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Comparison of Multivariate Allometric Coefficients in Red-Spot Prawn (*Metapenosis barbata*) from Adjacent Waters off Taiwan

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ABSTRACT

Multivariate allometric coefficients of red-spot prawn sampled from the adjacent waters of Tashi, Keelung, Taichung and Kaohsiung were estimated and compared to examine whether (1) allometry can be used to elucidate the genetic variation among groups and (2) the assumption that those groups compared share a common allometric pattern in some multivariate statistic method, e.g. Burnaby's method and shearing principal component analysis (PCA) for size correction, or common PCA and multiple-group PCA for multiple-group ordination, can be satisfied. The specimens were sampled during November and December in 1995. A total of 11 measurements was made for each individual. The first eigenvector extracted from the covariance matrix of log-transformed data was used to reflect the multivariate allometric coefficients. The bootstrap method was used to assess the accuracy of estimates. The dendrogram of four areas was constructed by unweighted pair-group method with arithmetic means (UPGMA) by using the angles between four first eigenvectors by sex. The results show that four areas were clustered into two distinct groups for each sex, one group included Tashi, Keelung and Kaohsiung; the other included Taichung. The hypothesis of one common multivariate allometric pattern was clearly rejected. This indicates that some multivariate statistic methods should not be used without testing this assumption. The geographic clusters are different from the one derived from shape analysis, so the examination in genetic variation among populations by multivariate allometric comparison may be not suitable for this species. Different water masses in winter and flow patterns of coastal current around sampling areas may be the main factors to result in the differences of allometric coefficients between two clusters.

Key words: *Multivariate allometric coefficient, Bootstrap, Dendrogram, Angle.*

INTRODUCTION

Allometry is mainly used to describe the relative growth between morphometric measurements in organisms (Klingenberg, 1996). Three different levels of allometry are frequently distinguished: static, ontogenetic and evolutionary allometry. This classification has also been used in most comparisons between levels of allometry. Studies on allometry may trace to the pioneer work of Huxley (1932). He derived a formula of allometry, $y=bx^{\alpha}$, where x and y are morphometric measurements and the constant α is often called the allometric coefficient. The special case when $\alpha=1$ is called isometry.

Multivariate analysis of a set of phenotypic characters is regarded as a more appropriate method than the use of a single character to separate stocks or determine morphological relationships between populations of a species (Thorpe, 1983; Winans, 1985; MacCrimmon and Claytor, 1986; Cawdery and Ferguson, 1988). Since a generalization of the allometry was proposed by Jolicoeur (1963), studies on the multivariate allometric pattern of organ-

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ism have increased. Most multivariate studies of allometry have used principal component analysis (PCA) (Klingenberg, 1996). The first eigenvector is roughly proportional to the slopes obtained in bivariate allometric regressions of the measurements on a measure of overall size (Shea, 1985). Therefore, the first eigenvector can be interpreted as multivariate allometric coefficients. When all loadings of the first eigenvector are equal with a value 1 divided by the square root of number of variable, the first eigenvector is called isometry vector (Jolicoeur, 1963; shea, 1985).

Multivariate allometric coefficients for comparisons among groups are also applied to some multivariate statistic approaches. For example, one assumption that these groups under consideration share a common multivariate allometric pattern is a basic precondition in Burnaby's method (Buranby, 1966) and shearing PCA for size correction (Humphries *et al.*, 1981) or multiple-group PCA (Thorpe, 1983) and common PCA (Airoldi and Flury, 1988; Flury, 1988) for multiple groups ordination. However, this assumption has rarely been examined (Klingenberg and Froese, 1991; Klingenberg, 1996).

Red-spot prawn, *Metapenaeopsis Barbara*, is one of the most abundant and widely distributed demersal resources in Taiwan Strait (Wu, 1984). Many studies on the fishery biology of this species (Tzeng and Yeh, 1995; Chiu, 1996) has been conducted, information of multivariate allometric coefficients is still unknown.

In this paper, comparisons of multivariate allometric coefficients of red-spot prawn from four adjacent waters off Taiwan were conducted to examine whether (1) allometry can be used to elucidate the genetic variation among populations and (2) the assumption that these groups compared share one common allometric pattern in some multivariate statistic methods can be satisfied.

