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COMPARATIVE MORPHOMETRIC ANALYSIS IN SELECTED SPECIES OF SNAKEHEAD FISHES (CHANNIDAE, PERCIFORMIS) TO ASSES EVOLUTIONARY TRENDS AND RELATIONSHIP

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ABSTRACT

Four species of genus *Channa* (Gronovius), *vi.,C. punctatus, C. gachua,C. striatus, and C. marulius*were selected for their morphometric character analysis to find out interspecific relationship. We have chosen 11-morphometric characters. All the measurements of head and body region were size-adjusted with the Head Length and Standard Length respectively. Morphometric analysis within and between the species were carried out with the help of Unscrambler ® version 9.8 software. Results of Line plot of Multivariate analysis show low level of variability in all the characters of population of each species. The pattern of variability in all the characters divides four channid species into two groups on the basis of similarities. One group consists of *C. punctatus*and *C. gachua*while the other one consists of *C. striatus, and C. marulius.* Maximum head-width is the most prominent feature in species of former group and dorsal fin base length is the most prominent feature in species of later group. Multivariate analysis of variance shows that the maximum head-width is the most significant character to assess variability in the channid species. Univariate analysis of variance shows that all the four species are different from each other in the character of dorsal-fin base length, pectoral-fin length and maximum head-width. However, in other characters they show various degrees of interspecific relationship. The results of Principal Component Analysis of pooled data of these four species after cluster analysis show that although, all four species are not closely related but can be grouped into two groups.

Key words: *Channa*, multivariate analysis, principal component analysis, Standard length, Unscrambler

INTRODUCTION

Snakeheads, are primary freshwater edible fishes, belong to the family *channidae*. They are also known as murrels. They are distributed in African and Asian continents with natural habitat in slow rivers, canals, reservoirs, swamps, marshes, ditches and rice fields. In India, the genus *Channa* (Gronovius) is represented by nine valid species after the discovery of *Channaaurantimaculata* in Dibrugarh, Assam by Musikasinthorn (2000). Most of them are locally distributed in northeastern and southern region of India (Day, 1876). Four species namely *Channapunctatus, C. gachua, C. striatus and C. marulius* are commonly found throughout the India and commonly known as Sowl or Sowly. They are sold in the market as live fish and are highly priced for their quality, taste, flavor and nutritive, recuperative and medicinal properties all over India (Haniffa*et al.*, 2004).

Snakehead fishes present a good example of phenotypic homoplasticity and form a morphologically unique group of primarily freshwater fishes. They are characterized by an elongated cylindrical body, long and entirely soft rayed dorsal and anal fins, rounded caudal fin, a large mouth with well-developed teeth, cycloid and ctenoid body scales, shield like scales on the head that superficially resembles with a snake and a suprabranchial organ in the head region to breathe atmospheric air (Musikasinthorn, 1998 and Musikasinthorn, 2003).

Recently several studies have been attempted on the taxonomy and phylogeny of snakehead fishes.

Molecular phylogenetic studies based on different mitochondrial DNA sequences such as ND2, (Li, Musikasinthorn and Kumazava 2006), cytochrome *b* (Abol-Munafi*et al*. 2007) and RAPD analysis (Ambak*et al*. 2006) have been carried out on various species of *Channa*. However, the systematics of the *Channidea* is a matter of continuous debate because of phenotypic homoplsticity. Vishwanath and Geetakumari (2009) described two phylecticgroup in nine species of genus *Channa*found in India on the basis of descriptive morphological and osteological characters. However, to the best of my knowledge, phylogenetic relationship among the channid species has been rarely studied by using morphometric analysis. Although studies on morphometric analysis are very important for being complementary to molecular studies, less expensive and highly informative on taxonomy and phylogeny of species.

In the present study we have attempted multivariate analysis of 11 morphological characters of four-channid species *viz*., *C. punctatus*, *C.gachua*, *C.striatus*, and *C. marulius*. The variability level and pattern within each species and the relationship between the species are presented here.

