

MORPHOMETRIC VARIATIONS OF TWO SNAKEHEADS (FAMILY-CHANNIDAE) FROM BAGO RIVER, YANGON REGION BASED ON LANDMARKS AND TRUSS NETWORK ANALYSIS

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Abstract

The present study was conducted by observing landmark-based morphometric variation of the two snakeheads, *Channa panaw* and *Channa striata* of family Channidae from the same stock of Bago river, Yangon Region. A total of 20 specimens of each of two *Channa* species were collected during December 2019 to March 2020. Set up the ten morphological landmarks and twenty one truss distances were measured. The significance of morphological differences of study species were carried out analysis of variance (ANOVA). Significantly differences were found in twenty one truss measurements ($p < 0.001$) were observed. Wilk's lambda of discriminant functional analysis, values of study species were nearly 0 and differences strongly significant (range is $0 < \lambda < 1$). The eigenvalues of factor analysis (FA) was indicated four factors of *Channa panaw* and three of *Channa striata*. The principal analysis (PCA) indicated size and shape variation and explained percentage of total variance, 86.602 and 87.723. Discriminant function analysis (DFA) accounted for four morphological indices (94.6 %, 3.9 %, 1.1 % and 0.4%) in *Channa panaw* and three morphological indices in *Channa striata* (73.3%, 25.0 % and 1.7 %) of with group variability. About 95% of individuals of two *Channa* species into their original group were correctly classified in discriminant space, as determined by discriminant function analysis. All statistically analyses were done using SPSS Package Version 26.

Keywords: Landmarks, Truss network, Morphometric variations, FA, PCA, DFA

Introduction

The snakeheads of the family Channidae comprises of two genera. The genus *Channa* comprises of 33 species in Asia (Courtenay and Williams, 2004). In India, 12 species including *Channa amphibeus* (McClelland 1845), *C. auranti-maculata* (Musikasinthorn 2000), *C. barca* (Hamilton 1822), *C. bleheri* (Vierke 1991), *C. diplogramma* (Day 1865), *C. gachua* (Hamilton 1822), *C. marulius* (Hamilton 1822), *C. melano-stigma* (Geethakumari & Vishwanath 2011), *C. orientalis* (Bloch & Schneider 1801), *C. punctate* (Bloch 1793), *C. stewartii* (Playfair 1867), *C. striata* (Bloch 1793) are reported. Fishes within this genus are characterized by an elongated cylindrical body, long and entirely soft-rayed dorsal and anal fins, a large mouth with well-developed teeth on both upper and lower jaws, and an accessory air-breathing apparatus known as the supra-brachial organ (Musikasinthorn, 1998, 2003). Snakeheads are of considerable interest as food fish and in aquarium trade and also as predators (Courtenay and Williams, 2004). Due to lack of information on its distribution, biology and population trends, this species was assessed as Data Deficient (Britz, 2010). Morphometric is defined as the study of quantitative analysis such as size and shape of living organisms, which for understanding the taxonomy as well (Park *et al.*, 2013). Morphometric parameters of a fish species has a major role to ensure whether there is any disparity between same species of different geographic region (Naeem *et al.*, 2012). The morphometric relationships between various body parts of fish can be used to assess the well-being of individuals and to determine possible difference between separate stocks of the same species (King, 2007). Landmark is a point of correspondence on an object that matches between and within population (Swain & Foote, 1999). The distance between the landmarks provide more comprehensive coverage of form for greater discriminating power (Strauss and Bookstein, 1982). The truss

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network system is considered superior to traditional morphometric that use morphometric traits to represent the complete shape of fish, which has been commonly used in the field of fish taxonomy and fisheries management. Truss network systems are powerful tools for stock identification. A sufficient degree of isolation may result in notable morphological, meristic and shape differentiation among stocks of a species which may be recognizable as a basic for identifying the stocks (Turan, 2004). So far the research dealt with the morphometric variations between different stocks in different localities and between different species was scarce. The present research is therefore designed;

- to examine the morphometric differences of within and between the species of *Channa*

Materials and Methods

Study area

The study area was chosen at Thatyapinchaung village of Bago river, Yangon Region. It was located between latitude 16° 54' 57.8" N and longitude 96° 20' 15.2" E.

Study period

The study was lasted from December 2019 to March 2020.

