

Genetic Divergence and Relationship among Fifteen Species of Genera *Trachurus*, *Decapterus*, *Selar* and *Selaroides*

Akihiro Kijima, Nobuhiko Taniguchi and Akira Ochiai

(Received October 9, 1987)

Abstract Genetic distance and the relationships among 15 species of genera *Trachurus*, *Decapterus*, *Selar*, and *Selaroides* were estimated from 18 electrophoretically detectable isozyme genes. Estimates of genetic distance (D) between every pair of species within the genus *Trachurus* ranged from 0.005 to 0.560 with a mean of 0.322, and from 0.484 to 1.868 with a mean of 1.022 within the genus *Decapterus*. Between species of different genera, estimates of D ranged from 0.786 to 2.863 with a mean of 1.784. From these results, *Decapterus* species could be considered as having evolved over a long period while *Trachurus* is a newly arisen genus. A relationship among species suggests that the *Decapterus* species are expanded to offshore and deep area after being divided into some groups, and that the *Trachurus* species are divided presumably into at least two groups, one group of which is coastal and the other of which is offshore. *Trachurus japonicus* and *Trachurus novaezelandiae* could be considered subspecies on the basis of allelic distribution and genetic distance.

In the previous report (Kijima et al., 1986a) the subfamily Caranginae could be divided into two large group on the basis of electrophoretically detectable isozyme genes, one of which was fusiform including the genera *Trachurus*, *Decapterus*, *Selar*, and *Selaroides* and the other was compressiform. Isozyme genes were very useful for analyzing the relationship within a certain taxonomic level as shown by Kijima et al. (1986a). Because of too many species in many genera surveyed in the previous paper, the number of loci available were limited for making a thorough analysis of the relationship among the species within a genus.

The fusiform group was also morphologically somewhat highly specialized, adapting to long migration around offshore water (Suzuki, 1962; Vergara, 1972). This is one of the main evolutionary trends in the family Carangidae. There are many species in the genera *Trachurus* and *Decapterus* of the four genera. Although a lot of morphological and ecological studies among species were published (Matsubara, 1955; Suzuki, 1962; Kishida, 1974; Berry and Cohen, 1974; Stephenson and Robertson, 1977; Shavoneyev, 1980; Gushiken, 1983), taxonomic relationships among species have not yet been thoroughly estimated. It would be necessary to analyse relationships among them by using another marker index such as isozyme genes. The objectives of

the present study are to estimate the degree of genetic divergence and to investigate relationships among species on the basis of electrophoretically detectable isozyme genes. Moreover relationships among species are discussed from the view point of adaptive radiation as compared with morphological studies.

Materials and methods

Table 1 shows fish species, number of fish tested and their sampling sites. The *Trachurus* species except *T. japonicus* were commercially imported from several countries as food or research samples. They were transported in frozen state. The other species including *T. japonicus* were collected from the southeast coast of Japan. Fish samples were immediately frozen and stored below -20°C until they were tested. Taxonomy and identification of species followed Berry and Cohen (1974), Shavoneyev (1980) and Gushiken (1983).

Eleven enzymes were surveyed in the liver, muscle and heart by two buffer-systems as shown in Table 2. The procedure for starch gel electrophoresis, detection of isozymes, and nomenclature of locus followed the same methods as previously reported (Kijima et al., 1986a, b). Since MDH isozymes cannot be confirmed as soluble or mitochondrial form, they are designated with

numbers. Alleles were numbered consecutively as A, B, C, . . . from the most anodal to the most cathodal. Allele frequency was calculated to three of four decimal points by directly counting phenotypes. Calculation of genetic distance, and construction of dendrograms also followed previous reports (Kijima et al., 1986a, b).

Results

Fig. 1 shows electropherograms of 11 enzymes surveyed in the liver, muscle and heart. The isozymes detected are summarized in Table 2. Only one zone appeared in ADH, PGM, 6PGD, SDH and SOD in all of the species examined, indicating one locus coding for each enzyme (Fig. 1). In α GPD and IDH, different bands were observed between liver and muscle, indicating different isozymes in each tissue. Two or more different zones were observed in the same tissue in AAT, LDH, MDH and ME, indicating that some isozymes coded by different loci were active in the same tissue (Fig. 1). From the results, eighteen isozymic loci were estimated from 11 enzymes examined as shown in Table 2.

Allele distributions and frequencies at the 18 loci in 15 species belonging to 4 genera are shown in Table 3. There are 9 alleles (A-I) at the *Adh*

locus, 10 (A-J) at α Gpd-A, 11 (A-K) at α Gpd-B, 15 (A-O) at Aat-A, 8 (A-H) at Aat-B, 12 (A-L) at *Idh-A* and *Idh-B*, 8 (A-H) at *Ldh-A*, 3 (A-C) at *Ldh-B*, 7 (A-G) at *Mdh-1*, 5 (A-E) at *Mdh-2*, 4 (A-D) at *Mdh-3*, 5 (A-E) at *Mdh-4*, 9 (A-I) at *Me-A*, 11 (A-K) at *Pgm*, 10 (A-J) at *6Pgd*, 17 (A-Q) at *Sdh* and 2 (A-B) at *Sod*, considering all species. Allelic divergence was remarkably large at *Aat-A* and *Sdh*, and small at *Ldh-B* and *Sod*. The observed number of phenotypes is consistent with that expected at all loci examined.