Material and method

Sample collection

Fresh specimens were collected from fishing sites of Meerut, Uttar Pradesh, India during the period from July to November 2009. After morphometrics all specimens were preserved in 10 % formalin and then submitted to Museum of Department of Zoology, R.G College, Meerut. Identification of different species that dealt in the study was easily 1.done on the basis of key (Srivastav 2004).

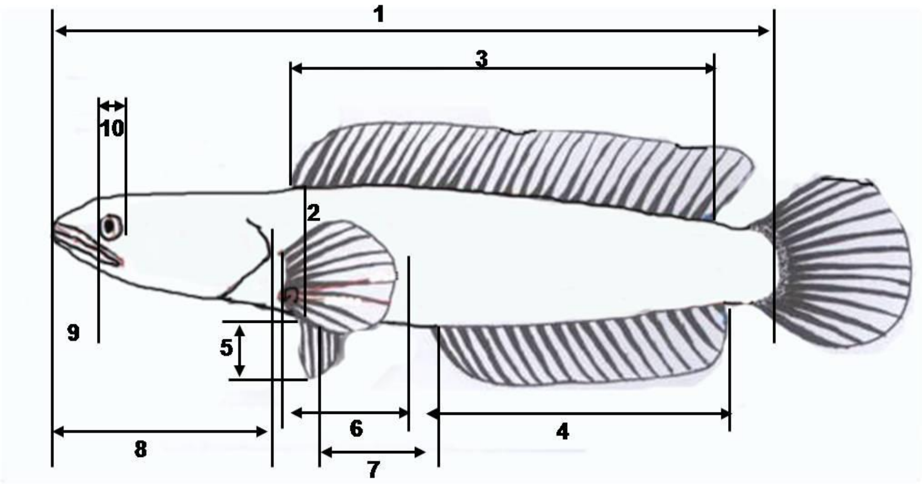

Fig. 1:

DATA COLLECTION

11-morphometric characters (fig.1)were measured according to the method of Hubb and Lagler (1958) with some modifications by using dial calipers with least account of 0.1 mm. Ocular diameter is the distance between anterior and posterior eye through pupil. Inter orbital distance is the distance between the bony margins of eye in the dorsal position. Standard length was measured from snout tip to the base of caudal fin. Head length was measured from the tip of snout to the post opercular margin. Pelvic to anal-fin distance was measured between the middle of the base of pelvic fin and the origin of the anal fin. The measurements of head and body region were then size adjusted with the Head length and Standard length respectively and then the data were used for further analysis. (Tab.1 to Tab.5)

Table 1. Variable statistics of morohometric characters in *Channapunctatus*

	Characters	Range	Mean	SDev.	Skewness
1	BD max.	0.210 - 0.245	0.228	0.0092	-0.0771
2	DFBL	0.539 - 0.576	0.561	0.0096	-0.7820
3	AFBL	0.372 - 0.395	0.383	0.0068	0.1114
4	VFL	0.112 - 0.150	0.130	0.0124	-0.1574
5	PFL	0.186 - 0.210	0.198	0.009	0.0246
6	P-AFD	0.149 - 0.185	0.164	0.0098	0.1613
7	HL	0.337 - 0.387	0.362	0.0149	-0.1658
8	HWmax.	0.537 - 0.718	0.631	0.0542	-0.1600
9	SNL	0.119 - 0.184	0.153	0.0199	-0.1881
10	Oc.D	0.114 - 0.157	0.140	0.0131	-0.5066
11	IOD	0.210 - 0.268	0.244	0.0167	-0.3633

BDmax: Maximum Body-Depth, DFBL: Dorsal-Fin Base Length, AFBL: Anal-Fin Base Length, VFL: Ventral-Fin Length, PFL: Pectoral-Fin Length, P-AFD: Pelvic to Anal Fin Distance, HL: Head Length, HWmax.: Maximum Head-Width, SNL: Snout Length, Oc.D: Ocular Diameter, IOD: Inter Orbital Distance.