MATERIALS AND METHODS

The specimens used in this study were collected from the adjacent waters off Tashi, Keelung, Taichung and Kaohsiung (Fig. 1) during November and December in 1995. Sex was identified and separated. A total of 11 measurements was made on each specimen (Fig. 2). They were rostrum length (RL), antennal spine width (ASW), hepatic spine width (HSW), carapace length (CL), Diagonal carapace length (DCL), first abdominal segment length (FSL), first abdominal segment width (FSW), first abdominal segment height (FSH), second abdominal segment length (SSL), sixth abdominal segment height (SSH) and body length (BL). Restricting ranges of carapace length of samples to specific length classes was conducted in this study. The sample size, range of carapace length and relative information is in Table 1.

The Jolicoeur's method (1963) was used to estimate the multivariate allometric coefficients. The first eigenvector was derived by using the covariance matrix of log-transformed data of red-spot prawn for each area and sex. A bootstrap technique (Effron and Tibshirani, 1986) was used to

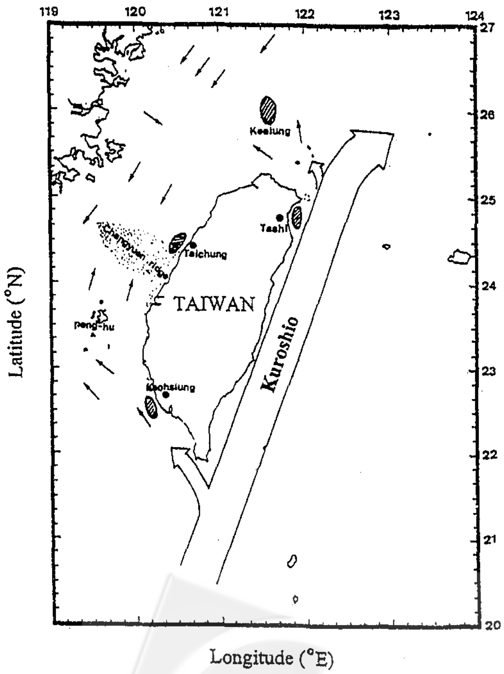

Fig. 1. Map showing sampling area (shadowed area) and current pattern in the vicinity seas of Taiwan in winter.

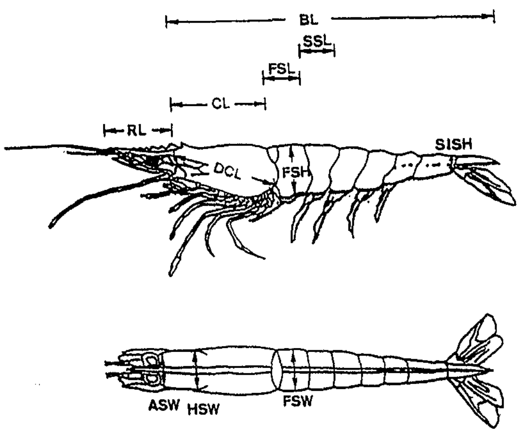

Fig. 2. Diagram of *Metapenaeopsis barbata* showing the meristic measurement.

assess the accuracy of estimates. A bootstrap sample of corresponding sample size was drawn at random, with replacement. For each analysis, one thousand bootstrap iterations were performed.

The angles between four multivariate allometric coefficients were calculated to indicate their similarity. If the angle increases, the similarity decreases. The angle α is the arc cosine of the inner product of pair of the first eigenvectors (Gibson *et al.*, 1984), $\alpha = \arccos(b \times c) \times 180/\pi$, where b and c are the first eigenvectors. These angles were considered as distance coefficients, and four sampling areas were regarded as operation taxonomic units. The dendrogram was constructed by unweighted pair-group method with arithmetic means (UPGMA) by using those angles by sex. The angles between isometric vector and those first eigenvectors were also computed, respectively.

The SAS for windows version 6.08 (1993) and SAS IML (Interactive Matrix Language) were used to compute all the statistics in this study. NTSYS (Numerical Taxonomy for Systematic, version 1.8) (Rohlf, 1993) was used for UPGMA computing and the establishment of dendrogram.

