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Genetic divergence among genetic groups of Gir crossbreds

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ABSTRACT

Comparative evaluation of FG (50% HF + 50% Gir), IFG (*Interse* of FG), FJG (50% HF + 25% Jersey + 25% Gir), IFJG (*Interse* of FJG) and R (50% HF + 12.50% Jersey + 37.50% Gir) crosses of Gir was done on the basis of age at first conception (AFCon), lactation length (LL) and 300 days milk yield (300 DMY) of first, second and third lactations using Mahalanobis D^2 statistics. The genetic group differences were significant for each trait separately and simultaneously (V-stat) in all the three lactations. The differences in the D^2 values among genetic groups in all three subsets were significant except IFG with R genetic group in first lactation. The total D^2 values for AFCon, LL and 300 DMY were 18.85, 1.29 and 8.53 in first; 19.65, 1.90 and 6.91 in second and 21.22, 1.32 and 6.83, in third lactation, respectively. The per cent contribution of AFCon to the total D^2 value was maximum followed by 300 DMY and lowest of LL in first, second and third lactation, respectively. Based on D^2 values, in first lactation, the FG and FJG (F_1) genetic groups were placed in cluster 2 and IFG, IFJG and R genetic groups in cluster 1. In second and third lactations, IFG and IFJG genetic groups formed cluster 1, FG and FJG groups grouped in to cluster 2 and R genetic group formed cluster 3. The magnitude of inter-cluster distance was greater than intra-cluster distance.

Key words: AFCon, Canonical analysis, D^2 value, Genetic divergence, Gir, LL, 300 DMY

Diverse roles and diverse conditions gives rise to the need for a range of different species and breeds and a pool of genetic diversity within each breed. Diversity enables livestock populations to adapt to changing environmental conditions and provides the raw material for breeding programmes aimed at improving productivity and meeting the needs of livestock keepers, consumers and society at large (FAO 2015). It is essential to estimate the genetic divergence among various genetic groups for making an appropriate breeding policy. The genetic diversity of these groups calculated from actual performance may give better understanding of grades in comparison to diversity based on expected inheritance. Multivariate analysis has been widely used in studies of breed characterization and genetic diversity as it provides descriptive analysis of the differences between populations, considering all variables together (Arandas *et al.* 2017). It is essential to use some sound multivariate analysis technique which would take into consideration maximum number of economically important traits for comparative evaluation of performance of different crossbreds. Therefore, genetic group differentiation was done by using D^2 statistics by combining information on important characters and the relative contribution of characters in different combinations were estimated.

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MATERIALS AND METHODS

The genetic divergence among 5 genetic groups, viz. FG (50% HF + 50% Gir), IFG (*Interse* of FG), FJG (50% HF + 25% Jersey + 25% Gir), IFJG (*Interse* of FJG) and R (50% HF + 12.50% Jersey + 37.50% Gir) on the basis of reproduction and production traits was studied by the method of multivariate analysis using Mahalanobis D^2 statistics. The traits studied were age at first conception (AFCon), lactation length (LL) and 300 days milk yield (300 DMY) of first, second and third lactation, indicated as first, second and third subset. Data were collected from Research Cum Development Project on Cattle, MPKV, Rahuri, for the period of 44 years from 1972 to 2015 and analysed with the help of two programmes namely Harvey (1990) and SAS version 9.3 (2013). Least-squares analysis of variance was carried out for AFCon, LL and 300 DMY by considering the effects of period and season of birth/calving (Harvey 1990). The data were corrected for the significant effects due to period and season of birth/calving as suggested by Gacula *et al.* (1968). The analysis of variance and covariance for the traits studied was done for testing the differences among the genetic groups for each character by F-test. Analysis of dispersion was done for the simultaneous test of differences between all the traits

Table 1. Total D^2 values and character-wise D^2 values with ranks for each genetic group combination

