000
sMDH-A	100	1.000	1.000	0.929	1.000
	120	0.000	0.000	0.071	0.000
sMDH-B	65	0.010	0.000	0.000	0.000
	100	0.990	1.000	0.000	1.000
	130	0.000	0.000	1.000	0.000
mMDH	100	1.000	0.000	0.000	0.000
	153	0.000	0.000	0.000	1.000
	200	0.000	1.000	1.000	0.000
ME-1	100	1.000	0.000	0.000	0.000
	101	0.000	0.000	0.000	1.000
	103	0.000	0.000	1.000	0.000
	107	0.000	1.000	0.000	0.000
ME-2	50	0.000	0.000	1.000	0.000
	100	1.000	1.000	0.000	0.000

**Table 1.** (Cont.)

Locus	allele	<i>Z. pachycephalus</i>	<i>Z. platypus</i>	<i>C. barbatus</i>	<i>A. kikuchii</i>
<i>ME-2</i>	120	0.000	0.000	0.000	0.917
	145	0.000	0.000	0.000	0.083
<i>MPI-1</i>	95	0.028	0.000	0.000	0.000
	100	0.706	0.937	1.000	0.000
	105	0.266	0.069	0.000	0.000
	110	0.000	0.000	0.000	1.000
<i>PGDH-1</i>	100	0.787	0.962	1.000	0.000
	110	0.000	0.000	0.000	1.000
	125	0.213	0.038	0.000	0.000
<i>PGI-A</i>	22	0.000	0.000	0.000	0.889
	72	0.000	0.000	0.000	0.111
	-40	0.023	0.938	1.000	0.000
	-100	0.926	0.062	0.000	0.000
	-140	0.051	0.000	0.000	0.000
<i>PGI-B</i>	75	0.000	1.000	0.000	0.083
	100	1.000	0.000	0.000	0.417
	115	0.000	0.000	0.435	0.000
	125	0.000	0.000	0.224	0.500
	135	0.000	0.000	0.341	0.000
<i>PGM-1</i>	75	0.000	1.000	0.000	0.000
	100	1.000	0.000	0.000	0.000
	102	0.000	0.000	0.000	1.000
	120	0.000	0.000	1.000	0.000
<i>PGM-2</i>	75	0.000	1.000	0.000	0.000
	100	1.000	0.000	0.000	0.000
	102	0.000	0.000	0.000	1.000
	120	0.000	0.000	1.000	0.000

ns: not scorable.

**Table 2.** Nei's (1972) genetic distance (below diagonal) and modified Roger's genetic distance (above diagonal) among *Zacco pachycephalus*, *Z. platypus*, *Candidia barbatus*, and *Aphyocypris kikuchii*

Species	<i>Z. pachycephalus</i>	<i>Z. platypus</i>	<i>C. barbatus</i>	<i>A. kikuchii</i>
<i>Z. pachycephalus</i>	—	0.328	0.817	0.782
<i>Z. platypus</i>	0.285	—	0.806	0.790
<i>C. barbatus</i>	1.115	0.951	—	0.857
<i>A. kikuchii</i>	1.045	1.061	1.521	—

*Z. pachycephalus* and *Z. platypus* is 0.285 (or  $I = 0.752$ ). *Z. platypus* has fixed alleles at *mMDH\*200*, *ME-1\*107*, *PGI-B\*80*, *PGM-1\*75*, and *PGM-2\*75*, while *Z. pachycephalus* has fixed alleles at *mMDH\*100*, *ME-1\*100*, *PGI-B\*100*, *PGM-1\*100*, and *PGM-2\*100*. In the Shuanghsi River where 2 *Zacco* species live sympatrically, 2  $F_1$  natural hybrids have occurred, judging from the occurrence

of intermediate zymograms at the following 5 loci shown in Fig. 2: the one between alleles *ME-1\*107* and *ME-1\*100*; *mMDH\*200* and *mMDH\*100*; *PGI-B\*100* and *PGI-B\*80*; *PGM-1\*100* and *PGM-1\*75*; and *PGM-2\*100* and *PGM-2\*75*. Morphologically, the 2  $F_1$  hybrids resemble *Z. pachycephalus* in having a wider mouth cleft and smaller scale size than in *Z. platypus*.