Collection of specimens

A total of 40 snakeheads comprising *C. panaw* and *C. striata* (20 specimens for each species) were collected with the help of fishermen immediately after catch. Specimens were transferred into the ice-box for further identification. Identified and classified of the collected species were follow after Talwar and Jhingran, 1991, Courtenay and Williams, 2004 and Froese and Pauly, 2018.

Truss network analysis

Pattern of size and shape variation of snakeheads, *C. panaw* and *C. striata* were evaluated by means of truss network analysis. The specimen was laid on the drawing graph sheet into a right body position. This sheet was sandwiched between plastic film sheet and pop block. A total of ten morphological landmarks were identified on the specimens (Table 1). The choosing landmarks were pierced with long round head pin. After removing the specimen from the drawing graph sheet, these landmarks were joined with the help of permanent marker as a series of a truss network. Measurements were taken 21 inter-landmarks between ten showing a degree of correspondence landmarks (i.e. 1 to 2, 2 to 3 etc.) using a standard truss network protocol (Table 2 and Figure 1) (Strauss and Bookstein, 1982).

Statistical analysis

Prior to the analysis, size effects from the data set were eliminated. Variations were attributed to body shapes and size differences of the fish. In this research, there were significant network morphometric variation among all measured characters and total length of the fish. Therefore, it was necessary to remove size-dependent variations for all the characters. An allometric formula given by Elliott *et al.* (1995). $M_{adj} = M (L_s / L_o)^b$, where M is the original measurement, M_{adj} = The size-adjusted measurement, L_s is the overall mean of the total length samples in each analysis, L_o is the total length and b is the slope of the regression coefficient, was calculated for each character from the observed data as the slope of $\log M$ on $\log L_o$. The efficiency of the size adjustment transformations was assessed by testing the significantly correlation between a transformed variable and the TL. Analysis of variance (ANOVA) was carried out to test the significance of morphological differences. In addition to size-adjusted data were standardized and submitted to multivariate techniques such as Factor Analysis (FA), Principal Component

Analysis (PCA) and Discriminant Functional Analysis (DFA) in SPSS software (version 26) (Veasey *et al.*, 2001).

Table 1 Morphological landmarks selected for the study fish

Landmark	Particular of landmark
1	Tip of the snout
2	Upper end of the operculum
3	Origin of the dorsal fin base
4	End of the dorsal fin base
5	Upper origin of the dorsal fin
6	Lower origin of the dorsal fin
7	End of the anal fin based
8	Origin of the anal fin based
9	Origin of the pelvic fin base
10	Lower end of the operculum

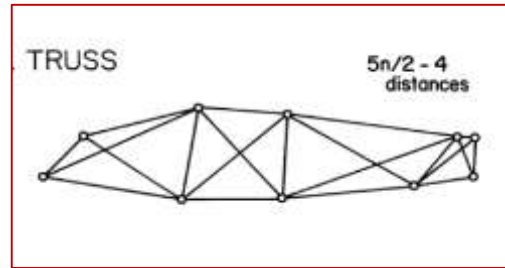


Figure1 The truss box of the 10 external landmarks design patterned

Landmark (n=10)

$$\begin{aligned} \text{Truss distance} &= \frac{5n}{2} - 4 = \frac{5 \times 10}{2} - 4 \\ &= \frac{50}{2} - 4 = 25 - 4 = 21 \end{aligned}$$

(Strauss and Bookstein, 1982)

Table 2 Morphometric measurements made for two *Channa* species

Measurement number	Network measurement	Distance code	Distance
1	1-2	HL	Head Length
2	2-3	BL1	Body Length 1
3	3-4	DFL	Dorsal fin length
4	4-5	BL2	Body Length 2
5	5-6	CL	Caudal Length
6	6-7	BL3	Body Length 3
7	7-8	AFL	Anal fin Length
8	8-9	BL4	Body Length 4
9	9-10	BL5	Body Length 5
10	1-10	ML	Mouth Length
11	2-8	BD1	Body diagonal 1
12	2-9	BD2	Body diagonal 2
13	2-10	HD	Head diagonal
14	3-8	BD3	Body diagonal 3
15	3-9	BH1	Body height 1
16	3-10	BD4	Body diagonal 4
17	4-7	BH2	Body height 2
18	4-8	BD5	Body diagonal 5
19	4-9	BD6	Body diagonal 6
20	5-7	BD7	Body diagonal 7
21	5-8	BD8	Body diagonal 8

Results

The length range and mean with standard deviation for each specimen were shown in table 3. Among the morphometric measurement, one-way ANOVA test showed that all truss measurements of two species were highly significant ($P < 0.001$) with Wilk's lambda value were highly significant (nearly zero) of discriminant function (Table 4).

