Biological Forum – An International Journal 12(1): 51-57(2020)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Phenotypic Characterisation and Multivariate Analysis of Biometric Traits of Diara Buffalo of Bihar, India

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(Received 10 April 2020, Accepted 18 June, 2020)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT : For Phenotypic characterization and multivariate analysis, measurements on 20 biometric traits in 400 Diara buffalo were recorded and incorporated into PCA analysis with varimax rotations. The phenotypic correlations were mostly positive and significant correlations. This suggest high predictability among the different traits and also making suitable for PCA analysis. After Varimax Rotation of the matrix of the components, three PCs with (eigenvalues greater than 1) with variance ratio of 90% were extracted for biometric traits of Diara buffalo. First component accounted for 48% of the variation. It was represented by significant positive high loading of PG, FW, NC, BLO, CG, BL, DBH, HBL, HBH, BH and HL. First component seemed to be explaining the maximum of general body conformation in Diara Buffaloes. The second component explained 14% of total variance with high loading of FL, EL and HC. The third component explained 28% variation of biometric traits with high loading of LG, NL and EL. The communality ranged from 0.68 (LG) to 0.99 (BLO) for all these 20 different biometric traits of Diara buffalo. The principal PC_1, PC_2 and PC_3 components together explain highest variation 90% in BLO trait and lowest 68% in LG trait. These components could be exploited in the evaluation and comparison of animals and provide criteria to select animals on the basis of small group of characters rather than individual characters. These differences indicate that each population has its own characteristics. The selection criteria should be determined taking into account the specificity of population or breed.

Keywords: Varimax, Morphometric Traits, Principal Component Analysis, Buffalo, Bihar.

INTRODUCTION

The mixed farming system is followed by the farmers in Bihar with cropping of cereal and livestock rearing. The livestock farming ensures round the year income in rain fed and semi-arid regions of Bihar and used them as an alternative source of income with production of milk and milk products. The buffalo among different livestock is found more in number because of more sustainable in production in rural masses in all harsh condition and low input management systems. India harbours all the recognized and high milk producing breeds of buffalo of the world. India has been the centre of dispersion of good germplasm of buffaloes for improvement of the species. Genetic resources of buffalo in India are represented by superior well-defined breeds namely, Murrah, Nili Ravi, Jaffarabadi, Bhadawari, Mehsana, Banni, Surti, Marathwadi, Pandharpuri, Nagpuri etc. The defined breeds of buffalo in India which constitutes about 30% of the total buffalo population in the country. However, 70% of the total buffalo population in the country is classified as non-descript type because efforts have not been made to characterize them phenotypically and genetically. The average productivity of indigenous is lower than that of national average (5.47 Kg/day). The lesser known group of buffalo population reared under area of South and North Gangetic plains of Bihar. They are phenotypically homogenous in certain characteristics, popularly known as Diara buffalo. They are well adapted to submerged condition of land in rainy season with water of the river Ganga. These buffalo are fully adapted to the agro-climatic and socio-economic conditions of the state under low-input management system in the Taal and Diara area of the river Ganges, Sone and Gandak. Diara buffalo serve the dual purposes of farmer milk and draught power having well adaptation to wide environmental conditions without affecting their production, reproduction and growth performance. The phenotypic characterization ofDiara buffalo is the first towards its improvements and documentations. The improvements in productivity required to ensure livelihood security of rural people. The phenotypic characterization of domestic animals consists of describing the biometric traits of buffalo population which differs from other groups (Canelón, 2005). This characterization included the biometric measurements of each animal's body structure related to Body size and conformation. The measurement of biometric traitshelps to study the individual conformation, allowing the racial characterization and classification of the population. In addition, this characterization explore variation, comparison between and inside genetic groups and establishes the association between the animal's conformation and function. These traits also contribute to the selection process in identifying the superior animals (Carvalho *et al.*, 2010). The body measurements of adult buffaloes and their correlations can aid in predicting the potential and aptitudes of these animals (Agudelo-Gómez *et al.*, 2015).