## DISCUSSION

The genetic distance of 0.285 between *Z. pachycephalus* and *Z. platypus* is beyond the range of the populational level of variation (Shaklee et al. 1982) but it fits well within the same genus. Some external differences including lateral line scales, the size of mouth cleft, and the shape of jaws can further distinguish these as 2 valid species. When fish species share a common spawning ground, the incidence of yielding natural hybrids between any 2 closely-related species is expected (Hubbs 1955). The occurrence of 2 F<sub>1</sub> hybrids between *Z. platypus* and *Z. pachycephalus* from the Shuangshi and Peihsi Rivers is an example. The habitat of these 2 species are sympatric in northern Taiwan and both have the same spawning season which commences in early spring and ends in late summer (Liu 1984, Wang et al. 1995). This would facilitate the production of natural hybrids. Successive generations of hybridization would lead to continuous intergradation of phenotypes and fusion of the participating species (Sakai and Hamada 1985). If this happens, the pooled gene frequency of these 2 species would approach the Hardy-Weinberg equilibrium, because of high gene flow. The pooled allozyme data for these 2 species in the same collection site reveal a great departure

from the Hardy-Weinberg equilibrium, however, indicating the existence of a reproductive isolating mechanism between them.

Though *Z. platypus* was reported to be distributed throughout western Taiwan from the Kao-ping River in the south the Lanyang River in the north (Oshima 1923, Liang 1984, Tzeng 1986), in fact, we confirmed that the species is not found outside the northern part of Taiwan during our recent investigation. Several other reports are in agreement with this result (Lee 1995, Fang et al. 1996). After close examination of *Z. platypus* specimens described by Liang (1984), we have determined that they are a misidentification of *Z. pachycephalus*. For these reasons, we consider that the previous report on the distribution of *Z. platypus* from regions other than northern Taiwan is in error due to the misidentification of *Z. pachycephalus*.

A new species *Z. taiwanesis* from the Choshui River described by Chen (1982) is considered to be a synonym of *Z. pachycephalus*. The species characters designated including a smaller head and more anteriorly positioned dorsal fin origin can be considered within the range of intrapopulational variation. The above 2 morpho-types of *Zacco* species collected during this study period showed the same allozyme patterns.

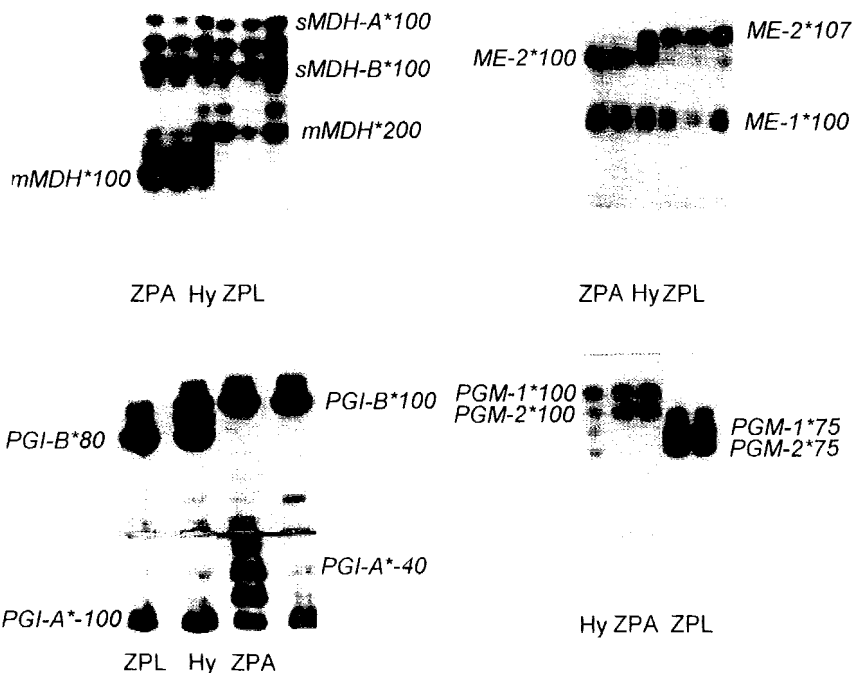


Fig. 2. Electrophoresis patterns of malate dehydrogenase (MDH), malic enzyme (ME), phosphoglucose isomerase (PGI), and phosphoglucomutase (PGM) in *Z. pachycephalus* (ZPA), *Z. platypus* (ZPL), and their hybrid (Hy).