Twenty-one truss morphometric measurements of *C. panaw* and *C. striata* (Plate 1) yielded four factors and three factors explaining 86.602 % of the total variance (60.542 % for factor 1 and 10.966 % for factor 2, 9.130 for factor 3 and 5.964 for factor 4) and 87.72% of the total variance (66.58% for factor1, 12.99% for factor2 and 8.15% for factor3) in the entire dataset with eigenvalues of 13.319, 2.413, 2.009, 1.312 and 14.648, 2.858, 1.749 respectively (Table 5 and Figure 2A and 2B).

As the extraction in PC analysis of *C. panaw*, PC1 was the four truss network measurements of weak factors loading (BL2, BL3, BL5 and HD), among them the low standardized score was BL3 (-0.095) showed and component plot in rotated space also revealed the low neuroticism. Variable BL2 in PC1 and PC2 was weak factor loading, thus variable was also showed that the low neuroticism. These results showed size variation of morphological structure was BL2 and BL3 (Table 6 and Figure 3A).

PC2 in *C. panaw* was the four truss network measurements of weak factors loading as BL1, BL2, BL5 and ML but low variable was BL1 (-.294), showed the low standardized and component plot in rotated space also did not revealed the low outgoingness in table 6 and figure 3A. These results indicated that no shape variation of morphological structure.

As the extraction in PC1 of *C. striata* was the three truss network measurements of weak factor loading (BL1, AFL and BD5). Among them the low standardized score was AFL and BD5 showed and component plot in rotated space also revealed the low neuroticism in table 6 and figure 3B. These finding examined that size variation of morphological structure was AFL and BD5.

PC2 in *C. striata* was the six truss network measurements of weak factors loading as HL, BL2, CL, AFL, BD5 and BD6 but these low standardized scores and component plot in rotated space also did not revealed the low outgoingness (Table 6 and Figure 3B). The outcome of present results indicated that no shape variation of morphological structure.

The two studied species showed four and three morphological indices defining 94.6% (DF1), 3.9% (DF2), 1.1% (DF3) and 0.4% (DF4) the morphological differences in *C. panaw* and 73.3% (DF1), 25.0% (DF2) and 1.7% (DF3) the morphological differences in *C. striata*. The truss distances with important loading on DF1 were shown with total variance of 94.6% and 73.3% in both studied species and the largest absolute correlation between each variable and any discriminant function of DF1 the total variance were not shown in *C. panaw* and *C. striata* (Table 7).

All of these distances were described as morphometric measurements cover the whole body of the fish. The largest absolute correlation between each variable and any discriminant function of DF2 elucidated 3.9% in *C. panaw* and 25.0% in *C. striata* of the total variance were four network measurement as significance loading BD2, BD3, BH1 and BH2 in *C. panaw* and seven network measurements as BL3, BL4, BD1, HD, BD4, BD6 and BD7 in *C. striata* (Table 7).

The DF3 elucidated 1.1% in *C. panaw* and 1.7% in *C. striata* of the total variance were seven network measurements as significance loading DFL, BL2, CL, BL3, BL4, HD and BD6 in *C. panaw* and fourteen network measurements in *C. striata* (Table 7).

The rest ten measurements contributed to DF4 elucidated 0.4% in *C. panaw* of total variance (Table 7).

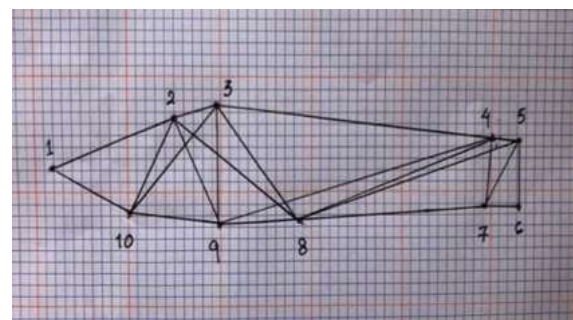
Although the largest absolute correlation between each variable, a correct classification of individuals into their original population of *C. panaw* and *C. striata* varied 98.5% by discriminant analysis (DF1 and DF2) and 95% of individual group cases (Table 8) and 98.3% by discriminant analysis (DF1 and DF2) and 95% of individuals group cases (Table 9) could be classified in their correct a priori grouping according to plotting of canonical discriminant functions of *C. panaw* and *C. striata*, which showed a more of them (20 individuals) overlapping for both morphometric (total length) and truss 21 measurements in discriminant space except total length 150 & 151 in *C. panaw* and total length 176 and 190 in *C. striata* (Fig. 4A and 4B).