Analysis of variance and product moment correlations were widely used to characterize phenotypic and genetic relationships among traits in a breeding program (Dietl *et al.*, 2005). However, principal component analysis is a more refined technique for analyzing data on measurements of biometric traits. Principal components are linear combinations of the original traits and are estimated in such away that the first principal component can explain the largest percentage of the total phenotypic variance. It is multivariate analytical tool that transforms a number of possibly correlated variables into as maller number of uncorrelated variables known as Principal Components(PC). It is arranged in such away that the first few retain most of the variation present in the original variables (Jolliffe, 2002). The factor extracted from PCA analysis can be used in breeding programs with sufficient reduction in number of first redundant traits to be recorded for explanation of maximum variability for prediction of performance traits (Ratwan *et al*. 2017). The phenotypic characterization of buffalo using Biometric traits and its multivariate analysis was reported by various workers in literature (Espinosa-Núnês *et al.*, 2011; Johari *et al.*, 2009; Vohra *et al.*, 2015; Mirza *et al.*, 2015; Dhillod *et al.*, 2017; Divier-Gomez *et al.*, 2015) in buffalo. There is some association between the body measurements, the productive and reproductive traits in buffaloes (Thomas and Chak-ravarty 2000; Espinosa-Núnês *et al.*, 2011; Kern *et al.*, 2014) and in cattle (Lagrotta *et al.*, 2010; Silva *et al.*, 2011; Pundir *et al.*, 2011; Verma *et al.*, 2015; Pares-Casanova *et al.*, 2012; Tolenkhoma *et al.*, 2012). The present investigation explores variations and the relationships among body dimensions in Diara buffalo using Principal Component Analysis(PCA) with varimax rotations aiming to eliminate redundant biometric traits.

MATERIAL AND METHODS

Place of research. The Diara buffaloes belonging to the breeding tract lies between 25°N and 26°N latitude and between 84°E and 90°E longitude in the middle Gangetic plains of India were taken into present study. Different body measurements for 20 biometric traits from 2017 to 2019 were recorded on 400 adult animals of different sex. All measurements were recorded using measuring tape twice by the same recorder to minimize the error and to avoid between recorder effects. The Biometric traits of Diara buffalo Height at wither (HW) - Distance from the highest point of wither to the ground; Body length (BL) - Distance from the point of the shoulder joint to the point of the pin bone; Oblique Body length (BLO) - Distance from the point of the Neck to the point of the pin bone; Heart girth (HG) - Circumference of the heart circumference around the chest; Paunch girth (PG) - Circumference around the chest; Leg length (LG) - Distance from the point of the shoulder joint to ground; Neck length (NL) - Distance from neck attachment to breast; Neck diameter (ND) - Girth of the neck from mid neck; Face length (FL) - Distance from between the horn site to the lower lip; Face width (FW) - Distance between front of both the eyes; Ear length (EL) - Distance from the point of attachment of ear to the tip of the ear; Horn Length (HL) - Distance between base to tip of horn; Horn Circumstance (HC) – Circumference at base of horn; Distance between horns (DBH) – Distance between two horns; Hip Bone Length (HBL) – Distance between hip point to ischia point; Hip Height (HBH) - Distance between hip point to ground; Pin Bone Length (PBL) - Distance between left and right pin bone point; Distance between Hip and Pin Bone (DHP) - Distance between Hip point to Pin point; Tail length (TL) - Distance between base of tail to tip of tail excluding Swiss hair length; Tail length (TLS) - Distance between base of tail to tip of tail including Swiss hair length were recorded and taken into study. The data were standardized for outliers. No specimens had missing measurements. Ethical approval was not necessary as animals were minimally manipulated. Appropriate precautions were taken to avoid measuring unhealthy animals and pregnant females. While recording special care was taken to measure the animals in a vertical position on the flat surfaces.