In order to estimate the degree of genetic divergence quantitatively, the genetic distance between every pair of species in 4 genera was calculated from allele frequencies as shown in Table 4. The minimum genetic distance was observed between *Trachurus japonicus* and *Trachurus novaezelandiae* (D=0.005), and the maximum between *Trachurus declivis* and *Decapterus tabl* (D=2.863). The genetic distance among species ranged from 0.005 to 0.560 with a mean of 0.322 within 15 pairs of the genus *Trachurus*, and from 0.484 to 1.868 with a mean of 1.022 within 21 pairs of the genus *Decapterus*. The genetic distance

Table 2. Enzymes surveyed, tissues and buffer-systems used, isozymes detected and loci coded.

Enzyme	Tissue	Buffer	Isozyme	Locus
ADH	liver	C-AEA	ADH	<i>Adh</i>
α GPD	muscle	C-APM	α GPD-A	α Gpd-A
	liver	C-AEA	α GPD-B	α Gpd-B
AAT	liver	C-AEA	AAT-A	<i>Aat-A</i>
	liver	C-AEA		<i>Aat-B</i>
IDH	muscle	C-AEA, C-APM	IDH-A	<i>Idh-A</i>
	liver	C-AEA	IDH-B	<i>Idh-B</i>
LDH	muscle	C-AEA, C-APM	LDH-A	<i>Ldh-A</i>
	heart	C-AEA, C-APM	LDH-B	<i>Ldh-B</i>
MDH	muscle	C-APM	MDH-1	<i>Mdh-1</i>
		C-APM	MDH-2	<i>Mdh-2</i>
		C-APM	MDH-3	<i>Mdh-3</i>
		C-APM	MDH-4	<i>Mdh-4</i>
ME	muscle	C-AEA, C-APM	ME-A	<i>Me-A</i>
		C-APM		
PGM	muscle	C-APM	PGM	<i>Pgm</i>
6PGD	liver	C-AEA	6PGD	<i>6Pgd</i>
SDH	liver	C-AEA	SDH	<i>Sdh</i>
SOD	liver	C-AEA	SOD	<i>Sod</i>
			11	18
			18	18

Table 1. Sampling site and the number of individuals in each species of the genera *Trachurus*, *Decapterus*, *Selar* and *Selaroides* examined.

Species	Sampling area	Number of fish
<i>Trachurus trecae</i>	west coast of Africa	15
<i>T. japonicus</i>	Japan (Kochi)	50
<i>T. novaezelandiae</i>	New Zealand	40
<i>T. trachurus</i>	Netherland	33
<i>T. murphyi</i>	Chile	50
<i>T. declivis</i>	New Zealand	1
<i>Decapterus russelli</i>	Japan (Okinawa)	12
<i>D. macrosoma</i>	Japan (Nagasaki)	50
<i>D. macarellus</i>	Japan (Kochi)	50
<i>D. muroadsi</i>	Japan (Kochi)	50
<i>D. maruadsi</i>	Japan (Kochi)	50
<i>D. akaadsi</i>	Japan (Miyazaki)	40
<i>D. tabl</i>	Japan (Kochi)	30
<i>Selar crumenophthalmus</i>	Japan (Kochi)	40
<i>Selaroides leptolepis</i>	Japan (Okinawa)	10

among species of different genera ranged from 0.786 to 2.863 with a mean of 1.784 in 69 pairs. The genetic distance in the present study generally increased on higher taxonomic levels.

A dendrogram revealing the relationships among them was constructed on the basis of the genetic distances as shown in Fig. 2. From the dendrogram, 15 species were clearly divided into two groups at a distance of 2.313, one of which included all *Decapterus* species tested and the other group was divided into two other groups, one of which was the genus *Trachurus* at a distance of 1.555. The remaining group which includes two genera, *Selar* and *Selaroides*, was divided at a distance of 0.786. The degree of genetic divergence between species, however, was largely different in each genus. The genus *Decapterus* was the most divergent species group, and *Trachurus* was the least.

The dendrogram also revealed that the species of *Trachurus* could be divided into three groups, namely 1) *T. declivis* and *T. murphyi*, 2) *T. trachurus*, and 3) *T. trecae*, *T. novaezelandiae* and *T. japonicus* at genetic distances of 0.468 and 0.410 respectively. Also there were four groups in the genus *Decapterus*, namely 1) *D. russelli* and *D. maruadsi*, 2) *D. macarellus*, *D. muroadsi* and *D. akaadsi*, 3) *D. tabl*, and 4) *D. macrosoma*.