RESULTS

Multivariate allometric coefficients and the first eigenvalues are shown in Table 2. All the first eigenvalues explained the largest part of total variance. The maximum percentage was 93.3% estimated from the female sample from Tashi. The smallest one was 74.86% estimated from the male sample from Kaohsiung. The estimates of multivariate allometric coefficients were considered fairly stable, as indicted by the relatively small standard errors of the estimates.

The theoretical value for isometry was 0.3015. Allometric coefficients for some characters were clearly different from this value. The angles between these first eigenvectors and isometric vector are also shown in Table 2, which value from 7.2769° to 3.1807°. The multivariate allometric coefficients estimated from Taichung's sample for both sexes had the most deviant from isometric vector than the others.

The angles between four multivariate

Table 1. Sample size, sampling areas, means and ranges of carapace length (CL) (mm) by sex.

Sampling area	sex	sample size	means of CL	ranges of CL
Tashi	Female	108	18.60	15.21-23.52
	Male	105	16.74	14.34-22.17
Keelung	Female	97	20.76	16.24-23.42
	Male	69	18.36	16.56-20.84
Taichung	Female	104	20.95	16.29-23.64
	Male	102	18.47	15.12-21.02
Kaohsiung	Female	94	21.36	16.97-24.38
	Male	100	18.74	16.47-20.55

Table 2. Multivariate allometric coefficients, percentages of total variance exlained by the first eigenvalues and corresponding standard errors (in parentheses) of red-spot prawn from four sampling areas. Angle1 indicates the angle (degree) between multivariate allometric coefficients and isometric vector.

	Sampling area							
	Tashi		Keelung		Taichung		Kaohsiung	
Variable	Female	Male	Female	Male	Female	Male	Female	Male
RL	0.3231	0.3278	0.3190	0.2933	0.2411	0.2252	0.2896	0.3132
	(0.0168)	(0.0116)	(0.0196)	(0.0407)	(0.0169)	(0.0198)	(0.0208)	(0.0268)
ASW	0.2935	0.3007	0.3075	0.3015	0.2664	0.2630	0.2933	0.2929
	(0.0106)	(0.0070)	(0.0116)	(0.0227)	(0.0099)	(0.0137)	(0.0156)	(0.0177)
HSW	0.33530	0.3299	0.3607	0.3567	0.3157	0.2849	0.3557	0.3234
	(0.0095)	(0.0056)	(0.0075)	(0.0192)	(0.0137)	(0.0156)	(0.0138)	(0.0143)
CL	0.3069	0.3361	0.3444	0.3312	0.3401	0.2914	0.3392	0.2960
	(0.0058)	(0.0049)	(0.0077)	(0.0153)	(0.0083)	(0.0112)	(0.0132)	(0.0126)
DCL	0.2953	0.3069	0.3269	0.3015	0.3285	0.3013	0.3207	0.2983
	(0.0067)	(0.0065)	(0.0081)	(0.0153)	(0.0087)	(0.0096)	(0.0084)	(0.0146)
FSL	0.2993	0.2853	0.2864	0.2890	0.2835	0.2894	0.2884	0.2843
	(0.0122)	(0.0088)	(0.0133)	(0.0273)	(0.0125)	(0.0142)	(0.0166)	(0.0148)
FSW	0.2815	0.2935	0.2929	0.2799	0.3114	0.3299	0.3126	0.2998
	(0.0076)	(0.0063)	(0.0082)	(0.0189)	(0.0085)	(0.0124)	(0.0127)	(0.0154)
FSH	0.3001	0.2965	0.2807	0.2819	0.3453	0.3401	0.2772	0.3185
	(0.0135)	(0.0084)	(0.0163)	(0.0336)	(0.0162)	(0.0192)	(0.0153)	(0.0192)
SSL	0.3034	0.2727	0.2518	0.2578	0.2792	0.2815	0.2705	0.3404
	(0.0174)	(0.0096)	(0.0150)	(0.0293)	(0.0133)	(0.0162)	(0.0196)	(0.0225)
SSH	0.3041	0.2680	0.2973	0.2772	0.2985	0.2992	0.2739	0.2531
	(0.0102)	(0.0073)	(0.0125)	(0.0222)	(0.0138)	(0.0238)	(0.0116)	(0.0160)
BL	0.2687	0.2906	0.2666	0.2926	0.3409	0.3823	0.2823	0.2878
	(0.0062)	(0.0050)	(0.0077)	(0.0191)	(0.0104)	(0.0136)	(0.0127)	(0.0099)
%var.	0.9003	0.9330	0.8818	0.8937	0.8595	0.8114	0.8242	0.7468
angle1	3.1807	4.0088	6.4629	5.111	6.9627	7.2769	4.9632	4.0779