GG combination	1st lactation				2nd lactation				3rd lactation			
	Total D^2	AFCon	LL	300 DMY	Total D^2	AFCon	LL	300 DMY	Total D^2	AFCon	LL	300 DMY
FG-IFG	5.80**	3.04 (1)	0.24 (3)	2.52 (2)	4.96**	3.04 (1)	0.03 (3)	1.89 (2)	4.48**	2.18 (2)	0.04 (3)	2.26 (1)
FG-FJG	0.82**	0.00 (3)	0.01 (2)	0.81 (1)	0.34**	0.00 (3)	0.00 (2)	0.34 (1)	0.59**	0.01 (3)	0.02 (2)	0.56 (1)
FG-IFJG	4.44**	1.98 (2)	0.34 (3)	2.12 (1)	4.09**	2.06 (1)	0.15 (3)	1.88 (2)	4.13**	2.35 (1)	0.30 (3)	1.48 (2)
FG-R	6.23**	4.10 (1)	0.13 (3)	2.00 (2)	6.01**	4.40 (1)	0.48 (3)	1.13 (2)	6.42**	5.01 (1)	0.02 (3)	1.39 (2)
IFG-FJG	3.69**	3.05 (1)	0.17 (3)	0.47 (2)	3.73**	3.04 (1)	0.06 (3)	0.63 (2)	3.15**	2.48 (1)	0.11 (3)	0.56 (2)
IFG-IFJG	0.13**	0.11 (1)	0.01 (3)	0.01 (2)	0.13**	0.09 (1)	0.04 (2)	0.00 (3)	0.20**	0.00 (3)	0.12 (1)	0.08 (2)
IFG-R	0.12	0.08 (1)	0.01 (3)	0.03 (2)	0.48**	0.12 (2)	0.26 (1)	0.10 (3)	0.68**	0.58 (1)	0.00 (3)	0.10 (2)
FJG-IFJG	2.56**	2.00 (1)	0.25 (3)	0.31 (2)	2.89**	2.06 (1)	0.21 (3)	0.62 (2)	3.34**	2.65 (1)	0.47 (2)	0.22 (3)
FJG-R	4.45**	4.11 (1)	0.08 (3)	0.26 (2)	5.21**	4.40 (1)	0.58 (2)	0.23 (3)	5.72**	5.46 (1)	0.08 (3)	0.18 (2)
IFJG-R	0.43**	0.38 (1)	0.05 (2)	0.00 (3)	0.62**	0.44 (1)	0.09 (2)	0.09 (3)	0.66**	0.50 (1)	0.16 (2)	0.00 (3)
Total D^2	28.67	18.85	1.29	8.53	28.46	19.65	1.90	6.91	29.37	21.22	1.32	6.83
% Contribution	100	65.75	4.50	29.75	100	69.04	6.68	24.28	100	72.25	4.49	23.26
Rank total		13	28	19		13	24	23		15	25	20

Values given in parentheses are ranks. **P<0.01.

studied and for all the genetic groups. The significance of dispersion was observed using V-statistics test, where Wilk's criteria was used as described by Rao (1952). The transformation of correlated variables to uncorrelated variables and the test of significance of D^2 values were carried as described by Rao (1952). The diversities between the genetic groups based on various characters were estimated by using Mahalanobis D^2 Statistics (Mahalanobis 1928). The percentage contribution of each character to overall diversity was calculated on the basis of D^2 values and rank basis. Genetic groups were grouped in to various clusters by Tocher's method (Singh and Choudhary 1985) and canonical variate analysis was carried out to verify the clustering pattern (Rao 1948).

RESULTS AND DISCUSSION

Analysis of variance indicated that genetic group differences were significant (P<0.01) on AFCon, LL and 300 DMY separately and simultaneously (V-stat) in all the three lactations.

Relative diversities: All inter-genetic D^2 values differed significantly from each other except between IFG with R genetic group combination in first lactation. Maximum D^2 values (6.23, 6.01 and 6.42) were observed between FG and R group in first, second and third lactation, respectively. Maximum D^2 values between two groups indicate higher differences in performance of the traits. The inter-genetic D^2 values were least between IFG with IFJG groups in second lactation (0.13) and third lactation (0.20) which indicated that there was not much variation in performance between these *interse* groups. Yakubu *et al.* (2010) revealed that the Mahalanobis distance (7.19) between Bunaji and Sokoto Gudali cattle breeds of Nigeri was maximum and highly significant (P<0.001).

D^2 values and character-wise D^2 values with ranks: The per cent contribution of AFCon to the total D^2 value was maximum followed by 300 DMY and lowest of LL in first, second and third lactation (Table 1).

The contribution of 300 DMY in FG-IFG genetic group combination was higher in first (2.52), second (1.89) and third lactation (2.26), respectively. In FG-FJG genetic group combination, D^2 values in second and third lactation were 0.34 and 0.59, in which 300DMY accounted for highest divergence (0.34 and 0.56). These results indicated that FG group had higher milk producing ability which increases the conversion values of 300 DMY as compared to FJG group. These findings were supported by Sangwan and Singh (1995) in Hariana crosses who reported minimum diversity (0.0863) between FH and FJH genetic groups. Jagtap and Shingte (1991) in Gir crossbreds noticed minimum diversity (0.36) between FG and FJG groups.

The highest rank total was in LL followed by 300 DMY and lowest in AFCon in all lactations. It indicates lower contribution of LL and higher contribution of AFCon towards diversity.

Contribution of each character to overall genetic diversity: The overall rank wise contribution of age at first conception, lactation length and 300 days milk yield was 76.66, 6.66 and 16.66%, respectively. The lower contribution of LL on rank basis to the total divergence than present study was noticed by Sangwan and Singh (1995) in Hariana crosses as zero per cent.

Cluster formation: Based on D^2 values in first lactation, the FG and FJG (F_1) genetic groups were placed in cluster 2 and IFG, IFJG and R genetic groups in cluster 1. In second and third lactation, IFG and IFJG genetic groups formed cluster 1, FG and FJG groups grouped in cluster 2 and R genetic group formed cluster 3 (Figs 1A–3B).