Statistical analysis. The data collected were analysed using fixed effect model, by considering district effect as fixed so as to adjust the data for significant effect of district if any as per following statistical model (Harvey, W. R. 1987).

$$Y_{ij} = \mu + D_i + e_{ij}$$

where, Y_{ij} is the phenotypic observation for one of the 16 Biometric traits, μ is the overall mean; D_i is fixed effect of District, while e_{ij} is the random error associated with each record which is NID $(0, \sigma_e^2)$. The main statistical values (Mean, standard deviation and coefficient of variation) of Biometric traits were calculated using the Pastec package of r-software. Pearson correlation coefficients and variance and covariance among the body measurements of Biometric traits were estimated. From variance and covariance matrix, the data required for Principal Component Analysis (PCA) was generated. The correlation matrix obtained was subjected to Bartlett's sphericity test whether it was an identity matrix.

Principle Component Analysis (PCA). The KMO test on the adequacy of sampling and the Bartlett's test of Sphericity were computed to establish the validity of data set. The KMO value should be greater than 0.5 for statistical factor analysis to proceed; Bartlett's test if it is significant it means that the correlation matrix is not an identity matrix. The goal of PCA is to replace a large number of correlated variables with a smaller number of uncorrelated variables while capturing as much information in the original variables as possible.

These derived variables called principal components are linear combinations of the observed variables. Specifically, the first principal component

$PC_1 = a_1X_1 + a_2X_2 + \ldots + a_kX_k$

is the weighted combination of the k observed variables that accounts for the most variance in the original set of variables Where, X was observed variables; a is a matrix of eigenvectors (weights). The second principal component is the linear combination that accounts for the most variance in the original variables under the constraint that it's orthogonal (uncorrelated) to the first principal component. Each subsequent component maximizes the variance accounted for while at the same time remaining uncorrelated with all previous components. Theoretically, you can extract as many principal components as there are variables. Rotations of principal components was through the transformation of the components to approximate a simple structure. The raw varimax criterion of the orthogonal rotation method was employed for the rotation of the factor matrix (the aim of varimax rotation is to maximize the sum of variances of a quadratic weight). Scree test was used to retain number of principal components which lies above the bended elbow of scree plot. Further, principal components to be retained based on its obtained Eigenvalue > 1 criterion (Kaiser, 1958). Each observed variable contributes one unit of variance to the total variance. All analyses were performed using standard statistical and PCA procedure with different required packages available from R software.

RESULTS AND DISCUSSION

The effect of non-genetic factor District was investigated in the study and presented non-significant effect on all traits. It indicates that different morphometric traits across districts of Diara buffalo are similar and not significantly different between each other. The descriptive statistics for all the biometric traits of Diaraalong with standard deviation (SD), coefficient of variation (CV) has been shown in Table 1. Mean of biometric traits (cm) studied in Diara buffaloes were 121.75 ± 4.35 for BH, 113.16 ± 6.34 for BL, 123.66 ± 6.56 for BLO, 173.83 ± 10.03 for CG, 196.33 ± 11.72 for PG, 72.41 ± 2.31 for LG, 41.33 ± 2.23 for NL, 80.5 ± 4.97 for ND, 41.08 ± 1.84 for FL, 17.25 ± 0.69 for FW, 24.91 ± 1.25 for EL, 27.41 ± 3.33 for HL, 15.5 ± 1.60 for HC, 27.41 ± 1.49 for DBH, 41.58 ± 3.59 for HBL, 120.08 ± 4.01 for HBH,23.75 ± 2.08 for PBL, 36.08 ± 1.83 for DHP, 82.08 ± 4.14 for TL and 92.5 ± 4.4 for TLS. Diara buffalo for morphometric traits. The obtained results are in agreement with Chandran *et al.* (2015). The means of biometric traits that Diara buffaloes were medium to larger in body size. Based on comparison of biometric traits, Diara buffalo are slightly smaller in height and length of Gojri buffaloes and Nilli Ravi buffaloes (Nivsarkar *et al.* 2000; Ahmad *et al.* 2013; Vohra *et al.*, 2015). This may due to poor management condition given to Diara Buffalo and harsh climatic condition of the region. Results show that the higher value of CV% (>0.20%) in the biometric traits were found in CG, PG, HL, HC and HBL and the other traits had moderate values (0.10<CV<0.20) as presented.

Table 1: Descriptive statistics for all thebiometric traits along with standard deviation.

