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Temporal and Spatial Variation of Morphology for the Red Scad (*Decapterus kurroides*) in the Adjacent Waters off Taiwan

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ABSTRACT

Multivariate morphometric variation was used to elucidate the stock structure of the red scad (*Decapterus kurroides*) off Taiwan. A total of seven samples from the northeastern (Keelung and Nanfangao) and southwestern (Kaohsiung and Tungkang) Taiwan were collected during spawning and non-spawning seasons. Nineteen characters for each individual were size–standardized by multiple group principal component analysis (MGPCA). The adjusted measurements were used to construct the dendrogram of seven samples by unweighted pair-group method with arithmetic means (UPGMA) method using Manhattan distance values. A randomization test was used to examine the significance of the morphometric difference between each pair of groups derived from the cluster analysis. The results obtained from cluster analyses and randomization tests indicate (1) that the morphology of red scad is significantly different between spawning and non-spawning seasons and (2) that the morphometric difference between populations from northeastern and southwestern Taiwan is significant without respect to spawning or non-spawning seasons. There appear to be at least two morphologically distinguishable stocks of this species off Taiwan, but further verification of the stock structure may be essential.

Key words: *Decapterus kurroides, Morphometric variation, Stock structure.*

INTRODUCTION

Information on stock structure is essential for any exploited species undergoing assessment and management (Ihssen *et al.*, 1981). Morphometric variability among different geographical populations would be attributed either to distinct genetic structure or to environmental conditions in each area (Kinsey *et al.*, 1994). Organisms, therefore, having the same morphometric characteristics, are often assumed to constitute a stock, and that has been utilized widely in stock discrimination studies (Avsar, 1994).

However, morphological traits of an organism are not independent and changes in various aspects of morphology are coordinated (Zelditch *et al.*, 1992), so, unless a specific morphometric character is known to have a genetic foundation, morphology is best described by multivariate techniques which accommodate the intercorrelated nature of characters (Thorpe, 1983).

Morphometric characters usually have two independent components: size and shape (Humphries *et al.*, 1981). Most of the variability in a set of multivariate

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characters is due to size (Junquera and Perez-Gandaras, 1993). Thus, morphometric data analyzed should be free from the effect of size to avoid misinterpretation of the results (Strauss, 1985). Several multivariate techniques for size adjustment can be used to obtain size-free morphometric data, e.g. Burnaby's method (Buranby, 1966), multiple group principal component analysis (MGPCA) (Thorpe, 1983; Thorpe, 1988).

Red scad (*Decapterus kurroides*) is mainly distributed off the eastern coast of Africa and the west Pacific, from the Japan to Australia, and it is one of the most important commercial species in Taiwan. The population biology of red scad in Taiwan, e.g. maturity and fecundity (Chang *et al.*, 1972a), digestive system and stomach contents (Chang *et al.*, 1972b), and age and growth (Chang and Shaw, 1975), have been well documented, but information on stock structure is still unavailable. The objective of this paper is to examine the extent of multivariate morphometric variability to elucidate the stock structure of the red scad off Taiwan.

MATERIALS AND METHODS

A total of seven samples were separately collected off Keelung, Nanfangao, Kaohsiung and Tungkang (Fig. 1) between March 1998 and February 1999. The sample size, sampling date and relative information are shown in Table 1. A total of 19 measurements were made on each specimen (Table 2; Fig. 2). All were taken to the nearest 0.01 mm, except the body length was taken to the nearest 0.1 cm.

MGPCA was used to remove the influence of size from the raw data. The first principal component obtained is usually considered to be a vector describing size, while the remaining components relate to shape. However, it is frequently argued that this separation may be quite arbitrary as it is only based on the orthogonality of the components and that the first and subsequent components could separately share information on shape and size (Humphries *et al.*, 1981). Therefore, we followed the method of Corti *et al.* (1988) to examine the information on size contained in all components. In this method the relation coefficients of body length were calculated, as an independent measure of size, on all principal components. The MGPCA was programmed and executed by Interactive Matrix Language (IML) in Statistical Analysis System (SAS, 1985).

To obtain a size-free shape analysis, the component score from the MGPCA size vector was excluded in sequent analysis. Dendrogram of seven samples was constructed by unweighted pair-group method with arithmetic means (UPGMA) in NTSYS (Rohlf, 1993), using Manhattan distance values (Sneath and Sokal, 1973) between seven samples to illustrate the relationship among samples and to assess the degree of similarity between the samples. The Manhattan distance was chosen because it is invariant to differences in scale among variables (Dryden and Mardia, 1998).