Discussion

Genetic distance and relationships among genera. Kijima et al. (1986a) have estimated an average genetic distance of 0.880 for every pair of species, 2.046 for every pair of genera in 35 carangid species. They also indicated that these values were considered to be reasonable in comparison with the other fish species. Comparing these data with those of this study, infinite values of genetic distance estimated in the previous report were calculated as 1.462 (*D. macrosoma* and *D. macarellus*), 1.868 (*D. macrosoma* and *D. tabl*), and 2.819 (*D. macrosoma* and *Selaroides leptolepis*), respectively. The values between the other pairs were not very different from each other. The relationships between genera agreed well with the previous report. The present data thus support the previous study.

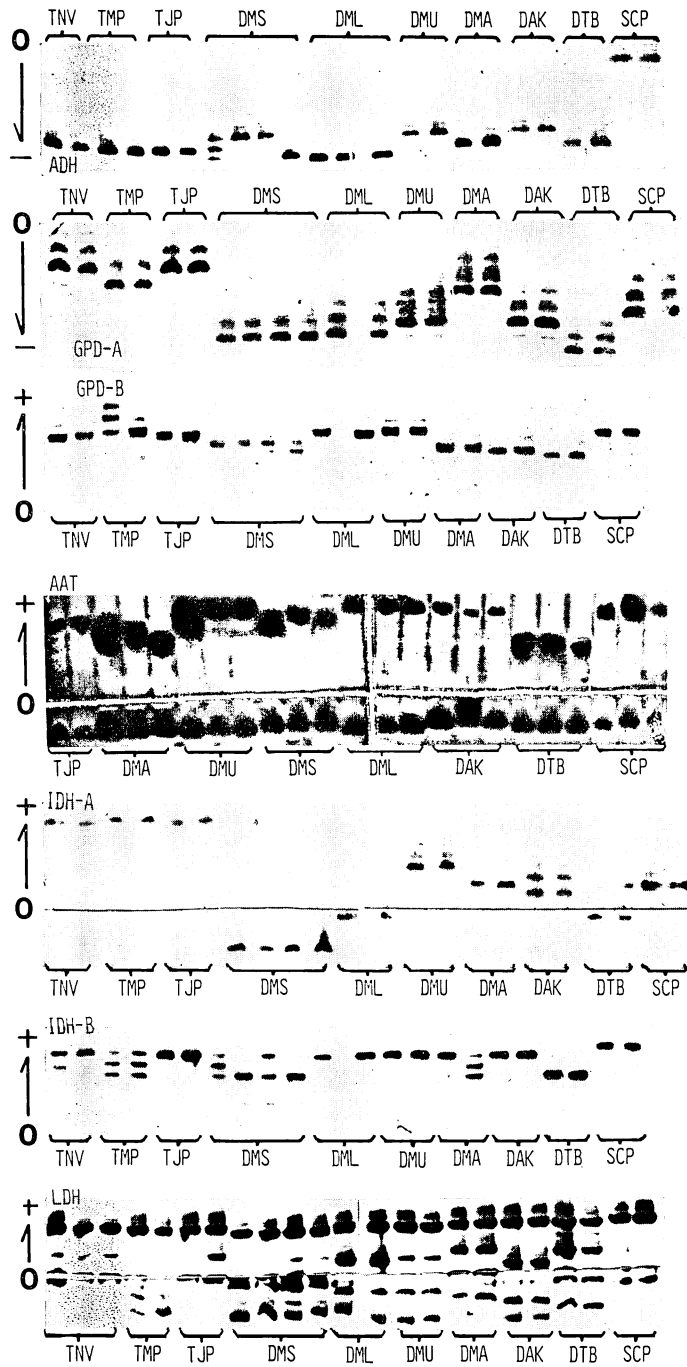
Isozymic alleles are changed by occurrence of amino acid substitution and are considered neutral or nearly neutral for natural selection. The rate

of amino acid substitution is considered to be large in proportion to evolutionary time. Genetic distance corresponds to the number of allelic change or the rate of amino acid substitution and therefore should increase in proportion to evolutionary time. Genetic distances between *Decapterus* species were distinctively larger than those between *Trachurus* species. It suggests that the genus *Decapterus* has arisen long over the past while *Trachurus* is a newly arisen one. In fact, morphological differences among *Trachurus* species are so small that some taxonomic controversy in species or subspecies levels have not been settled yet (Berry and Cohen, 1974; Shavoneyev, 1980).

Genetic relationship among *Decapterus* species. Of the Carangidae, *Decapterus* species are considered as the group which is morphologically and ecologically more highly adapted to migrate around offshore areas. Morphological adaptability for offshore areas is characterized by the body shape such as low body depth and by the large first dorsal fin. Although the size of the first dorsal fin compared to the second one is not obviously different, the body depth of *D. macarellus* is the lowest and next to *D. russelli*, *D. macrosoma*, *D. muroadsi*, *D. tabl*, *D. akaadsi* and *D. maruadsi* from the data of Gushiken (1983).