Sr. No.	Parameters	Code	Mean (cm)± SE	SD	CV (%)
1.	Height at wither (cm)	BH	121.75 ± 4.35	15.09	12.39
2.	Body length Horizontal (cm)	BL	113.16 ± 6.34	21.99	19.43
3.	Body length Oblique (cm)	BLO	123.66 ± 6.56	22.73	18.38
4.	Heart girth	CG	173.83 ± 10.03	34.76	20.01
5.	Paunch Girth	PG	196.33 ± 11.72	40.63	20.69
6.	Leg Length	LG	72.41 ± 2.31	8.02	11.08
7.	Neck Length	NL	41.33 ± 2.23	7.73	18.70
8.	Neck Circumstance (cm)	ND	80.5 ± 4.97	17.22	21.4
9.	Face Length	FL	41.08 ± 1.84	6.38	15.54
10.	Face Width	FW	17.25 ± 0.69	2.41	14.01
11.	Ear Length	EL	24.91 ± 1.25	4.33	17.4
12.	Horn Length	HL	27.41 ± 3.33	11.54	42.12
13.	Horn Circumstance (cm)	HC	15.5 ± 1.60	5.56	35.92
14.	Distance between horns	DBH	27.41 ± 1.49	5.19	18.92
15.	Hip Bone Length (cm)	HBL	41.58 ± 3.59	12.44	29.92
16.	Hip Height	HBH	120.08 ± 4.01	13.88	11.56
17.	Distance between Pin bones	PBL	23.75 ± 2.08	7.21	30.36
18..	Distance between Hip and Pin Bone (cm)	DHP	36.08 ± 1.83	6.35	17.6
19.	Tail length	TL	82.08 ± 4.14	14.35	17.48
20.	Tail Length up switch to Switch (cm)	TLS	92.5 ± 4.4	15.28	16.52

The coefficient of variation (CV) for different morphometric traits ranges between 42.12% (horn length) to 12.39 (Height at wither). Majority of the biometric traits showed higher consistency except for horn length and horn circumference which were comparatively more variable. In gojri buffalo, slightly lower variation ranged between minimum and maximum 3.32% (FL) to 19.41 (HL) CV% was reported by Vohra *et al*. (2015). The higher variability of traits (CG, PG, HL, HC and HBL) may be attributed to the fact that selection was not applied for these traits or that these parts respond more to the environment than others. Face length had little variability which may be due to the fact that it is a cephalic measurement and its close association with cranial bone. Majority of body measurements showed moderate variability, indicating that Diara buffaloes are almost similar in their body size. The standard deviations were well within the normal range in Diara buffaloes. This indicated that body measurements were less affected by environment. All biometric traits presented moderate variability indicating that Diara are almost similar in shape and size in their natural habitat. This might be due to natural selection for better adaptability for particular shape and size. Similar finding was also reported by Vohra *et al.* 2015 in buffalo and Tolenkhomba *et al.* (2013) in cattle of North East region. The variation among breeds can be caused by the difference of genetic, nutrition, management system and climate.

The correlation coefficients between studied biometric traits are given in Table 2 (a) and (b). Correlation coefficient estimated ranged between 0.20 (TL and HC) to 0.98 (TL and TLS) among various biometric traits. A total of 189 correlations (in all combinations) were estimated. Among these 147 correlations were significant and positive (Table 3). These correlations among all 147 correlations were moderate to high in magnitude. All other correlations were low to moderate in magnitude. The result is in agreement with the findings of phenotypic correlations in Gojri buffalo with slight disagreements where few correlations were negative (Vohra *et al.* 2015). The proportions of correlations (more than 75%) between measurements of biometric traits were positive and significant respectively in Kankrej cows (Pundir *et al*., 2011) and local hill cattle. The positive and significant (p<0.05/0.01) correlations among different biometric traits suggest high predictability among the different traits. Further, varying estimates of correlations in biometric traits could be attributed to the fact that postnatal growth does not take place proportionality in all tissue categories or body regions within those tissue categories.

Table 2 (a): Phenotypic Correlations among Biometric Traits.