Table 3 Descriptive data of snakeheads *C. panaw* and *C. striata*

Source of fish sample	Species	Sample size	Total length (mm)	
			Range	Mean ± SD
Bago river	<i>Channa panaw</i>	20	135-197	162.20 ± 17.82
	<i>Channa striata</i>	20	150-270	209.95 ± 30.08



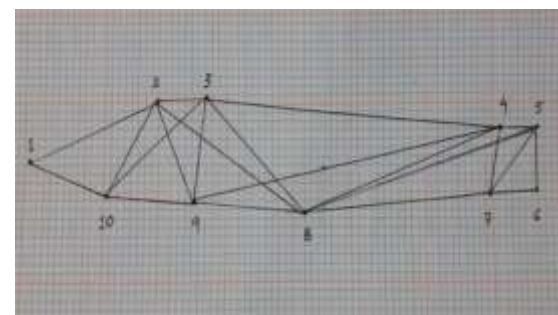
A. Location of landmarks of *C. panaw* (Musikasinthorn, 1998)



B. Scheme of truss network used *C. panaw*



C. Location of landmarks of *C. striata* (Bloch, 1793)



D. Scheme of truss network used of *C. striata*

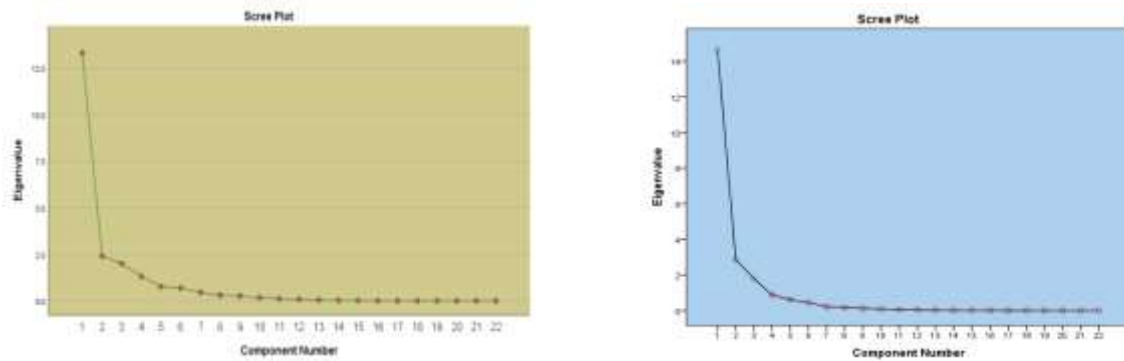
Plate 1 Morphometric analysis of *C. panaw* and *C. striata*

Table 4 Analysis of variance (ANOVA) testing differences within each species *C. panaw* and *C. striata*

Measurement numbers	Distance code	df		F-value		Wilk's lambda		P-value	
		1	2	<i>C. panaw</i>	<i>C. striata</i>	<i>C. panaw</i>	<i>C. striata</i>	<i>C. panaw</i>	<i>C. striata</i>
1	HL	1	38	943.72	563.89	0.04	0.06	0.000*	0.000*
2	BL1	1	38	1363.11	786.94	0.03	0.05	0.000*	0.000*
3	DFL	1	38	410.37	215.88	0.09	0.15	0.000*	0.000*
4	BL2	1	38	1445.39	850.70	0.03	0.04	0.000*	0.000*
5	CL	1	38	1335.75	814.34	0.03	0.05	0.000*	0.000*
6	BL 3	1	38	1442.05	820.10	0.03	0.04	0.000*	0.000*
7	AFL	1	38	657.72	443.84	0.06	0.08	0.000*	0.000*
8	BL 4	1	38	1144.72	546.92	0.03	0.07	0.000*	0.000*
9	BL5	1	38	1174.34	703.33	0.03	0.05	0.000*	0.000*
10	ML	1	38	1128.72	679.98	0.03	0.05	0.000*	0.000*
11	BD1	1	38	847.30	387.03	0.04	0.09	0.000*	0.000*
12	BD2	1	38	1130.13	659.02	0.03	0.06	0.000*	0.000*
13	HD	1	38	1150.54	718.52	0.03	0.05	0.000*	0.000*
14	BD3	1	38	982.58	502.62	0.08	0.07	0.000*	0.000*
15	BH1	1	38	1130.46	688.88	0.03	0.05	0.000*	0.000*
16	BD 4	1	38	984.52	608.13	0.04	0.06	0.000*	0.000*
17	BH2	1	38	1303.46	805.17	0.03	0.05	0.000*	0.000*
18	BD5	1	38	596.55	401.65	0.06	0.09	0.000*	0.000*
19	BD6	1	38	336.92	188.38	0.10	0.17	0.000*	0.000*
20	BD7	1	38	1234.64	747.23	0.03	0.05	0.000*	0.000*
21	BD8	1	38	489.39	322.98	0.07	0.11	0.000*	0.000*