Kishida (1974) investigated the habitat of five *Decapterus* species in the East China Sea. According to his conclusion, *D. maruadsi* has inhabited the coastal water, *D. akaadsi* and *D. tabl* have inhabited areas of 200 m depth or less at the front part of the continental shelf, while *D. macrosoma*'s habitat ranges from coastal water to the surface of the front part of the continental shelf. *D. russelli* has not been caught in the Kyushu and Shikoku area but in Okinawa, mixed with *D. macrosoma*. Morphological characters are well correlated with habitat in each species. Comparing the present data with the data reported by Kishida (1974), deep sea type and offshore type are together in the same group. This suggests that the *Decapterus* species have expanded to offshore and deep areas after dividing into some species groups. It could be reasonable because of the general tendency of long term evolution of fishes from coastal water to offshore or deep sea.

Genetic relationship among *Trachurus* species. Shavoneyev (1980) proposed that the genus *Trachurus* could be divided into three groups, that



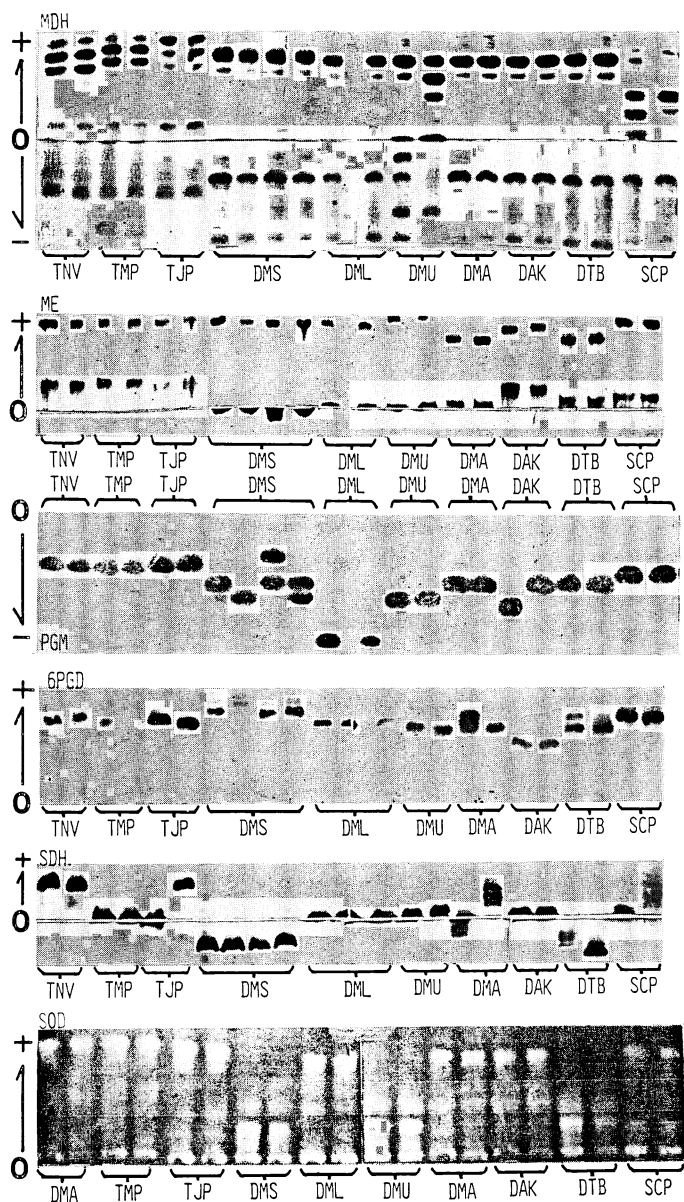


Fig. 1. Examples of electropherogram of 11 enzymes. See the text for nomenclature of allele. TTC, *Trachurus trecae*; TJP, *T. japonicus*; TNV, *T. novaezelandiae*; TDV, *T. declivis*; TTR, *T. trachurus*; TMP, *T. murphyi*; DRL, *Decapterus russelli*; DMS, *D. macrosoma*; DML, *D. macarellus*; DMU, *D. muroadsi*; DMA, *D. maruadsi*; DAK, *D. akaadsi*; DTB, *D. tabl*; SCP, *Selar crumenophthalmus*; SLL, *Selaroides leptolepis*.

Table 3. Allele frequencies in the populations of *Trachurus*, *Decapterus*, *Selar* and *Selaroides*. See Fig. 1 for the abbreviations for species. Figures in parentheses show the numbers of specimens.

