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Taxonomic Description of Three Shrimp Species (*Melicertus kerathurus*, *Metapenaeus monoceros*, *Penaeus semisulcatus*) Using Multivariate Morphometric Analyses

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Abstract: The pattern of taxonomic relationships and morphological divergence of three three species of shrimp, *Penaeus semisulcatus*, *Metapenaeus monoceros* and *Melicertus kerathurus,* collected from Iskenderun Bay, were investigated. A multivariate ANOVA using morphometric characters revealed highly significant inter-sample variation for most of the characters. In discriminant function analysis, the first discriminant function accounted for 77% and the second accounted for 23% of the between-group variability, showing clear between-species differentiation. Examination of the contribution of each variable to the first two discriminant functions showed high contributions from measurements 1_2, 4_5, 11_12, 8_11, 8_9, 4_15 in the first function, and 7_12, 3_16, 3_4, 12_13, 8_12 in the second function, indicating that these characters are key characters in discriminating between these species. The UPGMA cluster analysis produced two main clustering; *Melicertus kerathurus* was closest taxa to *Penaeus semisulcatus* being the sister group to the *Metapenaeus monoceros* which was the most divergent in this group. In the correct assignment of individuals into their original sample, the proportion of correctly classified the *Metapenaeus monoceros* to their original group was highest (92%), showing a clear separation from the other species.

Key words: Shrimp, taxonomy, morphometric analyses, truss network system

INTRODUCTION

Penaeid shrimps are important resources for worldwide fisheries and aquaculture[1]. Morphological variation studies within and among species penaeid shrimps in nature began over 35 years ago for purposes of fishery management. The results having been taken from these studies can be used for the purpose of aquaculture. The study of the morphological characteristics of shrimp species and the analysis of morphological relationships between broodstocks can be also a useful tool for their management because identification and discrimination of broodstocks are essential to successful rearing programs[2,3].

Penaeid shrimps differ in a variety of morphological characteristics that are the expression of genetic differences among them. There are, of course numerous studies of the morphological differences among species which can be used for taxonomic distinctions. These studies generally focus on the structures of genitalia, appendages, rostra and sculpturing of the carapace. Studies of the variation among the species in morphological characters related to size, shape or other commercial characters are quite limited.

Dimensions collected from photographs of shrimp in either dorsal or lateral view either dead or alive have been used in recent studies. Four species of Penaeus, *P. monodon, P. setiferus, P. stylirostris* and *P. vannamei* were investigated using morphological variables by digitizing a photographic image. The results showed that nearly all of the morphometric variation within the populations and species of Penaeus is related to the size of the shrimp[4].

Morphometric characters have been successfully used for taxonomic inferences. There are many well-documented morphometric studies that provide evidence for taxonomic dilemmas[4-6]. A new system of morphometric measurements called the truss network system[7] has been increasingly used for population and taxonomic studies[4,6,8]. Therefore in the present study the truss network system were constructed on the taxonomic description of shrimps species.

Penaeus semisulcatus de Haan, 1844, *Metapenaeus monoceros* (Fabricius, 1798) and *Melicertus kerathurus*

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(Forskal, 1775) are the most common penaeid shrimps and currently being fisheried commercially in the Eastern Mediterranean. Although, *Penaeus semisulcatus* and *Metapenaeus monoceros* are indo-Pacific species distributed along the coast of the Eastern Mediterranean. The shrimp *Penaeus kerathurus* is an endemic species in the Mediterranean[9,10]. Despite their high commercial value, there is little information available on descriptions and the taxonomic relationships of the shrimp species. Therefore, in the present study, the pattern of taxonomic relationships and morphological divergence of three genera, including three species, *Penaeus semisulcatus*, *Metapenaeus monoceros* and *Melicertus kerathurus,* living in the Mediterranean Sea, were investigated.

MATERIALS AND METHODS

The shrimps were caught off the Iskenderun Bay of the North-eastern Mediterranean in November 2005 by trawling. The species were identified according to Dall *et al.*,[11].

The truss network system described for fish body morphometrics[7] was used to construct a network on shrimp body, eighteen landmarks determining 35 distances were measured on the body, as illustrated in (Fig. 1). Significant correlations were observed between size and morphometric characters between the samples. Therefore transformation of absolute measurements to size–independent shape variables was the first step of the analyses. In order to eliminate any variation resulting from allometric growth, all morphometric measurements were standardized according to Elliott *et al.*,[12] $M_{adj} = M (L_s/L_o)^b$. where M is the original morphometric measurement, M_{adj} the size adjusted measurement, L_o the standard length of fish and L_s the overall mean of standard length for all fish from all samples for each variable. The parameter b was estimated for each character from the observed data as the slope of the regression of log M on log Lo, using all specimens. This allometric elimination was performed using the MorFISH program[13] . Correlation coefficients between transformed variables and standard length were calculated to check if the data transformation was effective in removing the effect of size in the data.

