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Phenotypic differentiation among cattle populations based on biometric traits

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ABSTRACT

An attempt was made to differentiate 3 cattle populations of Rajasthan state i.e. Kankrej (407), Sanchori (152) and Nari (175) by canonical discriminant analysis (CDA), a multivariate technique using 12 different biometric traits. Single trait analysis variance showed that Sanchori cows had largest size, Kankrej was intermediate and Nari was the smallest. The step-wise discriminant analysis showed that distance between hip bones, heart girth, horn length, face width, ear length, face width, horn diameter, height at withers, tail length without switch, tail length and body length were the most discriminating traits between these three cattle populations. The Mahalanobis distances between these cattle populations indicated that they are three distinct populations. The dendrogram based on the average linkage method showed that there are 2 clusters; cluster one includes Nari and Sanchori cows and cluster two Kankrej cows, clearly separated from cluster one. The individual assignment to different cattle populations by the cross-validation classification approach showed that 100% of the Kankrej cows, 98.08% of Sanchori cows and 98.98% of Nari cows were correctly assigned into their source populations. The present study revealed that the free canonical approach is proved useful and informative in differentiating between 3 cattle populations and suggested that Sanchori and Nari may be established/registers as a distinct breed.

Key words: Biometric traits, Canonical discriminant analysis, Indigenous cattle

Kankrej is one of the distinct and registered breed of Indian cattle. Sanchori and Nari cattle populations are not classified as distinct breeds to date and need status of a breed. All the 3 cattle populations represent important genetic resources in their environment and make up an integral part of livestock production system in the Rajasthan state. Univariate statistical analysis analyzes each variable separately and do not explain how the populations under investigation differ when all measured morphological traits are considered simultaneously (Dossa *et al.* 2007). Multifactorial discriminant analyses were more suitable in assessing variation within a population and can discriminate different population types when all measured morphological variables are considered jointly. Canonical discriminate analysis (CDA) is a multivariate statistical technique used to discriminate two or more populations based on a suite of continuous or discriminating variables. The purpose of the present study was to achieve similarity/dissimilarity between Kankrej, Sanchori and Nari cattle populations based on morphological traits, using size free canonical discriminate analysis and if found suitable register them as a distinct breed.

MATERIALS AND METHODS

Collection of data and location of study: Data consisted of 12 different morphometric traits of 735 indigenous cows of Kankrej (407, Palanpur district), Sanchori (153, Jalaur district) and Nari (175, Sirohi district) from Rajasthan state. All the measurements were recorded by the same recorder to avoid between recorder effects. All the traits were recorded from the near side of the cows. The circumference measurements were taken using a tape while the other measures were taken with the help of a measuring stick. The recorded biometric traits were body length (the distance from the point of the shoulder joint to the point of the pin bone), height at withers (the distance from the highest point of withers to the ground), heart girth (the circumference of the chest just behind the elbow joint), paunch girth (the circumference at paunch region just anterior to the hip joint), ear length (distance from the point of attachment of ear to the tip of the ear), face length (distance from the horn site to the lower lip), face width (distance between both the eyes), horn length (distance from part of horn attachment to the tip of the horn), horn diameter (circumference of the horn at base), tail length with switch (measured from the tail droop to the tip of the tail including switch), tail length without switch (measured from the root of tail droop to the tip of the tail excluding switch) and distance between hip bones (distance between both the hip bones).

Statistical analysis: Means, standard errors and coefficients of variation of the different morphometric traits were calculated using MEAN PROC (SAS 2009). The Duncan's multiple range tests were performed for pair-wise