Trait	BH	LG	NL	NC	BL	BLO	CG	PG	FL
BH	1								
LG	0.75**	1							
NL	0.91**	0.76*	1						
NC	0.9**	0.57**	0.75**	1					
BL	0.93**	0.6*	0.85**	0.94**	1				
BLO	0.93**	0.67*	0.86**	0.96**	0.97**	1			
CG	0.96**	0.66*	0.84**	0.96**	0.93**	0.97**	1		
PG	0.89**	0.52*	0.79**	0.94**	0.93**	0.96**	0.97**	1	
FL	0.88**	0.61*	0.86**	0.81**	0.9**	0.91**	0.89**	0.89**	1
FW	0.78**	0.58*	0.76**	0.72**	0.77**	0.84**	0.82**	0.82**	0.76**
EL	0.52	0.67*	0.66*	0.31	0.39	0.4	0.42	0.31	0.56
HL	0.9**	0.7*	0.9**	0.9**	0.91**	0.95**	0.91**	0.87**	0.9**
HC	0.5	0.45*	0.5^{ns}	0.24	0.48	0.39	0.37	0.33	0.66
DBH	0.64*	0.47*	0.42^{ns}	0.73**	0.63**	0.67**	0.65**	0.55**	0.41
HBL	0.81**	0.61*	0.8**	0.83**	0.85**	0.91**	0.86**	0.89**	0.89**
HBH	0.96**	0.75*	0.9**	0.9**	0.89**	0.92**	0.93**	0.88**	0.78**
PBL	0.84**	0.69*	0.89**	0.83**	0.86**	0.88**	0.83**	0.8**	0.76**
DHP	0.85**	0.65*	0.76**	0.86**	0.82**	0.85**	0.86**	0.79**	0.87**
TL	0.87**	0.7*	0.83**	0.86**	0.84**	0.84**	0.85**	0.77**	0.68**
TLS	0.81**	0.59*	0.73**	0.86**	0.78**	0.78**	0.8**	0.73**	0.57

**<0.01; *<0.05

The PCA was applied on 20biometric traits of Diara Buffaloes. The value of KMO measure of sampling adequacy (MSA) was obtained as 0.907. This value fits with the acceptable threshold criterion of KMO (> 0.5) which permits to proceed with PCA analysis .The estimate of sampling adequacy KMO revealed the proportion of the variance in different biometric traits caused by the underlying components (Kaiser, 1958). The overall significance of the correlation matrix was tested with Bertlett's test of sphericity for the biometric traits (chi-square was 3575.5 p<0.01) was significant, it means correlation matrix is not an identity matrix and provided enough support for the validity of the factor analysis of data. Yakubu *et al*. (2009) reported in close agreement of our estimates of sampling adequacy were 0.90 and 0.92 in age groups of 1.5 to 2.4 years and 2.5 to 3.6 years, respectively in White Fulani cattle. However, Vohra *et al*. (2015); Pundir *et al*. (2011) reported lower estimates of sampling adequacy as 0.74 in Gojri buffalo and 0.891 in Kankrej cows, respectively.

Table 2 (b): Phenotypic Correlations among Biometric Traits.

Trait	FW	EL	HL	HC	DBH	HBL	HBH	PBL	DHP	TL	TLS
FW	1										
EL	0.16	1									
HL	0.73**	0.55	1								
HC	0.31	0.55**	0.4	1							
DBH	0.63*	-0.08**	0.61	0.04	1						
HBL	0.74*	0.38**	0.93	0.39	0.49*	1					
HBH	0.81*	0.45**	0.88	0.29	0.67*	0.78**	1				
PBL	0.64*	0.58**	0.94*	0.24	0.5	0.83**	0.87**	1			
DHP	0.57	0.62**	0.91*	0.49	0.57	0.8**	0.77**	0.77**	1		
TL	0.57	0.56**	0.85	0.2	0.56	0.7*	0.88**	0.93**	0.75**	1	
TLS	0.48	0.44**	0.78	0.06	0.59*	0.61*	0.85**	0.86**	0.71*	0.98**	1