A multivariate discriminant analysis (SAS, 1985) was also performed to investigate the honesty of all groups derived from cluster analysis. Firstly, specimens in the same group were pooled regardless of locations. Each individual was allocated to the group with the nearest centroid, and the proportion of individuals allocated to each group was calculated. The proportion of individuals correctly re-allocated was taken as a measure of the integrity of that group. In such a case the proportion of individuals that are misclassified is low if all groups discriminated by cluster analysis does not derived by chance alone (Soriano *et al.*, 1988).

To test the significance of the morphometric differences between each pair of group derived from cluster analysis, randomization tests were performed (Solow, 1990). Specimens in the same group were first pooled regardless of location. All specimens were each randomly assigned to one of two groups.

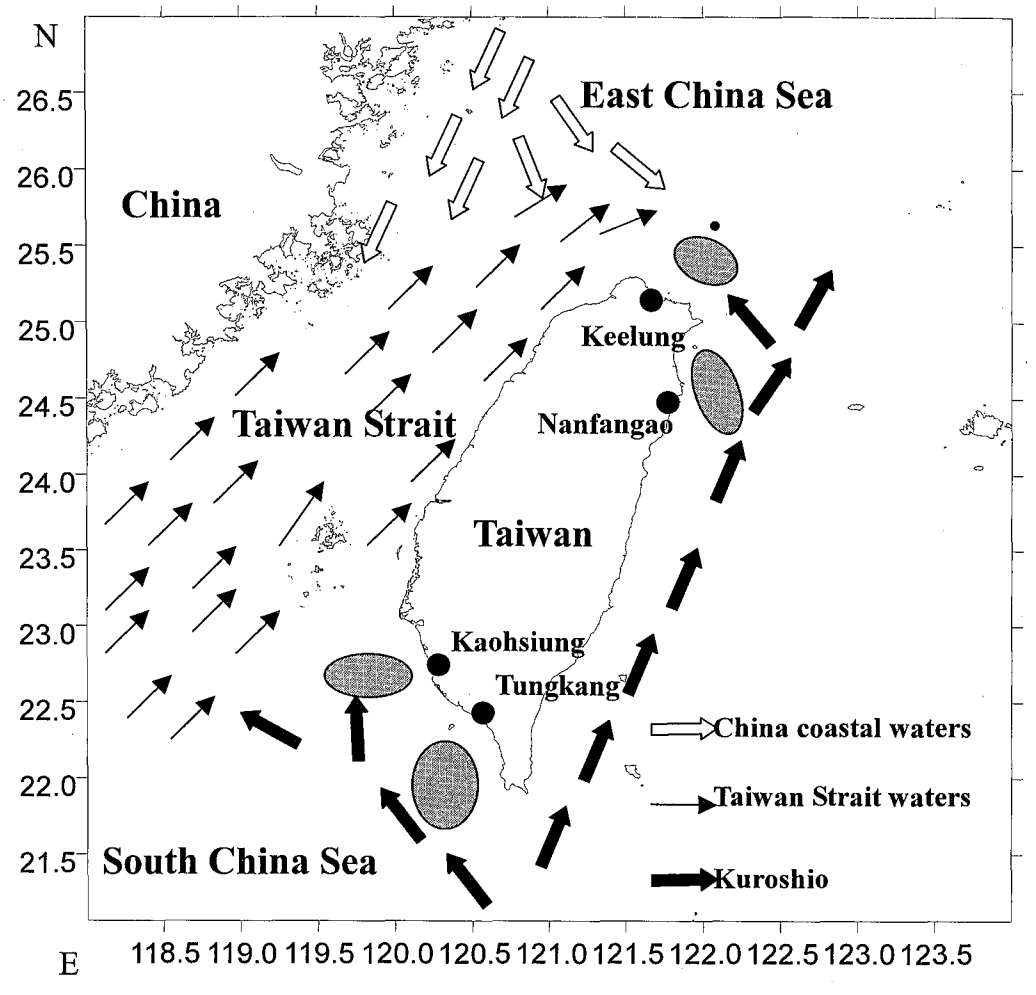

Fig. 1. Shadowed areas showing the sampling areas.

Table 1. Sampling date, sampling area, means and ranges of fork length (FL) (cm). The figure in the first column represents the sampling month.