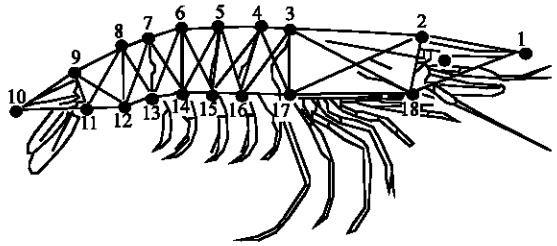

Fig. 1: Application of the truss network system on the body of shrimp

Discriminant Function Analysis (DFA) was used for multivariate analysis of three shrimp species. Discriminant function analysis combines a selection of body measures in a linear fashion to produce a mathematical function which can be used to classify individuals into groups. Discriminant function scores were used in hierarchical cluster analyses using SPSSv13.0. In hierarchical cluster analyses UPGM dendrogram was used that does not plot actual distances but rescales the distance to numbers between 0 and 25. The degree of similarity among samples in the overall analysis and relative importance of each measurement for group separation were assessed by stepwise Discriminant Function Analysis (DFA) with jack-knifed classification. Population centroids with 95% confidence ellipses derived from the DFA were used to visualize relationships among the individuals of groups.

RESULTS

A multivariate ANOVA (MANOVA) using morphometric characters revealed highly significant inter-sample variation for most of the characters (Table 1).

In discriminant function analysis, the first DF accounted for 77 % and the second accounted for 23 % of the between-group variability, showing clear between-sample differentiation (Fig. 2). Examination of the contribution of each variable to the first two discriminant functions showed high contributions from measurements 1_2, 4_5, 11_12, 8_11, 8_9, 4_15 in the first function and 7_12, 3_16, 3_4, 12_13, 8_12 in the second function (Table 2). This indicates that these characters are key characters in discriminating between these species.

The UPGMA cluster analysis of morphological data produced two main clustering (Fig. 3). *Melicertus kerathurus* was closest taxa to *Penaeus semisulcatus* being the sister group to the *Metapenaeus monoceros* which was the most divergent in this group.

The overall assignment of individuals into their original sample by the DFA was 87 % (Table 3). The proportion of correctly classified *Metapenaeus monoceros* to their original group was highest (92%), showing a clear separation from all others. Whereas, *Melicertus kerathurus* and *Penaeus semisulcatus* showed more similarity than the others.

DISCUSSION

In the present investigation, the taxonomic status of *Melicertus kerathurus* within the genera *Melicertus* and

Table 1: Test of equality of group means (ANOVA) between species for the characters

Characters	Wilks' Lambda	F	Sig.
1_2	0.347	670.805	0.000
2_3	0.628	210.290	0.000
3_4	0.593	240.665	0.000
4_5	0.403	530.294	0.000
5_6	0.572	260.932	0.000
6_7	0.761	110.316	0.000
7_8	0.767	100.925	0.000
8_9	0.457	420.821	0.000
9_10	0.794	90.348	0.000
10_11	0.774	100.532	0.000
11_12	0.424	480.999	0.000
12_13	0.801	80.951	0.000
13_14	0.891	40.399	0.016
14_15	0.756	110.590	0.000
15_16	0.892	40.359	0.016
16_17	0.894	40.268	0.018
17_18	0.979	0.778	0.463
18_1	0.992	0.280	0.757
1_10	0.495	360.679	0.000
2_18	0.984	0.590	0.557
2_17	0.940	20.314	0.106
3_18	0.921	30.099	0.051
3_17	0.889	40.496	0.014
3_16	0.517	330.680	0.000
4_17	0.869	50.408	0.006
4_16	0.924	20.970	0.058
4_15	0.494	360.859	0.000
5_16	0.939	20.348	0.103
5_15	0.695	150.771	0.000
5_14	0.459	420.511	0.000
6_15	0.909	30.584	0.033
6_14	0.765	110.038	0.000
6_13	0.612	220.787	0.000
7_14	0.976	0.887	0.416
7_13	0.876	50.110	0.008
7_12	0.636	200.566	0.000
8_13	0.934	20.564	0.084
8_12	0.765	110.047	0.000
8_11	0.498	360.259	0.000
9_12	0.849	60.378	0.003
9_11	0.913	30.444	0.037