*Zacco temmincki* is distributed in Japan, Korea, and southeastern China (Banarescu 1968, Hosoya 1993). There is a previous record of so-called *Z. temmincki* in Taiwan by Oshima (1919). However, *Z. temmincki* was not found during this study. The color pattern and lateral line scale counts in Oshima's *Z. temmincki* are more likely those of *Z. pachycephalus* rather than *Z. temmincki* of Japan and Korea. It is assumed that *Z. temmincki* of Oshima (1919) was actually a misidentified *Z. pachycephalus*. Therefore, we neither agree with Banarescu (1968) who claimed that there is only 1 species of *Zacco* (*Z. pachycephalus*), nor with that of Oshima (1919) who recorded the occurrence of *Z. temmincki* in Taiwan. There are 2 species of *Zacco* in Taiwan: *Z. platypus* and *Z. pachycephalus*.

Both *Zacco* and *Candidia* were previously placed in the genus *Opsariichthys* (Güther 1868, Regan 1908). However, as mentioned above, both were also recognized as valid genera (Jordan and Evermann 1902, Jordan and Richardson 1909). *C. barbatus* is externally similar to *Z. pachycephalus* except for the barbels (Regan 1908), which misled Banarescu (1968) to place this species under the genus *Zacco*. However, genetic distance between the genera *Zacco* and *Candidia* is much higher than that set for the interspecific level (Shaklee et al. 1982). The distance Wagner tree shows that the relationships between *Candidia* and *Zacco* is the same as between *Aphyocypris* and *Zacco* (Fig. 3). In addition, the lack of an elongated anal fin, and the possession of reddish spots below the eyes and at the anterior bases of the pectoral and ventral fins in mature males of *C. barbatus* indicate that it should not be a member of the genus *Zacco*.

The speciation that took place in genera *Zacco* and *Candidia* in Korea and Japan was discussed by Ming (1991) and Okazaki et al. (1991). Based on allozyme analyses, they confirmed that 3 pre-

sumptive valid species exist for the *Z. temmincki* complex, provisionally designated types A, B, and C, respectively. Types A and B are found in Japan, with types B and C in Korea. Ming (1991) concluded that the genera *Zacco* and *Candidia* were separated from one another in the early Pliocene (about 5 Mya), with 1 lineage of the *Z. platypus/pachycephalus* group and the other with the *Z. temmincki/Candidia* group. The latter laterally branched in the late Pliocene. According to morphological descriptions of Hosoya (1993), *Z. temmincki* Type A is more closely related to *C. barbatus* than to the other 2 types of *Zacco* with both elongated anal fin not reaching the caudal base even in sexually mature males, and the anterior bases of the pectoral and ventral fins being red instead of yellowish as in the other *Zacco* species. Therefore, we suggest that the recent split in the late Pliocene took place with 1 branch of *Z. temmincki* B and C types and the other with *C. barbatus* and *Z. temmincki* A type. The *Z. temmincki/Candidia* group differs from the *Z. platypus/pachycephalus* group by having a distinct lateral band on the body sides instead of having 10 more cross bars as in the latter group. We suggest that the taxonomic status of the *Z. temmincki* complex should be reconsidered.

The distribution pattern of the genus *Zacco* in Taiwan was probably influenced by geohistorical events. About 1.5-1 Mya, Taiwan was connected to the Asian continent with the rise of the Central Mountain Range and the regression of sea levels (Lin 1963). Because the distribution of the genus *Zacco* is restricted to western Taiwan, the time of colonization of this genus in Taiwan might not be earlier than the rise of Central Mountain Range. Therefore, the 1st invasion of the genus *Zacco* in Taiwan might have taken place at that time. The speciation event of *Z. platypus* and *Z. pachycephalus* might also have occurred simultaneously. The divergent time of about 1.3-1.4 Mya between these 2 species, estimated by genetic distance, supports this hypothesis. The early colonization by a *Zacco* population in Taiwan eventually evolved to the endemic species *Zacco pachycephalus*.