Table 2. Variable statistics of morohometric characters in *Channa.gachua*

	Characters	Range	Mean	SDev.	Skewness
1	BD max.	0.182 - 0.216	0.201	0.010	-0.351
2	DFBL	0.567 – 0.642	0.605	0.021	0.036
3	AFBL	0.245 – 0.375	0.351	0.036	-2.194
4	VFL	0.072 – 0.092	0.081	0.007	0.114
5	PFL	0.162 – 0.196	0.184	0.010	-0.698
6	P-AFD	0.138 – 0.214	0.165	0.022	0.485
7	HL	0.288 – 0.340	0.317	0.015	-0.438
8	HWmax.	0.625 - 0.789	0.696	0.050	0.279
9	SNL	0.122 – 0.218	0.164	0.030	0.432
10	Oc.D	0.125 – 0.161	0.144	0.011	-0.202
11	IOD	0.300 – 0.350	0.320	0.016	0.414

BDmax: Maximum Body-Depth, DFBL: Dorsal-Fin Base Length, AFBL: Anal-Fin Base Length, VFL: Ventral-Fin Length, PFL: Pectoral-Fin Length, P-AFD: Pelvic to Anal Fin Distance, HL: Head Length, HWmax.: Maximum Head-Width, SNL: Snout Length, Oc.D: Ocular Diameter, IOD: Inter Orbital Distance.

Table 3. Variable statistics of morohometric characters in *Channamraulius*

	Characters	Range	Mean	SDev.	Skewness
1	BD max.	0.135 - 0.185	0.159	0.015	0.337
2	DFBL	0.609 – 0.684	0.643	0.022	0.264
3	AFBL	0.365 – 0.442	0.401	0.024	0.214
4	VFL	0.085 – 0.107	0.101	0.006	-1.437
5	PFL	0.140 – 0.163	0.152	0.008	-0.174
6	P-AFD	0.166 – 0.229	0.200	0.024	-0.195
7	HL	0.272 – 0.315	0.297	0.015	-0.719

8	HWmax.	0.555 - 0.625	0.589	0.028	0.116
9	SNL	0.140 – 0.180	0.164	0.013	-0.377
10	Oc.D	0.104 – 0.155	0.123	0.015	0.753
11	IOD	0.231 – 0.266	0.255	0.011	0.999

BDmax: Maximum Body Depth, DFBL: Dorsal-Fin Base Length, AFBL: Anal-Fin Base Length, VFL: Ventral-Fin Length, PFL: Pectoral-Fin Length, P-AFD: Pelvic to Anal-Fin Distance, HL: Head Length, HWmax.: Maximum Head-Width, SNL: Snout Length, Oc.D: Ocular Diameter, IOD: Inter Orbital Distance.

Table 4. Variable statistics of morohometric characters in *Channastriatuss*

	Characters	Range	Mean	SDev.	Skewness
1	BD max.	0.160 - 0.181	0.171	0.008	-0.153
2	DFBL	0.554 – 0.628	0.589	0.022	0.041
3	AFBL	0.307 – 0.367	0.337	0.018	0.306
4	VFL	0.074 – 0.136	0.119	0.016	-1.885
5	PFL	0.158 – 0.183	0.169	0.006	0.034
6	P-AFD	0.170 – 0.234	0.188	0.018	1.187
7	HL	0.325 – 0.382	0.358	0.016	-0.374
8	HWmax.	0.500 - 0.559	0.534	0.021	-0.384
9	SNL	0.163 – 0.214	0.180	0.013	1.352
10	Oc.D	0.119 – 0.176	0.140	0.017	0.630
11	IOD	0.222 – 0.257	0.238	0.010	0.432

BDmax: Maximum Body-Depth, DFBL: Dorsal-Fin Base Length, AFBL: Anal-Fin Base Length, VFL: Ventral-Fin Length, PFL: Pectoral-Fin Length, P-AFD: Pelvic to Anal-Fin Distance, HL: Head Length, HWmax.: Maximum Head-Width, SNL: Snout Length, Oc.D: Ocular Diameter, IOD: Inter Orbital Distance.