**<0.01; *<0.05

The eigenvalues and percentages of the explained variance and cumulated variance for body morphometric traits are presented in Table 3. The results show that the first three components accounted for 90% of the total variance whose the eigenvalues were greater than 1(>1). The remaining seventeen PCs had lower variance. The first (PC_1), second (PC_2) and third (PC_3) principal components accounted for 75%, 9.00% and 6%, respectively of the total variance while the remaining 17 PCs jointly accounted for 10% of the total variation. Another criterion for determination of number of component is scree plot that could be used to decide the actual number of component to be retained for analysis. Scree plot can depict various components and the component having eigenvalue up to the bent of elbow are usually considered. Three Principal Components above the bend or elbow are indicated in plot (Fig. 1) which suggest its retention for extraction. Based on above criteria, three components are appropriate for summarizing the data of biometric traits of Diara buffalo.

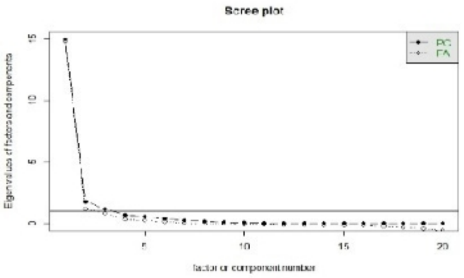

Fig. 1. Scree plot of components and eigenvalues for biometric traits of Diara buffalo.

The identified three components could explain cumulative percentage of variance of 90%. First component accounted for 75% of the variation. It was represented by significant positive high loading of BLO, BH, CG, HL, BL, HBH, NC, PG, NL, PBL, FL, TL, HB and DHP. The high loading of various traits indicates that length, height and diameter of Diara buffalo explain maximum of variation of biometric traits. First component seemed to be explaining the maximum of general body conformation in Diara Buffaloes. The second component explained 9% of total variance with high loading of biometric traits HC and EL. The extracted PCs with explaining 90% in our findings was slightly different than the reports of Vohra *et al*. (2015). They extracted four components in Gojri buffalo for a cumulative variance of 70.09%.

After Varimax Rotation of the matrix of the components, three PCs with (eigenvalues greater than 1) explained 90% variations of 20 biometric traits of Diara buffalo. The identified three components after orthogonal Varimax rotation contribute 90% of total variation of 20 biometric traits of Diara buffalo. The result shows that extracted 3 PCs are sufficient to identify the groups of variables necessary to improve the genetic performance of Diara buffalo. First component (PC1) accounted for 48% of the variation. It was represented by significant positive high loading of PG, FW, NC, BLO, CG, BL, DBH, HBL, HBH, BH and HL. First component seemed to be explaining the maximum of general body conformation in Diara Buffaloes. The second component explained 14% of total variance with high loading of FL, EL and HC. The second PCs explaining head features of Diara buffalo which corroborated with result in Gojri buffalo (Vohra *et al.*, 2015). The third component explained 28% variation of biometric traits with high loading of LG, NL and EL. Vohra *et al.* (2015) used factor analysis with Varimax rotation revealed 4 components in Gojri buffalo which explained about 70.86% which is slightly lower to the findings of present study in Diara Buffaloes. The extracted PCs sufficient to identify the groups of variables necessary to improve the genetic performance of Diara buffalo.

The communality ranged from 0.68 (LG) to 0.99 (BLO) for all these 20 different biometric traits of Diara buffalo. The principal PC_1, PC_2 and PC_3 components together explain highest variation 90% in BLO trait and lowest 68% in LG trait. The extracted PCs sufficiently explained the variability of data. Similar communality ranged from 0.44 to 0.83 for 13 different biometric traits in Gojri buffalo was reported by Vohra *et al.* (2015). In Egyptian buffalo the communalities ranged from 0.96 (height at hips, HT) to 0.78 (rump width) Shahin *et al.* (1993). The lower estimates of communalities of LG and DBH indicated that these have less contribution in the variation of body conformation in Diara Buffaloes. The lower estimates of communalities were reported for HL and PG traits of body conformation in Gojri buffaloes by Vohra *et al.* (2015). The lower estimates of communality indicate that components have lesser contribution in explaining the variation of traits.