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comparison of means. Variance components (REML) due to populations were estimated by VARCOMP procedure (SAS 2009). Step-wise discriminate procedure (SAS 2009) was applied using PROC STEPDISC to determine, which biometric trait have more discriminant power than others. The relative importance of the biometric variables in discriminating between the cattle populations was assessed using the level of significance, partial R^2 and F-statistic. The CANDISC (SAS 2009) procedure was used to perform univariate and multivariate one-way analysis that calculated the Mahalanobis distances between the three cattle populations. Based on the Mahalanobis distance, matrix dendogram was created using PROC CLUSTER (SAS 2009) in which Average Linkage Method was used. The ability of these canonical functions to assign each individual animal to its respective population was calculated as the percentage of correct assignment to each cattle population using the DISCRIM (SAS 2009) procedure by Nearest Neighbour Discriminant Analysis. The cross-validation approach was used for assignment of individual to their respective population in which one individual is removed from the original matrix and the discriminant analysis is then performed from the remaining observations and used to classify the omitted individual. It also provides an unbiased estimate of error. The proportion of individuals correctly re-allocated is taken as a measure of the morphological distinctness of the population.

RESULTS AND DISCUSSION

Kankrej breed is available in Gujarat and Rajasthan states of India and provide livelihood to many people by providing milk and draft power. Cows of the breed have high genetic potential for milk production. The average lactation milk yield was 2,331 kg in 304 days (Anonymous 2016). The breeding tract of Sanchori cattle lies between the breeding tracts of Tharparkar and Kankrej breeds of cattle i.e. Jalore district. Cows are generally white or grey in coat colour. Nari cattle are distributed in Bali tehsil of Pali district and entire Sirohi district of Rajasthan state.

The descriptive statistics of 3 different cattle populations for all the biometric traits are presented in Table 1. Body length, heart girth, paunch girth, horn length, horn diameter and distance between hip bones differ significantly between cattle populations. The estimates revealed that Sanchori cattle had more values with respect to these traits except horn length which was longer in Kankrej cattle. Height at wither, face length, face width and tail length without switch did not differ significantly in Kankrej and Sanchori, but these traits differ significantly with Nari cattle from both the populations. Tail length with switch did not differ significantly in Kankrej and Nari while it differ significantly with Sanchori cattle. The coefficient of variation of different biometric traits showed that horn length, horn diameter, ear width and distance between hip bones had more variability. The tail length with switch had more variability than the without switch indicating that tail switch had more variability. Face length and height at withers had little variability may be due to fact that it is a cephalic measurement and its close association with cranial bone. Our results revealed that size of Sanchori cows was the largest, Kankrej was intermediate and Nari was the smallest.

In Kankrej cows, estimates for body length, height at withers, heart girth were in close agreement with the reports of Pundir *et al.* (2011). Compared to Sanchori cows, in the present study, higher body length, height at withers and chest girth were reported by Nivsarkar *et al.* (2000) in Tharparkar cattle, the geographical neighbour. The horn length and horn circumference estimated in the present study were higher than Tharparkar cattle (Nivsarkar *et al,* 2000) but lesser than Kankrej cattle (Pundir *et al*. 2011). The face length and tail length of Sanchori cows were comparable to the Kankrej cows. The biometrical parameters of Sanchori cattle found in this study indicated that this population is different from Kankrej and Tharparkar breeds of cattle found in adjoining areas of Gujarat and Rajasthan and hence deserve a status of a separate breed of

Table 1. Descriptive statistics of different cattle breed/populations of Rajasthan