Table 5 Eigen values, percentage of variance and percentage of cumulative variance in *C. panaw* and *C. striata*

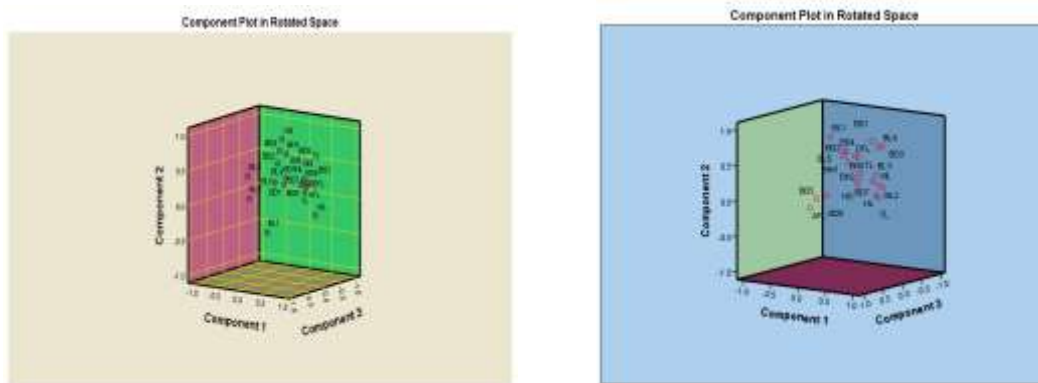
Factors	<i>C. panaw</i>			<i>C. striata</i>		
	Eigenvalues	(%) of Variance	(%) of Cumulative variance	Eigenvalues	(%) of Variance	(%) of Cumulative variance
1	13.319	60.542	60.542	14.648	66.580	66.580
2	2.413	10.966	71.508	2.858	12.990	79.570
3	2.009	9.130	80.638	1.749	8.153	87.723
4	1.312	5.964	86.602	-	-	-



A. *Channa panaw*

B. *Channa striata*

Figure 2 Showing of Eigen values by scree plot of two species of *Channa*



A. *Channa panaw*

B. *Channa striata*

Figure 3 Score plots on size-corrected truss variables of two species of *Channa*

Table 6 Result of factors extraction in PC analysis after varimax normalized rotation in *C. panaw* and *C. striata*

Network measurement	Distance code	<i>C. panaw</i>				<i>C. striata</i>		
		PC 1	PC 2	PC 3	PC 4	PC 1	PC 2	PC 3
1-2	HL	.635	.606	-.085	.326	0.871	0.164	0.323
2-3	BL1	.368	-.294	.741	.030	-0.125	0.861	0.094
3-4	DFL	.891	.373	.121	.087	0.541	0.705	0.404
4-5	BL2	.056	.177	.855	.054	0.869	0.249	0.154
5-6	CL	.715	.608	-.110	-.042	0.845	0.124	0.250
6-7	BL3	-.095	.462	.692	-.036	0.696	0.407	0.092
7-8	AFL	.855	.337	.201	.237	0.124	0.006	0.982
8-9	BL4	.510	.453	.367	-.411	0.587	0.747	-0.231
9-10	BL5	.067	.290	.064	.915	0.332	0.754	0.403
1-10	ML	.862	-.114	-.065	-.259	0.851	0.304	0.250
2-8	BD1	.624	.396	.582	-.024	0.513	0.850	-0.070
2-9	BD2	.388	.657	.445	.296	0.350	0.697	0.439
2-10	HD	.217	.931	.065	.206	0.645	0.388	0.479
3-8	BD3	.533	.674	.173	-.165	0.599	0.769	-0.113
3-9	BH1	.438	.771	.245	.072	0.437	0.611	0.442
3-10	BD4	.300	.802	.265	.349	0.403	0.753	0.442
4-7	BH2	.610	.680	.106	-.028	0.668	0.334	0.524
4-8	BD5	.852	.397	.177	.205	0.221	0.146	0.951
4-9	BD6	.832	.446	.251	-.004	0.581	0.689	0.387
5-8	BD7	.650	.350	.042	-.352	0.812	0.360	0.344
5-9	BD8	.820	.370	.331	.200	0.375	0.198	0.896