Sampling area	Sampling date	Sample Size	Means of FL	Ranges of FL
Tungkang2	Feb. 1999	18	22.36	21.5-23.1
Nanfangao3	Mar. 1998	30	25.31	23.7-27.0
Keelung4	Apr. 1998	29	24.23	22.2-26.8
Keelung9	Sep. 1998	27	27.98	25.0-30.8
Kaohsiung4	Apr. 1998	21	23.64	22.3-25.3
Kaohsiung10	Oct. 1998	30	24.39	23.3-25.2
Kaohsiung11	Nov. 1998	29	25.77	24.8-27.8

The new data set was then analyzed by multivariate discriminant analysis, and the cross-validation estimator (Pc) estimated (Solow, 1990). This estimator measures the proportion of individuals that are misclassified. Resampling was performed 1000 times, each with a different random permutation. This randomization test

Table 2. Morphometric variables analyzed.

No.	Name	Description
1	BL	Body length
2	ED	Eye diameter
3	D1L	Length of the third spine in the first dorsal fin
4	D2L	Length of the first spine in the second dorsal fin
5	P1L	Length of spine in pectoral fin
6	P2L	Length of spine in pevic fin
7	A1D	Length of the first detached spine of anal fin
8	A2D	Length of the second detached spine of anal fin
9	LC	Length of lower caudal fin
10	S-E	Distance between snout and eye
11	S-P1	Distance between the snout and insertion of pectoral fin
12	S-D1	Distance between the snout and the insertion of the first dorsal fin
13	S-P2	Distance between the snout and the insertion of the pevic fin
14	D1-D2	Distance between the insertions of the first dorsal and the second fins
15	D2M	Length of the second dorsal fin matrix
16	P-A	Distance between the insertions of the pevic and annl fins.
17	AM	Length of anal fin matrix
18	DF-AF	Distance between the insertions of the dorsal and anal finlets
19	CH	Minimum height of the caudal peduncl

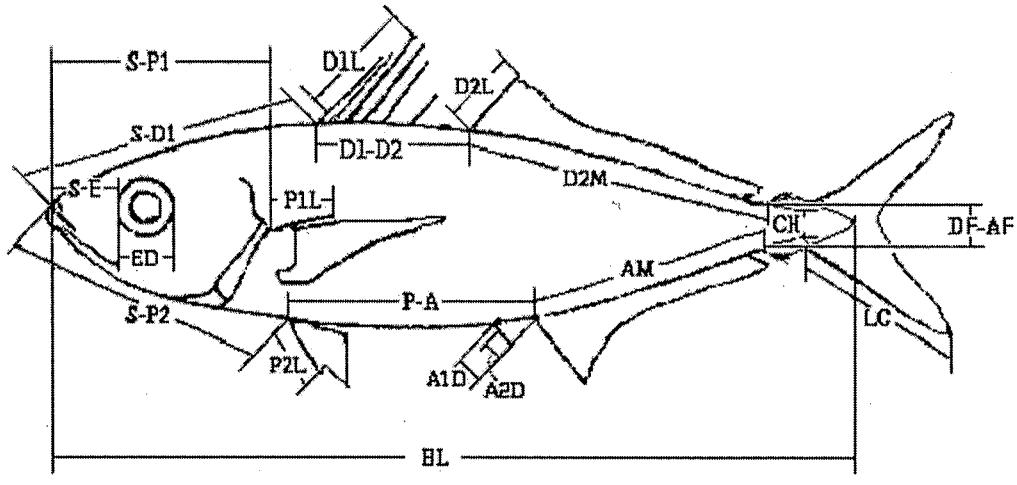

Fig. 2. Diagram of *Decapterus Kurroides* showing the body parts measured.

assesses the significance of misclassification rate by comparing the proportion of individuals (Po) that have been misclassified in the original data set to the proportion misclassified (Pc) in each randomized data set. This test was also programmed and executed by IML in SAS (SAS, 1985).

RESULTS

The MGPCA run on the 19 characters of all samples produced a clear "size" vector (with coefficients of similar magnitude and sign) associated with the largest eigenvalue (Table 3). The remaining components

Table 3. The 19 eigenvectors and eigenvalues, percentage of variance explained by each eigenvalue and relation coefficients (r) between body length and 19 principle component scores obtained from MGPCA.