Locus	<i>Trachurus</i>						<i>Decapterus</i>						<i>Selar</i>	<i>Selaroides</i>	
	TTC (15)	TJP (50)	TNV (40)	TDV (1)	TTR (33)	TMP (50)	DRL (12)	DMS (50)	DML (30)	DMU (50)	DMA (50)	DAK (40)	DTB (30)	SCP (40)	SLL (10)
<i>Adh</i>	<i>E.</i> 033 <i>G.</i> 967	<i>C.</i> 010 <i>G.</i> 990	<i>G</i>	<i>G</i>	<i>E.</i> 288 <i>G.</i> 712	<i>G</i>	<i>E.</i> 292 <i>G.</i> 708	<i>F.</i> 450 <i>I.</i> 550	<i>F.</i> 017 <i>I.</i> 983	<i>F</i>	<i>E.</i> 030 <i>H.</i> 970	<i>F.</i> 988 <i>H.</i> 012	<i>H</i>	<i>A.</i> 975 <i>B.</i> 025	<i>D</i>
<i>αGpd-A</i>	<i>B</i>	<i>B</i>	<i>B.</i> 987 <i>F.</i> 013	<i>C</i>	<i>A.</i> 015 <i>C.</i> 985	<i>C</i>	<i>G</i>	<i>I</i>	<i>H</i>	<i>G</i>	<i>D</i>	<i>G</i>	<i>J</i>	<i>E</i>	<i>E</i>
<i>αGpd-B</i>	<i>A.</i> 033 <i>G.</i> 967	<i>G</i>	<i>G</i>	<i>H</i>	<i>G.</i> 939 <i>J.</i> 061	<i>E.</i> 010 <i>H.</i> 930 <i>K.</i> 060	<i>D.</i> 958 <i>H.</i> 042	<i>E</i>	<i>G</i>	<i>H</i>	<i>D</i>	<i>C.</i> 975 <i>F.</i> 025	<i>B</i>	<i>I</i>	<i>I</i>
<i>Aat-A</i>	<i>F.</i> 033 <i>K.</i> 500 <i>M.</i> 467	<i>K.</i> 960 <i>M.</i> 040	<i>E.</i> 013 <i>K.</i> 924 <i>N.</i> 063	<i>M</i>	<i>F.</i> 167 <i>K.</i> 485 <i>M.</i> 348	<i>M</i>	<i>J</i>	<i>J.</i> 420 <i>L.</i> 550 <i>O.</i> 030	<i>N</i>	<i>I.</i> 010 <i>N.</i> 990	<i>B.</i> 010 <i>E.</i> 610 <i>H.</i> 320 <i>K.</i> 060	<i>N</i>	<i>A.</i> 017 <i>C.</i> 017 <i>D.</i> 949 <i>G.</i> 017	<i>M</i>	<i>M</i>
<i>Aat-B</i>	<i>F</i>	<i>E.</i> 010 <i>F.</i> 990	<i>F</i>	<i>F</i>	<i>F</i>	<i>F</i>	<i>F</i>	<i>B.</i> 010 <i>F.</i> 990	<i>H</i>	<i>A.</i> 010 <i>G.</i> 990	<i>F</i>	<i>F.</i> 975 <i>C.</i> 025	<i>G</i>	<i>D.</i> 275 <i>F.</i> 725	<i>C</i>
<i>Idh-A</i>	<i>I</i>	<i>G.</i> 030 <i>I.</i> 970	<i>G.</i> 313 <i>I.</i> 687	<i>H</i>	<i>I.</i> 712 <i>J.</i> 288	<i>I</i>	<i>K</i>	<i>L</i>	<i>K</i>	<i>D.</i> 020 <i>E.</i> 980	<i>C</i>	<i>B</i>	<i>K</i>	<i>A.</i> 050 <i>C.</i> 950	<i>F</i>
<i>Idh-B</i>	<i>G</i>	<i>F.</i> 020 <i>H.</i> 980	<i>H</i>	<i>E.</i> 500 <i>L.</i> 500	<i>C.</i> 030 <i>E.</i> 015 <i>F.</i> 576 <i>H.</i> 045 <i>I.</i> 076 <i>K.</i> 258	<i>A.</i> 010 <i>E.</i> 510 <i>H.</i> 480	<i>D</i>	<i>B.</i> 080 <i>D.</i> 650 <i>H.</i> 270	<i>H</i>	<i>H</i>	<i>B.</i> 010 <i>D.</i> 440 <i>E.</i> 020 <i>H.</i> 520 <i>K.</i> 010	<i>B.</i> 012 <i>H.</i> 988	<i>D.</i> 767 <i>H.</i> 233	<i>J</i>	<i>J</i>
<i>Ldh-A</i>	<i>A</i>	<i>A</i>	<i>A</i>	<i>E</i>	<i>A</i>	<i>E</i>	<i>F</i>	<i>H</i>	<i>G</i>	<i>G</i>	<i>C</i>	<i>G</i>	<i>D</i>	<i>B</i>	<i>A</i>
<i>Ldh-B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>A</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B.</i> 975 <i>C.</i> 025	<i>B</i>
<i>Mdh-1</i>	<i>F</i>	<i>F</i>	<i>F</i>	<i>F</i>	<i>F</i>	<i>F</i>	<i>D</i>	<i>C.</i> 010 <i>E.</i> 990	<i>B.</i> 017 <i>D.</i> 983	<i>D</i>	<i>D</i>	<i>D</i>	<i>D</i>	<i>A.</i> 013 <i>B.</i> 987	<i>G</i>
<i>Mdh-2</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>D</i>	<i>D</i>	<i>D</i>	<i>C</i>	<i>E</i>	<i>C</i>	<i>C</i>	<i>C</i>	<i>C</i>	<i>C</i>	<i>A</i>	<i>B</i>
<i>Mdh-3</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>B</i>	<i>A.</i> 697 <i>B.</i> 303	<i>B</i>	<i>C</i>	<i>C.</i> 990 <i>D.</i> 010	<i>C</i>	<i>A.</i> 660 <i>C.</i> 340	<i>C</i>	<i>C</i>	<i>C</i>	<i>C</i>	<i>A</i>
<i>Mdh-4</i>	<i>A</i>	<i>A</i>	<i>A</i>	<i>A</i>	<i>A</i>	<i>A</i>	<i>D</i>	<i>D</i>	<i>D</i>	<i>D</i>	<i>D</i>	<i>D</i>	<i>E</i>	<i>C</i>	<i>B</i>
<i>Me-A</i>	<i>E</i>	<i>E</i>	<i>D.</i> 013 <i>E.</i> 987	<i>E</i>	<i>D.</i> 152 <i>E.</i> 848	<i>E</i>	<i>A.</i> 083 <i>B.</i> 875 <i>C.</i> 042	<i>B.</i> 030 <i>D.</i> 940 <i>G.</i> 030	<i>D</i>	<i>C</i>	<i>C</i>	<i>C.</i> 212 <i>D.</i> 788	<i>C</i>	<i>F</i>	<i>H.</i> 800 <i>I.</i> 200