Table 7 Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions of landmark distance of *C. panaw* and *C. striata*

Network measurement	Distance code	<i>C. panaw</i>				<i>C. striata</i>		
		DF 1 (94.6 %)	DF 2 (3.9 %)	DF 3 (1.1 %)	DF 4 (0.4%)	DF 1 (73.3%)	DF 2 (25.0%)	DF 3 (1.7%)
1-2	HL	.240	.586	-.340	-.695*	.444	.246	.861*
2-3	BL1	.026	-.034	.275	.960*	-.101	.691	-.716*
3-4	DFL	.505	-.319	-.710*	.374	.399	.600	-.694*
4-5	BL2	.050	-.082	.995*	-.034	-.593	-.004	.805*
5-6	CL	-.202	-.559	-.803*	-.027	-.438	-.065	.897*
6-7	BL3	-.404	.617	.668*	-.098	-.150	.775*	-.613
7-8	AFL	.112	-.026	.171	.979*	.490	.552	-.675*
8-9	BL4	-.155	-.188	.956*	.162	.575	.818*	.021
9-10	BL5	-.228	-.225	-.266	-.909*	.548	.418	-.724*
1-10	ML	.289	.238	.422	.826*	.212	.491	.845*
2-8	BD1	.211	.158	.603	.753*	.231	.735*	-.637
2-9	BD2	-.067	.971*	-.022	-.229	.147	.372	-.917*
2-10	HD	-.231	.542	-.604*	-.536	.151	.837*	-.525
3-8	BD3	.524	.648*	-.206	.513	.479	.378	-.793*
3-9	BH1	.055	.988*	-.103	-.103	.146	.349	-.926*
3-10	BD4	-.337	.549	-.485	-.591*	.202	.742*	-.639
4-7	BH2	.057	.661*	.447	-.600	-.081	.654	-.752*
4-8	BD5	.272	.048	.023	.961*	.296	.606	-.738*
4-9	BD6	.281	-.186	.929*	.150	.369	.691*	-.622
5-8	BD7	-.081	.189	-.119	.971*	-.440	.783*	-.439
5-9	BD8	.237	-.018	.677	.697*	.341	.626	-.701*

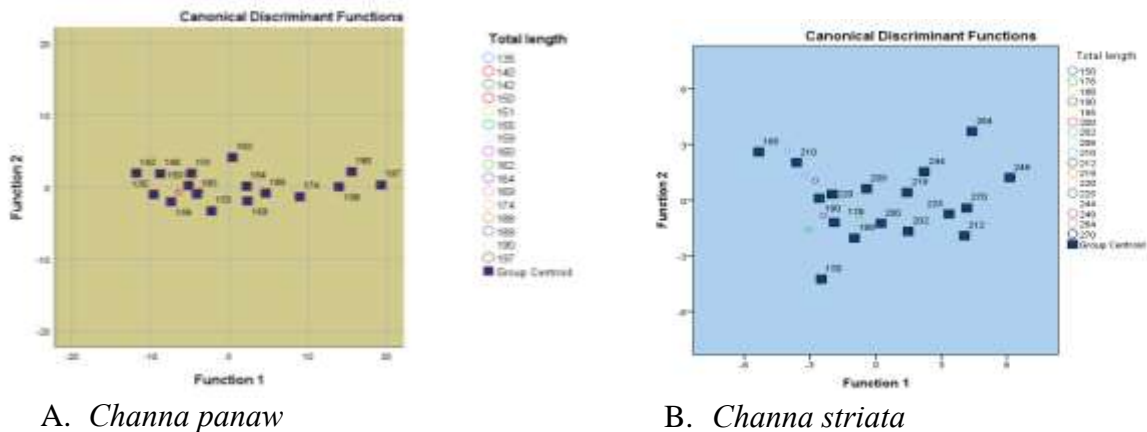


Figure 4 Sample centroids of discriminant function scores based on total length of two species of *Channa*