	Eigenvector																		
Variable	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
BD	0.230	-0.094	-0.019	-0.046	0.005	0.031	-0.077	0.051	-0.199	0.010	0.045	-0.003	0.020	0.076	0.046	-0.008	-0.018	-0.003	-0.936
ED	0.206	-0.176	0.057	-0.159	-0.161	0.048	0.258	0.101	0.224	-0.053	0.619	-0.012	-0.329	0.174	-0.382	0.042	0.240	-0.110	0.026
D1L	0.200	0.286	-0.257	0.483	0.271	0.630	0.185	-0.190	0.094	-0.059	0.074	-0.077	-0.068	0.083	0.032	-0.007	-0.039	0.001	-0.011
D2L	0.246	0.714	-0.214	-0.535	0.162	-0.164	0.176	0.083	0.004	-0.012	-0.042	0.063	-0.009	-0.003	-0.014	-0.031	0.005	0.000	0.001
P1L	0.208	0.401	0.780	0.103	-0.293	0.144	-0.206	-0.083	0.091	0.023	0.029	-0.001	0.096	0.038	0.012	-0.024	0.001	-0.003	-0.006
P2L	0.228	0.186	-0.270	0.527	-0.538	-0.447	0.198	0.087	-0.056	0.068	-0.060	0.101	-0.063	0.015	0.009	0.013	-0.022	0.010	-0.002
A1D	0.206	-0.073	0.265	0.211	0.551	-0.399	0.263	-0.044	0.051	0.473	0.161	-0.169	0.099	-0.086	0.062	0.016	-0.042	0.004	0.009
A2D	0.266	-0.155	0.223	0.104	0.308	-0.162	0.112	-0.029	0.060	-0.520	-0.331	0.493	-0.279	0.012	-0.048	0.003	0.035	-0.016	0.013
LC	0.257	-0.102	-0.005	0.031	0.008	0.103	-0.024	0.640	0.357	-0.078	-0.367	-0.434	0.100	-0.126	-0.130	-0.005	0.062	-0.001	0.004
S-E	0.248	-0.218	0.014	-0.234	-0.232	0.203	0.351	-0.424	-0.054	0.340	-0.474	-0.009	0.054	-0.068	-0.233	0.038	0.097	-0.145	0.022
S-P1	0.220	-0.167	0.008	-0.140	-0.139	0.091	0.205	-0.043	0.059	-0.069	0.122	0.025	0.073	-0.166	0.399	-0.164	0.122	0.756	0.057
S-D1	0.238	-0.131	0.005	-0.134	-0.083	0.055	0.012	0.028	-0.026	-0.041	0.099	-0.030	-0.073	0.012	-0.015	0.268	-0.891	0.048	0.103
S-P2	0.227	-0.023	-0.057	0.070	0.047	0.104	-0.116	0.117	-0.373	-0.090	0.234	0.239	0.429	-0.561	-0.345	0.045	0.078	-0.042	0.109
D1-D2	0.218	-0.046	-0.032	-0.022	0.047	0.000	-0.124	0.045	-0.238	-0.030	-0.023	-0.055	0.167	0.402	0.180	0.726	0.300	0.064	0.155
D2M	0.228	-0.100	-0.027	0.004	0.069	-0.035	-0.113	0.044	-0.345	-0.035	-0.027	-0.093	0.208	0.578	-0.206	-0.562	-0.070	0.084	0.197
P-A	0.232	-0.003	-0.008	-0.016	0.028	0.062	-0.336	0.060	-0.401	0.206	-0.044	-0.180	-0.684	-0.243	0.140	-0.087	0.106	-0.024	0.148
AM	0.225	-0.150	-0.030	-0.098	-0.093	0.068	0.093	0.075	0.041	-0.078	0.143	0.078	0.179	-0.030	0.630	-0.202	0.022	-0.610	0.106
DF-AF	0.202	-0.068	-0.207	-0.017	0.038	0.061	-0.476	0.044	0.440	0.454	-0.003	0.509	0.027	0.107	-0.021	-0.033	0.005	0.070	0.023
CH	0.259	-0.035	-0.183	-0.017	0.008	-0.282	-0.380	-0.554	0.281	-0.317	0.071	-0.390	0.083	-0.129	-0.060	-0.015	0.047	-0.042	-0.007
Eigenvalue	0.040	0.006	0.005	0.005	0.005	0.003	0.003	0.002	0.002	0.001	0.001	0.001	0.001	0.001	0.000	0.000	0.000	0.000	0.000
% variance	0.514	0.082	0.071	0.068	0.060	0.044	0.037	0.026	0.020	0.018	0.016	0.012	0.011	0.007	0.006	0.003	0.003	0.002	0.000
r	0.98	0.10	-0.05	0.14	-0.06	0.35	-0.45	0.02	-0.30	0.01	0.20	0.06	-0.01	-0.07	0.07	0.12	-0.20	0.03	-0.16