After several periods of separation and reconnection, Taiwan was reconnected to the continent with the formation of the Miaoli Plateau about 240 000-150 000 years ago. We suggest that the 2nd invasion of genus *Zacco* might have taken place at that time. Because of the limitation of the Miaoli Plateau, *Z. platypus* was restricted to northern Taiwan. This may explain why *Z. platypus* is widely distributed in mainland China, but is restricted to

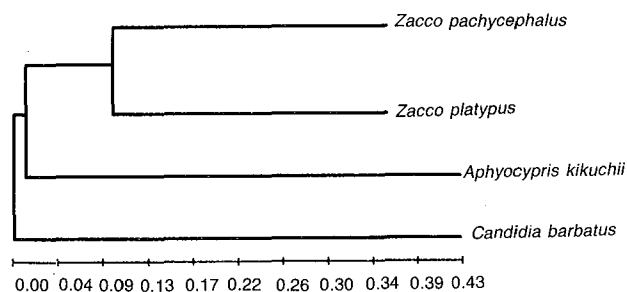


Fig. 3. Distance Wagner tree illustrating relationships among species, reconstructed from the added lengths of horizontal branches for modified Roger's genetic distance among taxa.

the northern part of the island of Taiwan.

**Acknowledgements:** The authors wish to express their sincere thanks to Dr. Shi-Kuei Wu, University of Colorado at Boulder for reviewing this manuscript. This study was supported by the Institute of Zoology, Academia Sinica.

## REFERENCES

- Banarescu P. 1968. Revision of the genera *Zacco* and *Opsariichthys* (Pisces, Cyprinidae). *Vestnik Cs. Spol. Zool.* **32**: 305-311.
- Chen IY. 1982. Revision of the fishes of genera *Opsariichthys*, *Zacco*, *Candidia* and *Parazacco*. *Ocean. Limnol.* **13**: 293-298.
- Chen JTF, MJ Yu. 1986. A synopsis of the vertebrates of Taiwan. 2nd rev. and enlarg. ed. Taipei: Commercial Book Co., pp. 283-296.
- Fang LS, IS Chen, CC Han. 1996. Fishes of Kaohsiung County. Kaohsiung County Government, 215 pp.
- Güther A. 1868. Catalogue of the fishes in British Museum, London. **7**: 295-297.
- Hosoya K. 1993. Cypriniformes. In T Nakabo, ed. Fishes of Japan, with pictorial keys to the species. Tokyo: Tokai Univ. Press, pp. 212-235.
- Hubbs CL. 1955. Hybridization between fish species in nature. *Syst. Zool.* **4**: 1-20.
- Jordan DS, BW Evermann. 1902. Notes on a collection of fish from the island of Formosa. *Proc. US Nat. Mus.* **25**: 322-323.
- Jordan DS, PE Richardson. 1909. A catalogue of the fishes of Formosa, or Taiwan, based on the collection of Dr. Hans Sauter. *Mem. Carneg. Mus.* **4**: 170.
- Lee DW. 1995. Fishes of Nantou County. Nantou: Taiwan Endemic Species Research Institute Press, pp. 1-60.
- Liang YS. 1984. Preliminary notes on the distribution of freshwater fishes found from Taiwan. *J. Taiwan Mus.* **37**: 59-70.
- Lin CC. 1963. Quarternary in Taiwan. *Taiwan Documents* **14**: 1-91.
- Liu J. 1984. Leuciscinae. In YT Chu, ed. The fishes of Fujian Province (I). China: Fujian Sci. Technol. Press, pp. 229-248.
- Ming MS. 1991. Systematic study on the genus *Zacco* (Pisces, Cyprinidae). Ph. D. thesis. Jen-Heh University, Korea.
- Murphy RW, JW Sites, DG Buth Jr., CH Hauffer. 1990. Proteins I: Isozyme electrophoresis. In DM Hillis, C Moritz, eds. *Molecular systematics*. Sunderland: Sinauer Associates Inc., pp. 45-68.
- Nei M. 1972. Genetic distance between populations. *Am. Nat.* **106**: 283-292.
- Okazaki T, M Watanabe, K Mizuguchi, K Hosoya. 1991. Genetic differentiation between two types of dark chub, *Zacco temminckii*, in Japan. *Jap. J. Ichthyol.* **38**: 133-140.
- Oshima M. 1919. Contributions to the study of the fresh water fishes of the island of Formosa. *Ann. Carneg. Mus.* **12**: 234-241.
- Oshima M. 1923. The distribution of Taiwanese fresh water fishes with reference to the geographic relationships between Taiwan and its adjoining regions. *Zool. Mag.* **35**(411): 1-49. (in Japanese).
- Pasteur N, G Pasteur, F Bonhomme, J Catalan, JB Davidian. 1988. *Practical isozyme genetics*. New York: Halsted Press, 215 pp.
- Regan CT. 1908. Descriptions of new fishes from Lake Candidius Formosa, collected by Dr. A. Moltrecht. *Ann. Mag. Nat. Hist., Ser. 8*: 358-360.
- Sakai H, K Hamada. 1985. Electrophoretic discrimination of *Tribolodon* species (Cyprinidae) and the occurrence of their hybrids. *Jap. J. Ichthyol.* **32**: 216-224.
- Shaklee JB, FW Allendorf, DC Morizot, GS Whitt. 1990. Gene nomenclature for protein coding loci in fish. *Trans. Amer. Fish. Soc.* **119**: 2-15.
- Shaklee JB, CP Keenan. 1986. A practical laboratory guide to the techniques and methodology of electrophoresis and its application to fish fillet identification. *Aust. CSIRO. Mar. Lab. Rep.* **177**: 1-59.
- Shaklee JB, CS Tamaru, RS Waples. 1982. Speciation and evolution of marine fishes studied by the electrophoretic analysis of proteins. *Pacif. Sci.* **36**: 141-157.
- Shen SC, SC Lee, KT Shao, HK Mok, CF Chen, CT Chen. 1993. Fishes of Taiwan. Taipei: Natl. Taiwan Univ., 960 pp.
- Sneath PHA, RQ Sokal. 1973. *Numerical taxonomy: the principles and practice of numerical classification*. San Francisco: Freeman.
- Sung WS, SC Lee, MJ Yu. 1993. Taxonomic status of the fishes of *Acrossocheilus formosanus* and *A. labiatus* (Cyprinidae: Barbinae) from Taiwan based on isozyme electrophoresis. *Bull. Inst. Zool., Acad. Sinica.* **32**: 127-139.
- Swofford DL, RB Selander. 1989. Biosys-1: a computer program for the analysis of allelic variation in population genetics and biochemical systematics. Champaign, Illinois: Illinois Natural History Survey.
- Temminck DJ, H Schlegel. 1846. *Fauna Japonica*. Leiden: E. J. Brill, p. 210.
- Tzeng CS. 1986. Distribution of freshwater fishes of Taiwan. *J. Taiwan Mus.* **39**: 127-146.
- Wang JT, MC Liu, LS Fang. 1995. The reproduction biology of an endemic cyprinid, *Zacco pachycephalus*, in Taiwan. *Environ. Biol. Fish.* **43**: 135-143.
- Wright S. 1978. *Evolution and the genetics of populations*. Vol 4, Variability within and among natural populations. Chicago: Univ. Chicago Press.