DATA ANALYSIS

Data analysis was done with the help of software Unscrambler® 9.8 version. First of all, Data of each species was subjected to descriptive variable statistics to calculate Range, Mean, SDev. And Skew ness of the data. Line plot of Multivariate analysis (MVA) were obtained for each species. Pooled data of four species were subjected to univariate analysis for each morphological character. Cluster analysis based on K-Mean methodology has been done. We grouped four channid species into two clusters with Absolute Pearson Distance value 0.02. We repeated the analysis with different number of iterations to get smallest value of sum of distance. Principal Component Analysis (PCA) after cluster analysis has been done for the pooled data of these four species.

Table 5. Variable statistics of morohometric characters of pooled data of*C.gachua*, *C.punctatus*, *C.marulius* and *C.striatus*

	Characters	Range	Mean	SDev.	Skewness
1	BD max.	0.159 - 0.228	0.190	0.031	0.192
2	DFBL	0.561 – 0.643	0.599	0.034	0.146
3	AFBL	0.337 – 0.401	0.368	0.029	0.037
4	VFL	0.081 – 0.130	0.108	0.021	-0.168
5	PFL	0.152 – 0.198	0.176	0.019	-0.086
6	P-AFD	0.164 – 0.200	0.179	0.017	0.145

7	HL	0.297 – 0.362	0.334	0.031	-0.121
8	HWmax.	0.534 - 0.695	0.612	0.067	0.066
9	SNL	0.153 – 0.180	0.165	0.011	0.246
10	Oc.D	0.123 – 0.144	0.136	0.009	-0.667
11	IOD	0.238 – 0.320	0.264	0.037	0.671

BDmax: Maximum Body-Depth, DFBL: Dorsal-Fin Base Length, AFBL: Anal-Fin Base Length, VFL: Ventral-Fin Length, PFL: Pectoral-Fin Length, P-AFD: Pelvic to Anal-Fin Distance, HL: Head Length, HWmax.: Maximum Head-Width, SNL: Snout Length, Oc.D: Ocular Diameter, IOD: Inter Orbital Distance.

RESULTS

Line plot of MVA of raw data for all characters of each species clearly shows the level and pattern of variability. *C. punctatus* and *C. gachua*show similar pattern of variability (Fig.2 and Fig.3) while *C. striatus* shows similarity with *C. marulius* (Fig.4 and Fig.5). Overall variability in almost all the characters in each species is of low level. Very low level of variability has been observed in maximum body depth, anal fin base length, and head length characters of *C. punctatus* and *C. gachua*while they show maximum variations in the