Table 3. (Continued)

Locus	<i>Trachurus</i>						<i>Decapterus</i>							<i>Selar</i>	<i>Selaroides</i>
	TTC (15)	TJP (50)	TNV (40)	TDV (1)	TTR (33)	TMP (50)	DRL (12)	DMS (50)	DML (30)	DMU (50)	DMA (50)	DAK (40)	DTB (30)	SCP (40)	SLL (10)
<i>Pgm</i>	B. 100 D. 900	D. 990 H. 010	D	D	A. 015 B. 985	D	G	C. 060 G. 600 H. 340	J. 983 K. 017	H	G	G. 863 I. 137	F	E	E
<i>6Pgd</i>	A. 067 E. 900 H. 033	D. 010 E. 990	D. 013 E. 987	E	E. 955 H. 045	E	E	G. 940 I. 060	C. 017 F. 983	B. 010 E. 990	E. 940 G. 060	C. 988 F. 012	F	D. 025 H. 975	J
<i>Sdh</i>	B. 267 F. 633 H. 067 N. 033	A. 060 F. 870 I. 040 K. 030	A. 025 F. 937 I. 038	B	B. 167 C. 015 E. 076 F. 621 G. 106 J. 015	B. 940 O. 060	M	B. 060 L. 940	B. 933 D. 017 L. 050	B. 870 D. 010 L. 120	B. 800 D. 030 L. 110 Q. 060	B. 950 L. 050	P	B. 974 D. 013 L. 013	C
<i>Sod</i>	B	B	B	B	B	B	B	A	B	A	B	B	A	B	B

Table 4. Genetic distance between every pair of species (below the diagonal) and its averages (above the diagonal). See Fig. 1 for the abbreviations.

	<i>Trachurus</i>						<i>Decapterus</i>							<i>Selar</i>	<i>Selaroides</i>
	TTC	TJP	TNV	TDV	TTR	TMP	DRL	DMS	DML	DMU	DMA	DAK	DTB	SCP	SLL
TTC															
TJP	0.077														
TNV	0.087	0.005			0.322									1.585	1.562
TDV	0.480	0.560	0.554												
TTR	0.313	0.325	0.334	0.432											
TMP	0.383	0.418	0.437	0.075	0.357										
DRL	1.300	1.313	1.302	1.298	1.247	1.291									
DMS	2.767	2.582	2.555	2.755	2.564	2.626	1.255								
DML	1.670	1.488	1.456	1.793	1.582	1.651	0.919	1.462			1.022			1.709	2.084
DMU	2.070	1.766	1.735	1.504	1.805	1.408	0.996	1.517	0.763						
DMA	1.391	1.330	1.316	1.272	1.325	1.224	0.484	1.333	0.856	0.951					
DAK	1.650	1.483	1.449	1.485	1.564	1.377	0.666	1.179	0.490	0.528	0.587				
DTB	2.833	2.658	2.646	2.863	2.758	2.750	1.098	1.868	1.046	1.139	0.971	1.357			
SCP	1.584	1.851	1.855	1.314	1.581	1.319	1.541	2.222	1.501	2.076	1.132	1.319	2.177		
SLL	1.340	1.471	1.473	1.769	1.559	1.761	1.762	2.819	1.776	2.567	1.737	1.751	2.175	0.785	