Breed/Trait	No	Overall		Kankrej		Sanchori		Nari	
		Mean±SE	CV	Mean±SE	CV	Mean±SE	CV	Mean±SE	CV
Body length	735	123.68**±0.28	6.33	123.44^{a}±0.37	6.05	129.32^{b}±0.65	6.23	119.28^{c}±0.36	4.08
Height at wither	735	122.20**±0.18	4.20	122.49^{a}±0.28	4.75	122.95^{a}±0.33	3.36	120.86^{b}±0.20	3.20
Heart girth	731	161.25**±0.41	6.96	162.56^{a}±0.56	6.97	167.02^{b}±0.75	5.55	152.97^{c}±0.56	4.82
Paunch girth	730	177.12**±0.52	7.96	178.95^{a}±0.70	7.91	183.54^{b}±0.96	6.52	166.93^{c}±0.72	5.67
Face length	735	44.06±0.08	4.97	44.09±0.10	4.85	44.07±0.19	5.53	44.01±0.15	4.72
Face width	636	15.47**±0.05	8.92	15.91^{a}±0.05	6.72	15.92^{a}±0.11	5.40	14.26^{b}±0.11	10.16
Horn length	731	42.52**±0.43	27.68	42.47^{a}±0.53	25.35	32.01^{b}±0.59	22.86	51.68^{c}±0.70	17.95
Horn diameter	728	23.86**±0.16	18.44	26.07^{a}±0.19	15.30	22.86^{b}±0.27	14.69	19.53^{c}±0.13	9.37
Ear length	732	30.33**±0.10	9.62	31.24^{a}±0.12	8.16	31.66^{a}±0.17	6.72	27.00^{b}±0.11	5.66
Tail length	730	113.12**±0.40	9.55	111.62^{a}±0.53	9.72	117.16^{b}±1.03	10.92	113.07^{a}±0.56	6.43
Tail length without switch	731	89.69**±0.29	8.79	89.34^{a}±0.34	7.80	87.37^{a}±0.80	12.77	92.63^{b}±0.52	7.36
Distance between hip bones	565	22.72**±0.37	39.56	17.28^{a}±0.10	12.32	37.94^{b}±0.23	4.58	36.07^{c}±0.17	4.91

Table 2. Intra-breed and inter-breed variance components

Breed/Trait	Inter-breed	Intra-breed (Residual)
Body length	25.10 (33.32)	50.22 (66.68)
Height at wither	1.02 (3.80)	25.97 (96.20)
Heart girth	50.81 (33.15)	102.47 (66.85)
Paunch girth	72.45 (30.51)	164.89 (69.49)
Face length	0	4.80 (100.00)
Face width	0.90 (39.57)	1.38 (60.43)
Horn length	96.14 (49.97)	96.24 (50.03)
Horn diameter	10.66 (46.94)	12.05 (53.06)
Ear length	6.61 (56.33)	5.12 (43.67)
Tail length	7.67 (6.37)	112.65 (93.63)
Tail length without switch	6.63 (10.06)	59.22 (89.94)
Distance between hip bones	130.62 (96.92)	4.15 (3.08)
Average of percentage	33.91	66.09

cattle of Indian origin.

In Nari cows, all the estimates of different biometric traits were lower than the Kankrej cattle except horn length (Pundir *et al.* 2011). The horn length of Nari cows estimated in this study was 51.68 cm, which was higher than Kankrej cows but the horn circumference obtained in this study was lower than that of Kankrej cows as reported by Pundir *et al.* (2011). This indicated that Nari cows are smaller in body conformation with longer but thinner horns as compared to Kankrej cows. The horn length of southern Indian cattle breeds like Hallikar, Bargur, Khillar and Pulikulam were lower than that of horn length of Nari cattle obtained in the present study, which clearly indicated that the horn of Nari cattle is perhaps longest among Indian cattle breeds. The face length of Nari cows (44.01cm) are comparable with Kankrej cows (44.09 cm) as reported by Pundir *et al.* (2011). The tail length of Nari cows as obtained in the present study was slightly higher than that of Kankrej cows (Pundir *et al*. 2011). The biometrical parameters of Nari cattle revealed that this cattle population is different from Kankrej and Sanchori of Rajasthan and deserve a status of a distinct breed of cattle of Indian origin.

Variance components were estimated using restricted maximum likelihood (REML) method to partition the variability in different biometric traits into inter- and intra-breed (residual) to asses the morphological divergence. Inter and intra-breed variance components for different biometric traits are given in Table 2. The percentage of intra-breed variation (66.09) was larger than the inter-breed (33.91). Similar observations were made by Aziz and Al-Hur (2013) in goats. The inter-breed variation ranged from 0 (face length) to 96.92% (distance between hip bones). The distance between hip bones and ear length had more than 50% inter-breed variation and rest all the traits had larger proportion of intra-breed variations. This showed that most of the variability was due to within breed differences. Klingenberg (1996) observed that discrimination between groups is difficult because of allometric variation within the groups. He further stated that amount of within group variation may exceed between group differences, which is in agreement with the present study.