Table 8 Showing classification results of canonical discriminant function based on all truss measurements of *Channa panaw*

		Classification results																	
		Predicted group membership																	
Total length		135	140	142	150	151	155	159	160	162	164	169	174	188	189	190	197	Total	
Original %	135	100.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	
	140	.0	100.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	142	.0	.0	100.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	150	.0	.0	.0	75.0	25.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	151	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	155	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	159	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	160	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	162	.0	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0
	164	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	.0	.0	100.0
	169	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	.0	100.0
	174	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	.0	100.0
	188	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	.0	100.0
	189	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	.0	100.0
	190	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	.0	.0	100.0
	197	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	100.0	100.0	100.0

95 % of original grouped cases correctly classified

Table 9 Classification results of canonical discriminant function based on all truss measurements of *Channa striata*

		Classification results																	
		Predicted group membership																	
Total length		150	176	188	190	195	200	202	209	210	212	219	220	225	244	249	264	270	Total
Original %	150	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
	176	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
	188	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
	190	0	50	0	50	0	0	0	0	0	0	0	0	0	0	0	0	0	100
	195	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	100
	200	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	100
	202	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	100
	209	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	0	100
	210	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0	100
	212	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	100
	219	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	100
	220	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	100
	225	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	100
	244	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	100
	249	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	100
	264	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	100
	270	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100

95 % of original grouped cases correctly classified

Discussion

In the present study, among the 21 truss measurements, all were highly significant different ($p < 0.001$) within species of same stock. Rahman *et al.* (2014) found all truss morphometric measurements significantly different ($p < 0.001$) in the Old Brahmaputra river. Kashyap *et al.* (2014) reported that all truss measurements were found to be highly significant ($p < 0.001$) of Freshwater Murrel, *Channa punctatus* from Northern and Eastern Regions of India.

Morphometric studies by statistical methods were based on a set of traditional measurements which were providing uneven and biased aerial coverage of the entire body form of the specimen explained Sathianandan (1999). Truss network provides a more systematic and geometric characterization of fish shape. Analysis of truss network measurements in the present study was done by principal component analysis (PCA). The study of PCA analysis indicated that the scores on the scatterplot of *both species* which were size variation in morphological structure but no shape effect variation in their populations.

Joseph (2000) explained that PCA does not require any prior information about the groups in the analysis of truss data. In this research, eigen values of the four and three principal components were over one by *C. panaw* and *C. striata* respectively. These eigenvalues were conducted a principal components analysis to determine how many important components are present data. Yakubu and Okunsebor (2011) explained that the morphological divergence is exclusively associated to body shape but not to size. Traits related to size can make the result error if not removed from the data during morphometric analysis. Two truss measurements (BL2 and BL3) of *C. panaw* and (AFL and BD5) of *C. striata* were skewed on the analysis but the size effect data was removed using allometric transformation.

These two studied species. were accepted on this analysis because missing measurements was adjusted on the analysis. PC analysis was used to observe the intraspecific variation by score plots, that PCs showed significant differences were in this research. PC1 of morphometric data as multivariate index of size and PC2 as shape indices was interpret by Cadrin, 1999. Therefore, the results of PC analyses clearly highlighted fish species and variability pattern relation.

In discriminant functional analysis (DFA), the first DF accounted for much more of the within-group variability than did the remaining other DFs. It was obvious that the other DFs explained much less of the variance than the first DF. According to no significance loading of morphological indices in DF1 (Discriminant Function Analysis) of both studied species in the present study, suggested that no shape variation of *Channa panaw* and *Channa striata*. About 95% of individuals of both studied species into their original group were correctly classified in discriminant space, as determined by discriminant function analysis. This finding is supported by Kashyap *et al.*, (2016) stated about in group classification using DFA, 100 percent of all the samples were correctly classified into their original subpopulation.

Conclusion

Truss network system has emerged as a new tool with more effective strategies for descriptions of size and shape, better data collection and diversified analytical tools. They offer powerful tool for testing and displaying morphological differences when combined with multivariate statistical method (FA, PCA and DFA). These analyses can be effectively applied to assess the variation of stock within each species in the present study. The present results were preliminary baseline information of studied species of same population in Bago River for further studies. More research based on genetic studies and investigations of the causes of environmental factors will be needed in future.

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