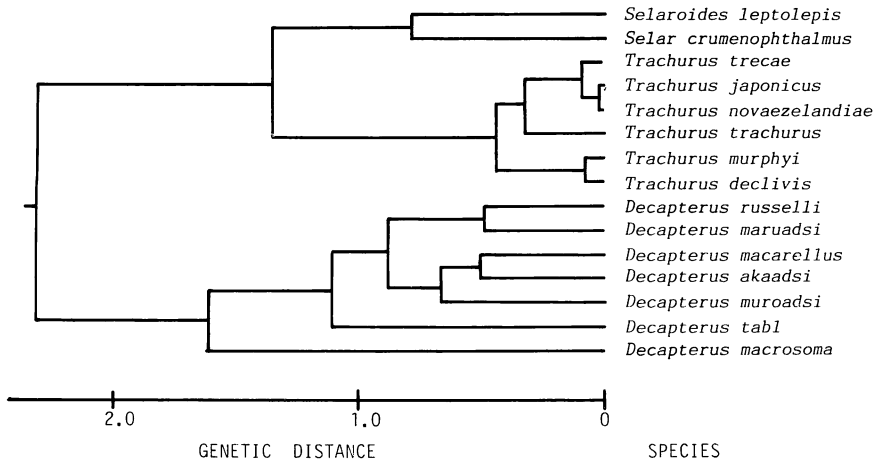


Fig. 2. Genetical relationship among 15 species of the genera *Trachurus*, *Decapterus*, *Selar*, and *Selaroides*.

is, “*mediterraneus*”, “*trachurus*” and “*picturatus*” on the basis of morphological and ecological characters. According to his hypothesis, members of the “*mediterraneus*” group (*T. mediterraneus*, *T. Trecae*, *T. lathami* and *T. indicus*) characterized by small scutes, high body depth and coastal area habitat are the most primitive. The members of the “*picturatus*” group (*T. picturatus*, *T. symmetricus* and *T. murphyi*) characterized by low body depth, a large number of scutes and habitat far beyond the continental shelf are the most advanced and phylogenetically close to members of the “*mediterraneus*” group, possibly linked by a common origin. The members of the “*trachurus*” group (*T. trachurus*, *T. delagoa*, *T. novaezelandiae* and *T. japonicus*) characterized by large scutes and by remnants of many primitive characters are an independent trend of development. He also suggested that *T. declivis* would be more properly regarded as an aberrant form, the evolution of which has occurred as a different course from that of all other members of *Trachurus*. His hypotheses are different at some points from the report of Berry and Cohen (1974). Berry and Cohen (1974) revealed that *T. novaezelandiae* and *T. japonicus* belonging to the “*trachurus*” group of Shavoneyev (1980) were morphologically similar to *T. lathami* which belongs to the “*mediterraneus*” group. They also revealed that *T. declivis* appeared to be closer to *T. murphyi* which belongs to the “*picturatus*” group. Comparing these reports with the present study, a close relation between *T. novaezelandiae*

and *T. japonicus* is just in agreement with both reports. These two next appeared to be close to *T. trecae* of Shavoneyev’s “*mediterraneus*” group while *T. declivis* appeared close to *T. murphyi* and is consistent with Berry and Cohen’s (1974) report. These results suggest that the size of the scute is not very clearly correspondent with evolutionary features and are against the hypothesis of Shavoneyev (1980). In fact, “*picturatus*” group is different from the other groups in number of rays and scutes and body depth, but the “*trachurus*” and “*mediterraneus*” groups are different from each other only in the depth of the largest scute according to the data from Shavoneyev (1980). Therefore, there are at least two groups in the *Trachurus* species and they would be adaptively radiated offshore such as the “*picturatus*” species. *T. declivis* may have been derived from an ancestor of *T. murphyi*. As only one individual of *T. declivis* could be tested, a deviation of allele frequency cannot be exactly estimated. However, because the probability of the appearance of a common allele at all loci should be high, a relationship between species could be assumed. These suggest that the two species in the south Pacific Ocean could be considered to come from different origins.