The canonical discriminant analysis indicated the characters those contribute most to discrimination among the populations (Neft and Marcus 1980). The step-wise discriminate analysis showed that distance between hip bones, heart girth, horn length, face width, ear length, face width, horn diameter, height at withers, tail length without switch, tail length and body length were the most discriminating variables between these three cattle populations (Table 3). Their respective partial R^2 were 0.9475, 0.3036, 0.2596, 0.2095, 0.1374, 0.0761, 0.0449, 0.0378, 0.0377, 0.0444 and 0.0163, with high significant values (P<0.0001). The corresponding F values for these traits were highly significant except body length.

These morphological variables obtained in the present study are more important and informative, and could be used to assign the 3 cattle populations into distinct populations, thereby reducing the errors of selection in future breeding and selection programmes. Similar to the

Table 3. Summary of step wise selection of different traits in different breed/populations of Rajasthan

Variable entered	Partial R-Square	F Value	Pr > F	Wilks' Lambda	Pr < Lambda	Average squared canonical correlation	Pr > ASCC
Distance between hip bones	0.9475	4996.13	<.0001	0.0525	<.0001	0.4737	<.0001
Heart girth	0.3036	120.54	<.0001	0.0365	<.0001	0.5249	<.0001
Horn length	0.2596	96.78	<.0001	0.0270	<.0001	0.6371	<.0001
Face width	0.2095	72.99	<.0001	0.0214	<.0001	0.6856	<.0001
Ear length	0.1374	43.80	<.0001	0.0184	<.0001	0.7096	<.0001
Face length	0.0761	22.63	<.0001	0.0170	<.0001	0.7295	<.0001
Horn diameter	0.0449	12.88	<.0001	0.0162	<.0001	0.7406	<.0001
Height at withers	0.0378	10.75	<.0001	0.0156	<.0001	0.7413	<.0001
Tail length without switch	0.0377	10.70	<.0001	0.0150	<.0001	0.7489	<.0001
Tail length	0.0444	12.66	<.0001	0.0144	<.0001	0.7589	<.0001
Body length	0.0163	4.52	0.0113	0.0141	<.0001	0.7595	<.0001

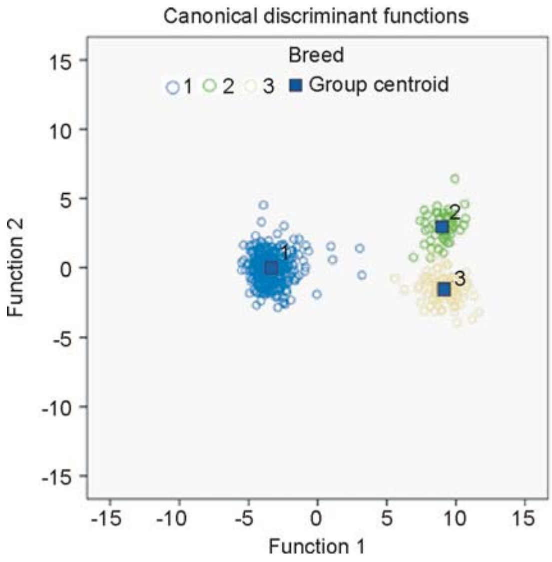

Fig. 1. Canonical discriminiant functions of different cattle populations of Rajasthan (Kankrej 1, Sanchori 2 and Nari 3).

present study, Yakuba *et al.* (2010) also reported height at wither and face length as most discriminating traits in 2 distinct cattle breeds. In an attempt to distinguish between brown and grey Bengal goats, Mukeherjee *et al.*(1979) reported significant differences between both breeds due to body length and chest circumference. The canonical discriminant function representation is shown in Fig. 1, which revealed well defined and non-overlapping 3 phenotypic groupings for 3 cattle populations under study i.e. distinct populations in the present study. This was supported by estimates of Mahalanobis distances presented in Table 4.

The pair-wise distances between Kankrej and Sanchori, Kankrej and Nari and Sanchori and Nari were 161.23, 158.75 and 20.16, respectively. All the estimates of distances were highly significant (P<0.001).