## 以遺傳學之證據釐清鱻屬與馬口魚屬之分類地位

王弘毅<sup>1,2</sup> 李信徹<sup>1</sup> 于名振<sup>2</sup>

以同功酶的資料分析採自臺灣六條河川中的鱻屬與馬口魚屬魚類。在 13 個酵素系統中共得到 26 個基因座，78 個對偶基因。鱻屬的二個種間（粗首鱻與平頷鱻）的 Nei's 遺傳距離為 0.285，相當於屬內的分化程度。粗首鱻具有較大的口裂，較多的側線鱗片數，以及在 *mMDH\*100*, *ME-1\*100*, *PGI-B\*100*, *PGM-1\*100*, 與 *PGM-2\*100* 等對偶基因上與平頷鱻有所區別。在屬間方面，若與菊池式細鱻比較，馬口魚顯然與鱻屬的二種魚類關係較遠，因此它們應為不同屬。馬口魚的嘴角有口鬚，並且在 *sAAT-1\*120*, *CK-A\*93*, *FH-1\*80*, *FH-2\*82*, *G<sub>6</sub>PDH-1\*80*, *IDHP-1\*113*, *IDHP-3\*120*, *ME-1\*103*, *ME-2\*50*, *PGM-1\*120*, 與 *PGM-2\*120* 等對偶基因上可明顯與鱻屬魚類有別。文中並討論鱻屬在臺灣的起源以及可能的種化時間。

關鍵詞：同功酶比較，鱻屬與馬口魚屬，河川棲地，臺灣。

<sup>1</sup> 中央研究院動物研究所

<sup>2</sup> 東海大學生物系