There is no completely divergent locus between *T. japonicus* and *T. novaezelandiae*, and the genetic distance between them is too small to be at the species level (Kijima, et al., 1986b, Taniguchi et al., 1986). Moreover there is no morphologically significant difference between them (Stephenson

and Robertson, 1977). There are two closely related subspecies inhabiting different areas south and north part of the earth, i.e. *T. trachurus trachurus* and *T. trachurus capensis* in the Atlantic Ocean and *T. symmetricus symmetricus* and *T. symmetricus murphyi* in the south and north part of the east side of the Pacific Ocean (Shavoneyev, 1980). On the west side of the Atlantic Ocean, only one species (*T. lathami*) has inhabited both parts. These are considered to be newly arisen and adaptively radiated north and south along the coast in each area. From these evidences, we could conclude that the two species, *T. novaezelandiae* and *T. japonicus*, are subspecies, and that they adaptively radiated from the Indian Ocean to the Pacific Ocean and then north and south along the coastal area.

Acknowledgement

We wish to thank Mr. F. Nishioka of the Tokai Regional Fisheries Research Laboratory, Mr. K. Takeshita of the Seikai Regional Fisheries Research Laboratory, Mr. S. Wada of the Fishery Research Institute of Shizuoka Prefecture, and Mr. S. Gushiken of the Gushiken Ichthyology Laboratory, for supplying the fish samples. This work was supported in part by grants-in-aid from the Ministry of Education, Science and Culture, Japan (60760148).

Literature cited

- Berry, F. H. and L. Cohen. 1974. Synopsis of *Trachurus* (Pisces, Carangidae). Quart. J. Florida Acad. Sci., 35(4): 177-211.
- Gushiken, S. 1983. Revision of the carangid fishes of Japan. Galaxea, 2: 135-264.
- Kijima, A., N. Taniguchi and A. Ochiai. 1986a. Genetic relationships in the family Carangidae. Proceedings of the Second International Conference on Indo-Pacific Fishes, p. 840-848.
- Kijima, A., N. Taniguchi and A. Ochiai. 1986b. Genetic divergence and morphological difference between the spotted and common mackerel. Japan. J. Ichthyol., 33(2): 151-161.
- Kishida, S. 1974. Fisheries biology of the scads (genus *Decapterus*) in the East China Sea-II. Specific distributoin and annual catch. Bull. Seikai Reg. Fish. Res. Lab., 45: 1-14. (In Japanese.)
- Matsubara, K. 1955. Fish morphology and hierarchy, I. Ishizaki Shoten, Tokyo. xi+789 pp (In Japanese.)
- Shavoneyev, Ye. 1980. Systematics, morpho-ecological characteristics and origin of carangids of the genus *Trachurus*. J. Ichthyol., 20(6): 15-25.
- Stephenson, A. B. and D. A. Robertson. 1977. The New Zealand species of *Trachurus* (Pisces: Carangidae). J. Roy. Soc. New Zealand, 7(2): 243-253.
- Suzuki, K. 1962. Anatomical and taxonomical studies on the carangid fishes of Japan. Rep. Fac. Fish. Pref. Univ. Mie, 4(2): 42-232.
- Taniguchi, N., M. Fujita and M. Akasaki. 1986. Genetic divergence and systematics in sparid fish from Japan. Proceedings of the Second International Conference on Indo-Pacific Fishes, p. 849-858.
- Vergara, R. 1972. Analisis taxonomico y consideraciones filogeneticas sobre las especies Cubanas del genero *Caranx*. (Teleostei, Perciformes, Carangidae). Cent. Invest. Pseq. Cuba, Contrib., 34: 1-138.
- (Department of Cultural Fisheries, Faculty of Agriculture, Kochi University, Monobe B-200, Nankoku 783, Japan; AK, present address: Department of Fisheries, Faculty of Agriculture, Tohoku University, Tsutsumi-dori Amemiya-cho, Sendai 980, Japan)

マアジ属, ムロアジ属, メアジ属, ホソヒラアジ属 15種の遺伝的分化と類縁関係

木島明博・谷口順彦・落合 明

アジ亜科で紡錘形のグループとされるマアジ属, ムロアジ属, メアジ属 および ホソヒラアジ属の合計 4 属 15 種間における遺伝的分化および類縁関係を 18 アイソザイム遺伝子を標識として調べた。その結果、遺伝的距離はマアジ属 6 種間で 0.005-0.560, 平均 0.322, ムロアジ属 7 種間で 0.484-1.868, 平均 1.022 であった。4 属間の遺伝的距離は 0.786-2.863, 平均 1.784 となり、分類群が高次になるに従って遺伝的距離が大きくなった。遺伝的距離をもとに作成した枝分れ図は各属がそれぞれ 1 つのグループを形成することを示し、形態による分類をよく反映した。これらのことから、ムロアジ属はより古い年代に分化し、マアジ属はより新しい年代に分化したと推定された。またマアジ属は沿岸性と沖合性の少なくとも 2 つのグループに大別された。日本のマアジとニュージーランドのマアジは最も新しい年代に適応放散によって西方より沿岸づたいに東進し、太平洋で南北に分化してできた種と考えられ、これらは亜種レベルにあると推定された。

(783 南国市物部乙 200 高知大学農学部; 木島, 現所属: 980 仙台市堤通雨宮町 1-1 東北大学農学部)