were considered as "shape" vectors (with coefficients of different magnitude and sign). The alternative measure of size (body length) is highly correlated with the "size" component (r=0.98), i.e. the first multiple group principal component (MGPC 1), and is uncorrelated with the "shape" components, i.e. MGPC 2-19 (Table 3), thereby confirming this interpretation of the components.

Dendrogram of seven samples were shown in Fig. 3. Seven samples were clustered into two groups (A and B), and each was further divided into two subgroups (A1, A2 and B1, B2). The A1 group includes Tungkang2 and Kaohsiung4; the A2 group includes Nanfangao3 and Keelung4; while B1 contains Keelung9; and B2 contains Kaohsiung10 and Kaohsiung11.

The results of discriminant analysis were shown in Table 4. The most well-defined group is B2 with only three misclassified individuals (5.08%). The second most well-defined group is A2 with 8.06% of misclassifications, most of them to the A1. The worst defined group is the A1 (17.95% of misclassifications), most of them to the A2. In the validation of the morphometrics analysis a total of 191 individuals (90.05%) were well classified. Based on above results, the discriminant analysis reasonably supports the result of cluster analysis.

Table 5 shows the results of randomization tests between each pair of groups derived from cluster analysis. The range of misclassified rates (Po) is very small (from 1.65% to 4.18%). All results of the randomization tests are all significant (p=0), which indicates that it is unlikely that the extremely low misclassification was due to chance alone and morphometric differences between four groups are all significant.

DISCUSSION

Our result obtained from the cluster analysis reveals that seven samples were

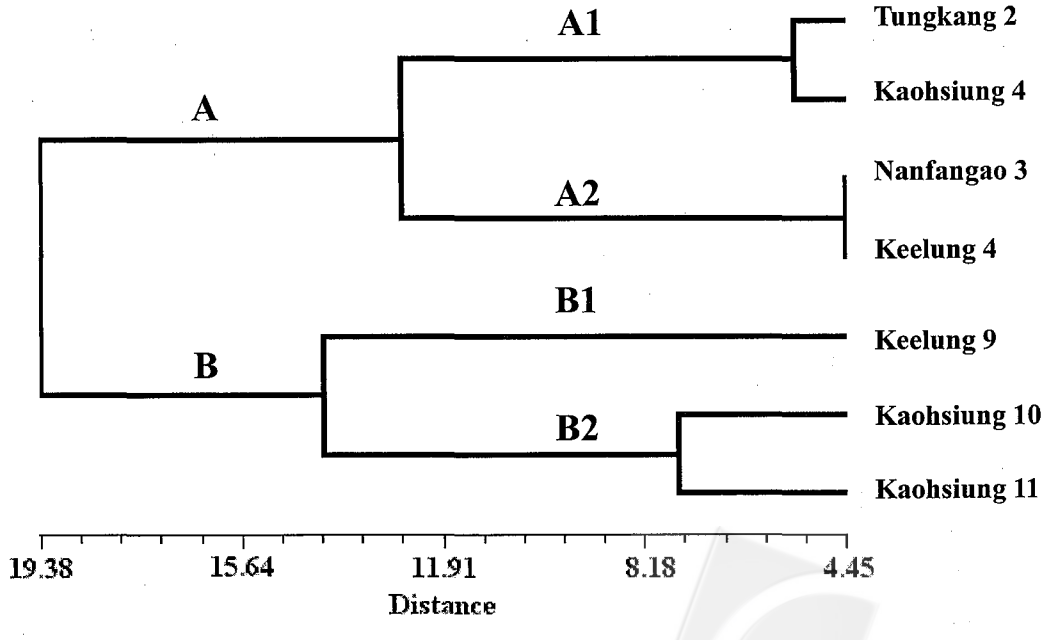

Fig. 3. Dendrogram of the cluster analyses for the seven samples based on the adjusted data by MGPCA.

Table 4. Number (and percentage) of individuals reallocated in each group in the validation of the cluster analysis based on the adjusted data by MGPCA.