Table 3: Component Matrix or Standardized loading of different Varimax Rotated Component for Biometric traits of Diara buffalo.

Traits	RC1	RC3	RC2	Communalities (h_2)
BH	0.74	0.54	0.32	0.95
LG	0.35	0.65	0.36	0.68
NL	0.57	0.62	0.43	0.9
NC	0.86	0.46	0.06	0.95
BL	0.82	0.43	0.29	0.93
BLO	0.86	0.44	0.25	0.99
CG	0.84	0.45	0.24	0.96
PG	0.87	0.34	0.23	0.92
FL	0.7	0.34	0.61	0.97
FW	0.86	0.12	0.24	0.81
EL	-0.11	0.77	0.6	0.97
HL	0.72	0.57	0.31	0.94
HC	0.16	0.07	0.91	0.87
DBH	0.79	0.18	-0.23	0.7
HBL	0.76	0.35	0.36	0.83
HBH	0.76	0.58	0.14	0.93
PBL	0.59	0.73	0.15	0.91
DHP	0.62	0.53	0.38	0.81
TL	0.56	0.81	0.02	0.97
TLS	0.56	0.78	-0.15	0.95

Table 4: Total Variance and Proportions of Variances explained by Varimax Rotated Components for Biometric traits of Diara buffalo.

Variance Name	RC1	RC3	RC2
SS loadings	9.5	5.64	2.78
Proportion Variance	0.48	0.28	0.14
Cumulative Variance	0.48	0.76	0.9
Proportion Explained	0.53	0.31	0.16
Cumulative Proportion	0.53	0.84	1

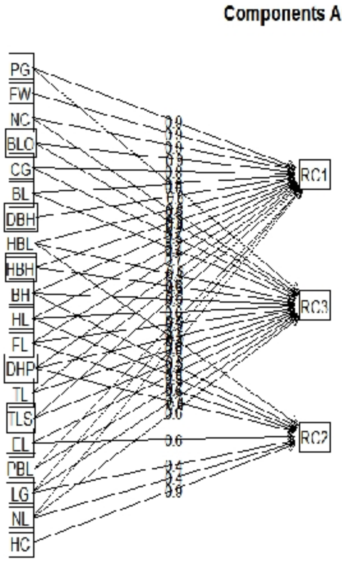

Fig. 2. Diagram of the Two Varimax Rotated Component Loading (Solution) for Biometric traits of Diara Buffalo.

CONCLUSIONS

The application of PCA pave way to explore the interdependence raw variables of biometric traits of Diara buffalo. Results of PCA suggest that the use of orthogonal synthetic variables principal component one (PC1), two (PC2) and three (PC3) provided a means of reduction in the number of biometric traits to be recorded in Diara buffaloes. They may be more reliable in explaining body conformation in adult Diara buffalo instead of individual trait. These components could be exploited in the evaluation and comparison of animals and provide criteria to select animals on the basis of small group of characters rather than individual characters. After varimax rotation, PC1 may be used in phenotypic selection as a means to explain biometric traits. Our results suggest that the present PCA provided a means for reduction in the number of biometric traits to be recorded in Diara buffalo (PG, FW, NC, BLO, CG, BL, DBH, HBL, HBH, BH and HL) which could be used in ranking programs as a mean to explain the body conformation. These differences indicate that each population has its own characteristics. The selection criteria should be determined taking into account the specificity of population or breed.

Acknowledgements. We sincerely extend thanks to Head of Department, Animal Genetics and Breeding, Bihar Veterinary College Patna (Bihar) for supporting and motivating me to carry out this work.We also thankful to the farmers for allowing us to take measurements of animals.

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How to cite this article: Singh, R.K., Kumar, B., Kumar, R., Kumar, S. and Mandal, K.G. (2020). Phenotypic Characterisation and Multivariate Analysis of Biometric Traits of Diara Buffalo of Bihar, India. *Biological Forum – An International Journal*, **12**(1): 51-57.