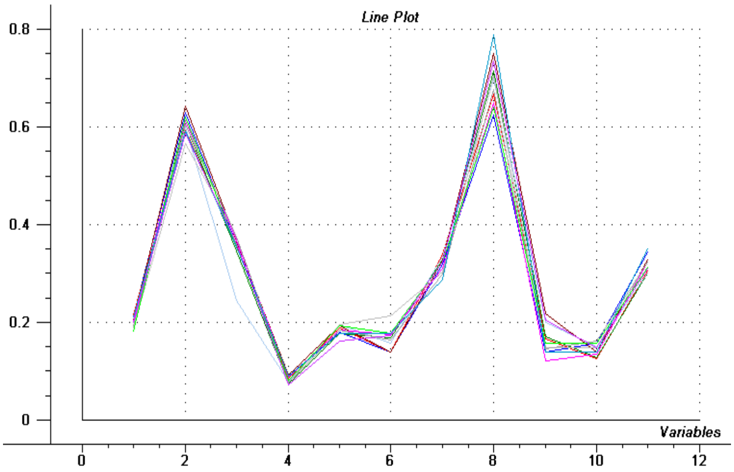

Fig. 2

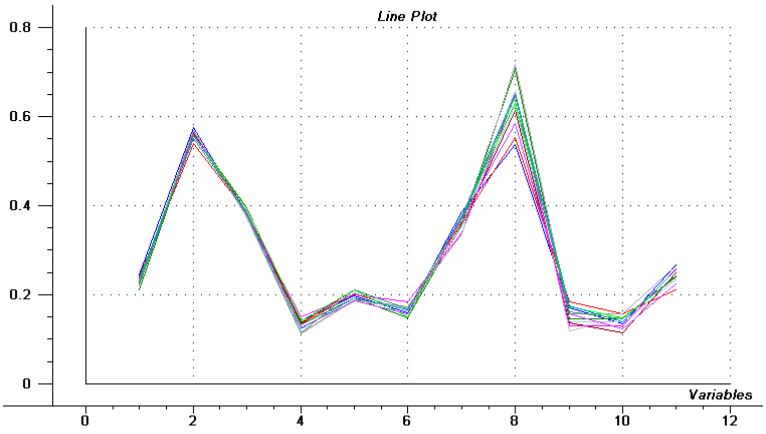

Fig. 3

length characters of *C. punctatus* and *C. gachua*while they show maximum variations in the character of maximum head length. The population of *C. striatus* and C. *marulius* show low level of variability in the characters of maximum body depth, pectoral fin length and snout length. Dorsal fin base length and maximum head width show higher magnitude of variability in comparison of other characters in the populations of *C. striatus* and *C. marulius.*Univariate analysis of variance of pooled data of the four species in each character provides information about interspecific variations. Results show that these species are different from each other in dorsal-fin base length, pectoral-fin length, and head-width maximum. In other characters they show various degrees of interrelationship. Ocular diameter appears to be a characteristic feature in C. *marulius* while inter orbital distance is characteristic in *C. gachua.*

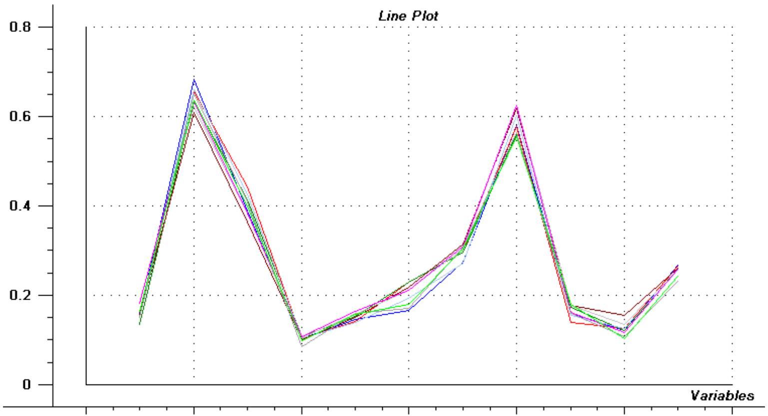

Fig. 4

Principal component analysis (PCA) of the pooled data before cluster analysis doesn't show that it fits into the data. Because the percentage of explained and residual variance was high viz., 58% and 31% in the score and loading plots of the projection results of PCA. The numerical value of Explained X Calibration and Explained X Validation show much difference for both PC1 and PC2. It shows that this model couldn't explain the data well.