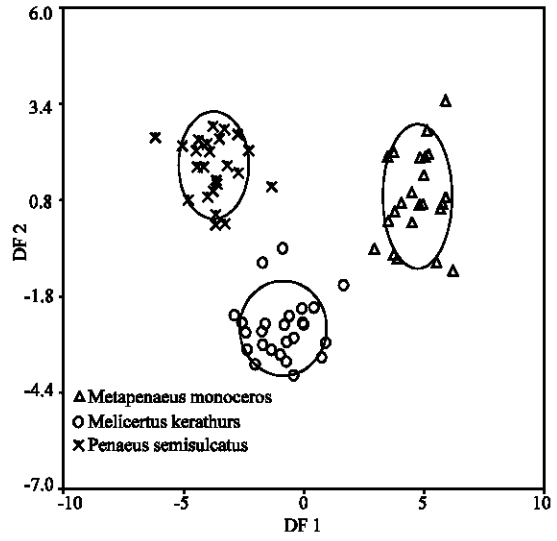

Fig. 2: Ninety five percent confidence ellipses of DFA scores for morphometric analysis

Table 2: Component loadings of discriminating variables. Variables ordered by absolute size of correlation within function. *Largest absolute correlation between each variable and any discriminant function

	Function	
Characters	1	2
1_2	0,367*	-0,198
4_5	0,339*	0,006
11_12	0,318*	0,126
8_11	0,288*	-0,191
8_9	0,287*	-0,184
4_15	0,268*	-0,191
1_10	0,258*	-0,208
5_14	0,237*	-0,180
5_6	0,224*	-0,163
2_3	-0,213*	0,035
5_15	0,175*	-0,106
6_14	0,154*	-0,022
7_8	0,137*	-0,126
6_15	0,110*	-0,024
9_12	0,108*	-0,029
4_17	0,105*	-0,050
7_13	0,094*	-0,086
3_17	0,087*	-0,086
5_16	0,053*	-0,041
7_14	0,044*	0,000
7_12	0,134	-0,298*
3_16	0,219	-0,290*
3_4	0,183	-0,259*
12_13	0,041	-0,244*
8_12	0,077	-0,237*
6_13	0,193	-0,201*
9_10	0,093	-0,197*
6_7	0,120	-0,184*
14_15	0,123	-0,182*
16_17	0,046	-0,154*
10_11	0,125	-0,154*
3_18	-0,004	-0,150*
13_14	0,056	-0,146*
2_17	0,026	-0,121*
9_11	0,042	-0,115*
15_16	0,081	-0,098*
4_16	0,062	-0,094*
8_13	0,063	-0,073*
17_18	0,017	-0,069*
2_18	0,009	-0,064*
18_1	0,004	0,045*

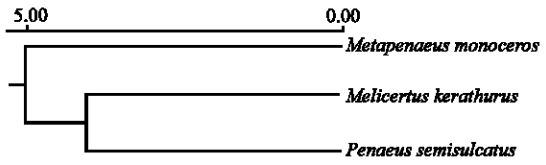

Fig. 3: Upgma cluster analysis of morphological data

Penaeus kerathurus as a species within the genera *Penaeus* and *Metapenaeus monoceros* as a species within the genera *Metapenaeus* were preliminary investigated. *Penaeus kerathurus* has been recently revised to *Melicertus kerathurus* on the bases of morphological

Table 3: Correct classification of individuals into their original species

		Predicted Group Membership			
Species		1	2	3	Total
Count	Melicertus kerathurus (1)	21	1	3	25
	Metapenaeus monoceros (2)	2	23	0	25
	Penaeus semisulcatus (3)	3	1	21	25
%	*Melicertus kerathurus*	84	4	12	100
	Metapenaeus monoceros	8	92	0	100
	Penaeus semisulcatus	12	4	84	100

characters. However in the present study, the topology produced from the UPGM tree for morphologic data revealed uncertainty on the present taxonomic status of these species. The amount of morphologic divergence was lower between *Melicertus kerathurus* and *Penaeus semisulcatus,* and higher between *Metapenaeus monoceros* and *Penaeus semisulcatus* within this family. Therefore, *Penaeus semisulcatus* showed least morphological differentiations and showed close morphological similarity to *Melicertus kerathurus*. These results lead us to reinvestigate the taxonomic status of *Melicertus kerathurus* within the genera *Melicertus* and *Penaeus*. This can be achived with detailed investigation using both morphological and molecular genetic markers.

Taxonomic description of a species has commonly relied on description of unique sets of morphological characters. Morphometric measurements from head of fish (1-2) and segments (4-5, 11-12, 8-9) were the most discriminative characters in the present classification. Such characters are phylogenetically informative to distinguish species of the penaeid shrimps.

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