allometric coefficients for female are shown in Table 3. Both multivariate allometric coefficients derived from data sets of Keelung and Taichung showed the maximal discrepancy, of which the angle was 8.858833°. The minimal angle, 3.712063°, was obtained from the comparison between Keelung's and Kaohsiung's samples.

Table 4 shows the angles between four multivariate allometric coefficients for male, ranged from 9.441357 to 3.719230. Both multivariate allometric coefficients estimated from Taichung's and Tashi's data had the smallest similarity, but both coefficients estimated from data sets of Tashi and Keelung had the highest similarity.

Figs. 3 and 4 show the dendrograms for female and male. Two results were the same. Four areas were clustered into two distinct groups, one group included Tashi, Keelung and Kaohsiung; the other included only the Taichung.

Table 3. The angles between four multivariate allometric coefficients for female.

	Tashi	Keelung	Taichung	Kaohsiung
Tashi	0			
Keelung	5.345330	0		
Taichung	8.503562	8.858833	0	
Kaohiung	4.685421	3.712063	6.634325	0

Table 4. The angles between four multivariate allometric coefficients for male.

	Tashi	Keelung	Taichung	Kaohsiung
Tashi	0			
Keelung	3.719230	0		
Taichung	9.441357	8.305453	0	
Kaohiung	4.781120	6.574487	8.993493	0

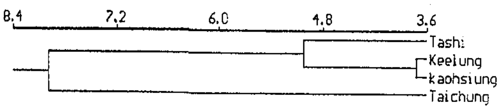

Fig. 3. Dendrograms of four sampling areas for female.

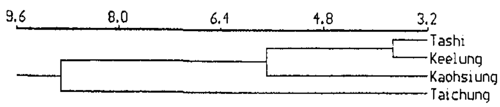

Fig. 4. Dendrograms of four sampling areas for male.

DISCUSSION

The range of the first eigenvalue was from 93.3% to 74.86% in this study. The majority of variance in each group was explained by the first eigenvalues, which revealed a good fit of the model of allometry to the data in all groups considered (Bjorklund, 1993). These similar results had been obtained in other multivariate studies of relative growth in other arthropods (Riska, 1981; Boitard *et al.*, 1982).

Allometry may be modified during growth process of organism (klingenberg, 1996). To elucidate the relationship among populations, shrink of the effect of growth variation within/between groups is necessary. Narrowing the differences of size among groups may be feasible to reduce such effect. Restricting group comparisons to specific length classes may disregard ontogenetic change within groups, and these information may be necessary for meaningful descriptions of group differences (Bookstein *et al.*, 1985). However, this effect may be not serious in this study, because the carapace length of each individual in each group was not all equal.

The multivariate allometric coefficients of red-spot prawn from Taichung was well separated from the others in this study. The hypothesis of one common multivariate allometric pattern is clearly rejected. Therefore, some multivariate statistic method should not be applied without testing this assumption for this species.

Although the resolution of allometric analysis in genetic variation among populations is believed to be inferior to shape analysis (Wiig, 1985), allometry has been found to be at least as heritable as shape (Atchley, 1983). The genetic variation among these four areas was also examined by shape comparison (Chiu, 1996). His results showed: (1) four areas were clustered into two distinct groups, one group included Taichung, Kauhsiung and Tashi; the other is Keelung; (2) male and female are clearly separately. These results are different from ours in this study, so the examination in genetic variation among populations by allometric comparison may be not suitable for this species.