The best-fitted model of PCA has been obtained after cluster analysis with Absolute Pearson correlation distance. PC Analysis has been done with cross validation test and Jack –

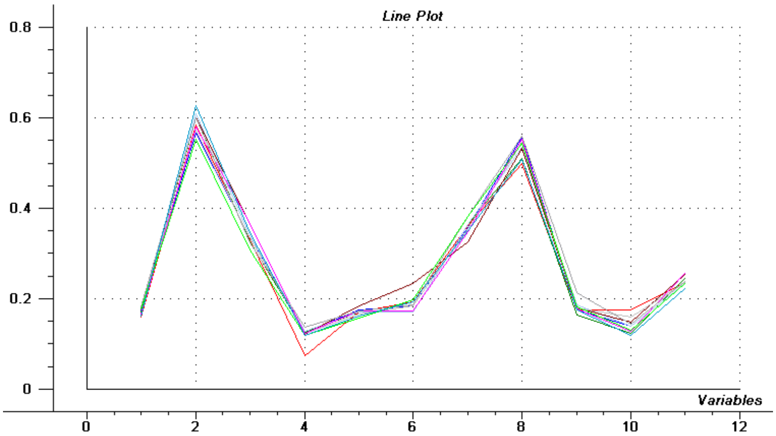

Fig. 5

-Knifing Uncertainty test. The number of PCs were two with full cross validation setup of four segments, each includes one species. The component score values for *C. gachua* and *C. punctatus* are -0.507 and -0.502, respectively. While the score values for *C.striatus* and *C. marulius* are 0.505 and 0.503 respectively (Fig. 6).

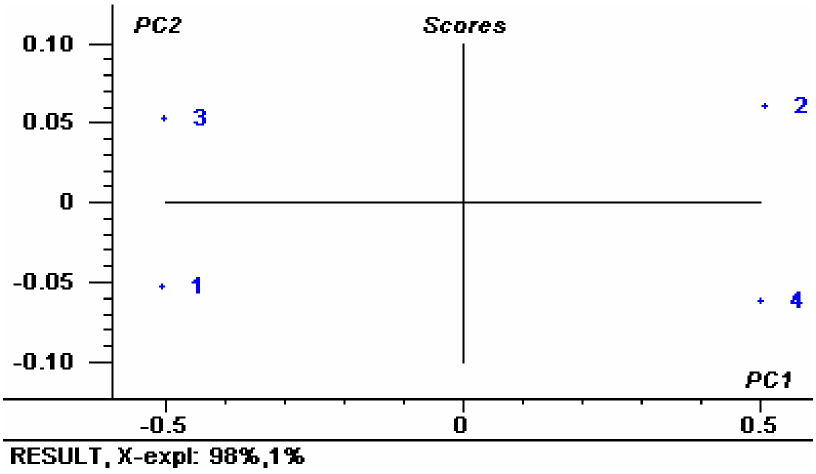

Fig. 6

The large numerical loading value of variables (characters) viz., dorsal fin base length (0.422), ventral fin length (-0.300), head length (-0.457) maximum head-width (0.522) and inter-orbital distance (0.425) shows them to be significant characters and theirlarge contribution in the variability within and among the species (Fig. 7). The negative and positive sign of the values show their corresponding relationship. The numerical values of total Calibration Explained Variance (Exp. X Cal.) and total Validation Explained Variance (Exp. X Val) for PC1 are 98.367% and 95.998%, and for PC2 s the values are 99.625% and 96.871% respectively (Fig.8). These values are very high and close to each other, which show high calibration and validation of the data.

DISCUSSION

The family *Channidae* is a specialized group of primary freshwater fishes.