Table 4. Mahalanobis distances between different breed/ populations of Rajasthan

Breed	Kankrej	Sanchori	Nari
Kankrej	0	161.23	158.75
Sanchori	P<.0001	0	20.16
Nari	P<.0001	P<.0001	0

The Mahalanobis distances between these cattle populations indicated 3 distinct populations. The dendrogram (Fig. 2) based on the average linkage method showed that there are 2 clusters; cluster one includes Nari and Sanchori cows and cluster two Kankrej cows clearly separated from cluster one. The distribution of the 3 populations shown in Figs 1 and 2 agrees with the results of Mahalanobis distances.

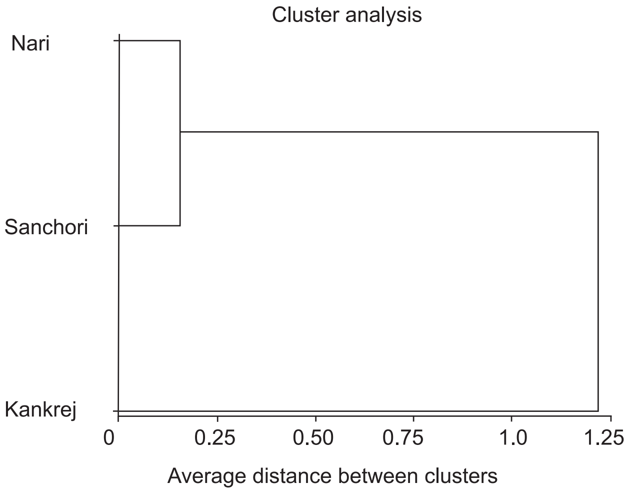

Fig. 2. Dendrogram showing similarity in different cattle populations of Rajasthan.

Yakuba *et al.* (2010) observed Mahalanobis distance between the 2 cattle populations as 7.19 which was high and significant and indicated that that they belong to genetically different groups. Aziz and Al-Haur (2013) observed Mahalanobis distance of 0.55 between 2 lines of goat and those between Ardi and each of Line1 and Line 2 were 25.03 and 21.45, respectively.

The individual assignment to different cattle populations was studied by cross-validation classification (Table 5). The proportion of individuals correctly assigned to their respective population is considered as a measure of the morphological distinctness of the population. In the present study, 100% of the Kankrej cows, 98.08% of Sanchori cows and 98.98% of Nari cows were correctly assigned into their respective source population. Low value of overall error 0.98% was observed indicating that they are distinct populations. The high morphological distances between the cattle populations coupled with correct assignment to source populations is an indication that they belong to different populations. There are few distinct physical traits like horn, body size and face which could differentiate these populations and confirm our findings. Yakuba *et al.* (2010) reported that 85.48% of Bunaji cattle and 96.55% of Sokoto Gudali classified into their source population assigned correctly by the Nearest Neighbour Discriminant Analysis.

Aziz and Al-Hur (2013) observed 100% assignment of Ardi animals into their genetic group and percentages of animals assigned in Line 1 and line 2 were 86.10 and 42.55, respectively. The use of multivariate discriminant analyses therefore could be successfully used in morphometric differentiation. In the present study, correct assignment of individual animals to their respective population ranged from 98.08 to 100% which revealed that they are 3 distinct populations. The observed morphological differences among the studied populations may support the hypothesis that much of this variation is under genetic control.

The results revealed that there was a clear grouping for 3 different cattle populations i.e. Kankrej, Sanchori and Nari by different statistical techniques used in the present study. The results were supported by physical traits of different cattle populations also. Both the cattle populations i.e. Sanchori and Nari can be possible candidate as a registered breed while Kankrej is already registered. Molecular characterisation studies in these breeds will provide further basis for registration of these two breeds. It is also concluded that the technique size free canonical discriminant analysis may be used for differentiation of other populations of cattle to confirm within breed similarity. Confirmation and registration of breed will be useful in genetic improvement programs, as breed is the basic unit for any developmental program.

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