	A1	A2	B1	B2	Total
A1	32 (82.05%)	5 (12.82%)	1(2.56%)	1 (2.56%)	39
A2	3 (4.84%)	57 (91.94%)	1 (1.61%)	1 (1.61%)	62
B1	1 (3.23%)	1 (3.23%)	27 (87.1%)	2 (6.45%)	31
B2	1 (1.69%)	1 (1.69%)	1 (1.69%)	56 (94.92%)	59

Table 5. Misclassified rate (Po) and results (*P*-values) of randomization tests between four groups derived from cluster analysis based on adjusted data by MGPCA.

	A1	A2	B1
A2	0.0418 (P =0)		
B1	0.0256 (P =0)	0 (P =0)	
B2	0.0298 (P =0)	0.0165 (P =0)	0.0331 (P =0)

clustered into two groups (A and B), and each was further divided into two subgroups (A1, A2 and B1, B2). This result was confirmed by the discriminant analysis. The results of randomization tests for each pair of four groups (A1, A2, B1 and B2) are all significant, which supports the morphological distinctness of these four groups.

The spawning period of red scad in Taiwan is between February and July (Chang *et al.*, 1972a). The sampling time for A and B groups is from February to April and from September to November, respectively. Therefore, the differences between A1 and B2 and A2 and B1 show that the morphology of red scad between spawning and non-spawning seasons is significant different.

The morphometric differences between A1 and A2 and B1 and B2 indicate the shape of red scad from northeastern and southwestern Taiwan is significantly different without respect to spawning or non-spawning seasons. Therefore, if a stock is considered as an intra-specific group of individuals that exhibit unique phenotypic attributes, then based on our results, we consider that there are at least two morphologically distinguishable stocks of the red scad in the adjacent waters off Taiwan. Other biological evidence supports indirectly our result. Chang *et al.* (1972b) indicated that the number of pyloric caeca of the red scad in northeastern Taiwan is higher than those in southwestern Taiwan. The growth of the red scad of Nanfangao is faster than that of Kaohsiung (Chang and Shaw, 1975).

Although morphometric studies have been proved valuable in providing insight into the discrimination of marine stocks, several factors may confound the analytical result of morphological relationship between geographical populations (Kinsey *et al.*, 1994), e.g. sexual dimorphism, allometric growth. In this study we attempted to minimize variances caused by these parameters through the use of size adjustment technique and narrowing the differences of size among specimens. No sexual dimorphism for red scad was found (Chang *et al.*, 1976). Restricting samples comparisons to specific range of body length may ignore ontogenetic variation within samples, and this information may be essential for significant portrayal of morphometric differences between samples. However, this effect may be not significant in this study, because the body lengths of individuals used in each sample were not all equal.

Morphometric differences between examined populations may reflect either genetic differences between the stocks or environmental differences between localities

(Kinsey *et al.*, 1994). The sampling areas in northeast of Taiwan are covered by the Kuroshio water masses, Taiwan Strait water masses, China coastal water and the water masses of South China Sea in specific season (Lee and Hu, 1998) (Fig. 1), but the sampling areas in the southwest of Taiwan are only covered by the Kuroshio water masses. This difference of water masses between sampling locations may result in parts of the morphometric variation at least.

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台灣附近海域產紅尾圓鯵形態形質之時空變異

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利用多變量形態形質之變異來推定台灣附近海域產紅尾圓鯵的系群結構。在本研究種之生殖與非生殖季期間，分別於台灣東北部(基隆和南方澳)及西南部(高雄和東港)共收集 7 個樣本，184 個體。每個體量測 19 個形態形質，所得之資料再以多群主成份分析法(MGPCA)校正個體大小變異所造成之影響。校正後之資料先計算各群間之曼哈頓距離，以未加權配對平均法建構 7 個樣本之系統樹。利用置換排列分析法檢定由集群分析法分析所得之各群間之形質差異是否顯著。分析之結果如下：(1) 紅尾圓鯵之外部形態形質，在生殖與非生殖季節間有顯著的不同；(2) 不管是生殖或非生殖季節，台灣東北部及西南部產之紅尾圓鯵外部形態形質皆有顯著的差異。根據以上之結果顯示，台灣附近海域產之紅尾圓鯵至少應有兩個外部形態不同的系群存在，然而，此結果仍須進一步的確定。

關鍵詞：紅尾圓鯵，形態形質，系群結構。

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