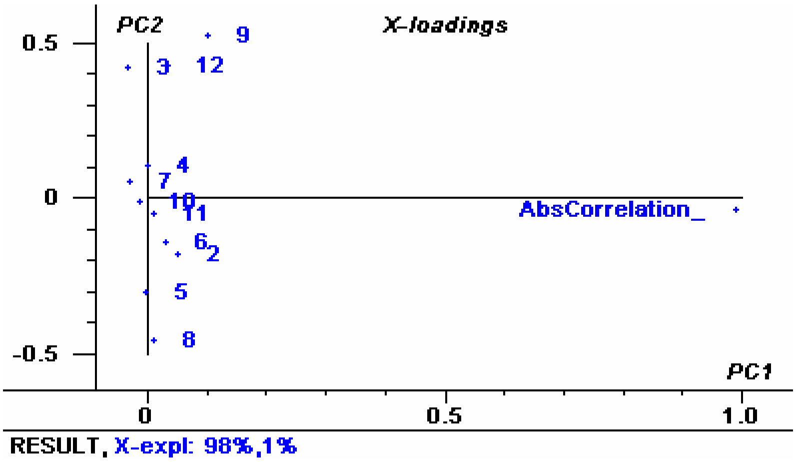

Fig. 7

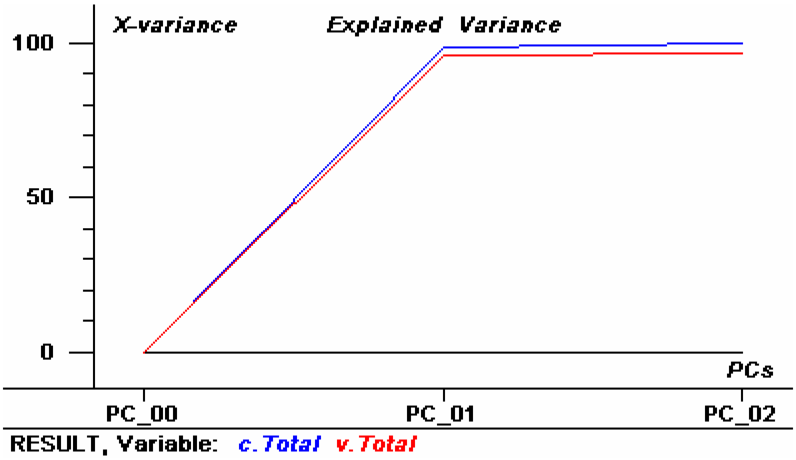

Fig. 8.

Morphologically Musikasinthorn and Taki (2001) divided the family *Channidae* into two major groups by presence or absence of a patch of scales at the chin (gular) region, which they called gular scales. All nine species of *Channa* found in peninsular India belong to the group in which gular scales are absent. They are monophyletic in origin and follow sympatric pattern of speciation because all channidspecies share several distinct morphological features shown in the introduction. Further Vishwanath and Geetakumari (2009) divided nine Indian channid species into two phylectic groups, Gachua and Marulius on the basis of morphological characterization. The marulius group comprises of *C. striatus*and *C .marulius* and gachua group comprises of *C. punctatus, C. gachua C. berca, C. amphibeus, C. aurentimaculata, C. bleheri, C. stewarti.* Our results of multivariate analysis (MVA) of morphometric data show notable consistency to this kind of classification of channid species. The present study strengthens the hypothesis that the member species of each group are descendents of a common direct ancestor. The level and pattern of variability in all eleven characters is almost similar in *C. punctatus,* and *C.gachua* and in *C. striatus*and *C .marulius.* This similarity clearly suggests that *C. punctatus* is close to *C. gachua* but distant to *C. striatus*and *C .marulius,* while *C. striatus*and *C .marulius*are close to each other.

Results of univariate analysis of variance of pooled data of the four species in each character show that these species are different from each other in dorsal-fin base length, pectoral-fin length, and head-width maximum. However, they have various degrees of relationship with each other in other characters. In principal component analysis of the data, grouped into two clusters we found that PC 1 includes C. *punctatus*, and *C. gachua* and PC 2 includes *C. striatus*and *C .marulius.* It described the interrelationship between the species of each component as we have observed in MVA. Maximum head- width, dorsal fin base length, ventral fin length, head length and inter-orbital distance are the significant characters to assess interrelationship among these four species.

Although there is a scope of further studies on morphometrics of more channid species by taking more characters of both shape and size and by using other more efficient methods, the present study establishes that phylogenetically they are close to each other enough to grouped into two phylectic groups. Morphologically, maximum head-width, dorsal-fin base length, ventral-fin length and the head length are the significant characters to confer interrelationship among these four species.

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