Combinations of genetic and environmental factors modify growth processes (Cock, 1966). The red-spot prawns from Taichung, Tashi and Kaohsiung should share common gene pool (Chiu, 1996), so environmental factor may play an important role for this variation among four multivariate allometric coefficients. There are different water masses surrounding Taiwan in distinct season (Wang and Chern, 1988, 1992). In the winter time, the Kuroshio water passes through the south of Taiwan, Taiwan Strait and the south of East China Sea, and the Kuroshio water mass covers offshore of Keelung, Tashi and Kaohsiung in the winter time. However, the branch of Kuroshio flew into Taiwan Strait does not cross to the Changyuen ridge (Fig. 1) (Fan, 1982; Wang and Chern, 1988). Therefore, the water mass around Taichung harbor is different from the others. The coastal currents of the north and south of Taiwan encounter in the middle of Taiwan Strait during rise of the tide, but the coastal current flow from the middle of Taiwan Strait to north and south of Taiwan during fall of the tide (Chu, 1963). Therefore, the flow pattern in Taichung harbor is also clearly different from the others. These differences may explaine why the multivariate allometric coefficients of red-spot prawn from Taichung were different from the others.

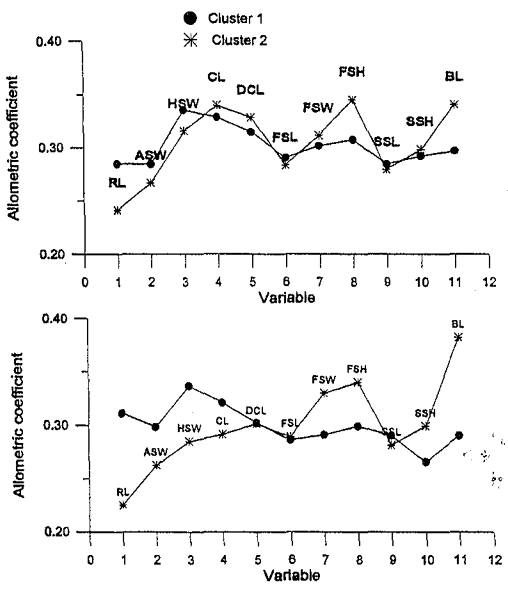

Fig. 5. Comparisons of allometric coefficients in two clusters for female (top) and male (bottom). The coefficients in cluster 1 is shown by the average of allometric coefficients derived from Tashi, Keelung and Kaohsiung, but the coefficients in cluster 2 is only derived from Taichung.

Differences between the average of allometric coefficients derived from Tashi, Keelung and Kaohsiung and the allometric coefficients estimated from Taichung was shown in Fig. 5. We found that BL, FSH and RL were three main characters to discriminate these two clusters for male and female. The similarity of multivariate allometric patterns between two clusters in female may be higher than in male.

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台灣附近海域產紅斑赤蝦(*Metapenosis barbata*)多變量異速成長係數之比較

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（1998年3月30日收件；1998年5月7日接受）

從大溪、基隆、台中和高雄等四附近海域產紅斑赤蝦之多變量異速成長係數的估計及比較，來檢視: (1)是否異速成長可用以解析不同族群間之遺傳變異；及(2)在某些多變量分析法中, 如大小校正法之Burnaby法、Shearing PCA及多群排序法之commom PCA、多群PCA，被分析之各群具有相同之多變量異速成長形態之假設是否成立。本研究中所使用之樣本於1995年11月至12月間取得。每一樣本測量11個外部形態形質；將所得之外部形態資料經對數轉換，計算其共變方矩陣，再以主成份分析法按各群及性別分別加以分析，所得之第一主成份向量，即爲多變量異速成長係數。估計值以bootstrap法評估其正確性。利用兩兩第一主成份向量間之夾角爲距離矩陣，四個採樣區視爲操作單位，再按性別利用未加權算數平均法建構其表型圖。結果顯示四個採樣區域之多變量異速成長係數，不論雌雄皆可分爲兩個集群。大溪、基隆及高雄爲一群，台中爲另一群。四地區之紅斑赤蝦具有相同異速成長形態之假設被不被接受。因此，引用假設各分析群中具有相同之多變量異速成長形態之多變量統計法，使用前須先檢視此一假設是否成立。兩個集群中所含之區域與形狀分析之結果不同，故對本研究種而言，利用多變量異速成長之比較以檢視族群間之遺傳差異是不適當的。採樣地區在冬季時被不同的水團覆蓋及漲退潮時具有不同的沿岸流型式，可能是造成兩個群集之多變量異速成長係數差異的主因。

關鍵詞：多變量異速成長係數，Bootstrap，表型圖，角度。

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