Intra and inter-cluster distance: The magnitude of inter-cluster distance was greater than intra-cluster distance (Figs 1–3). This showed distinct difference between grades belonging to two clusters. The inter-cluster distance between cluster 2 and 3 was maximum in second (2.37) and third lactation (2.46), respectively. The intra-cluster D^2 values

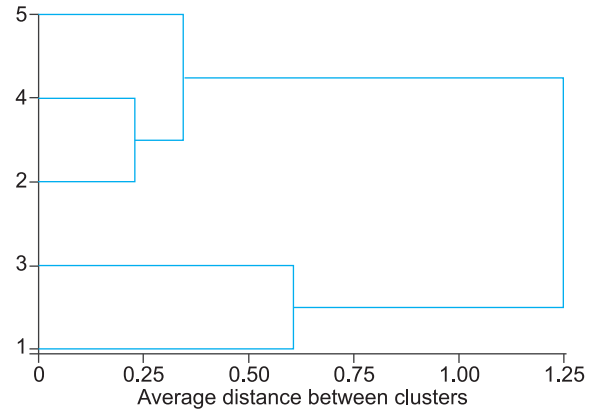

Fig. 1A. Dendogram of first subset.

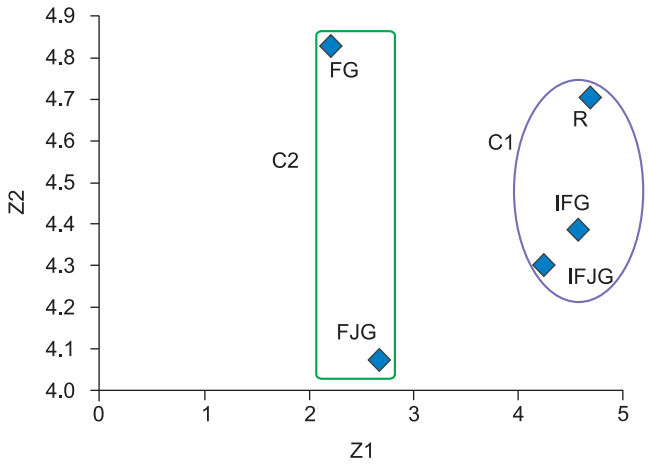

Fig. 1B. Clustering pattern plotted with 2-dimensional diagram of first subset.

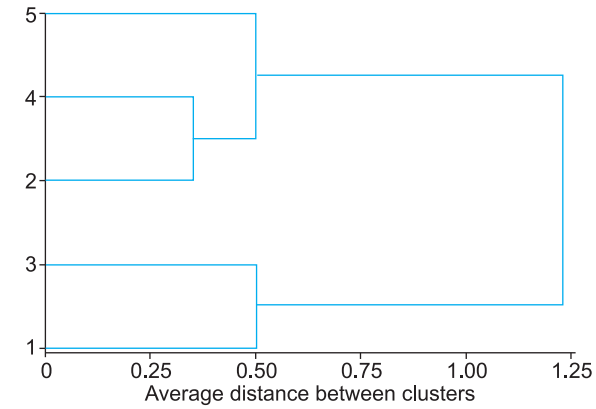

Fig. 3A. Dendogram of third subset.

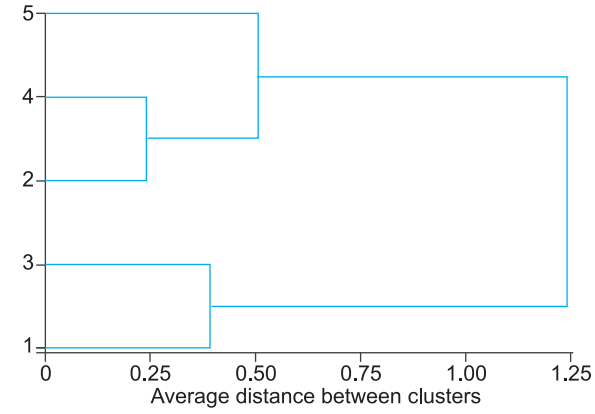

Fig. 2A. Dendogram of second subset.

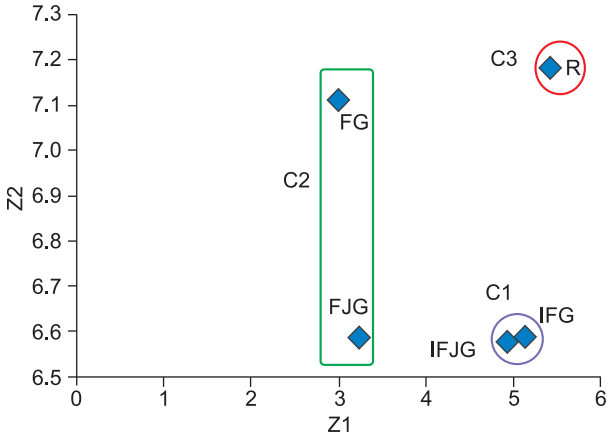

Fig. 2B. Clustering pattern plotted with 2-dimensional diagram of second subset.

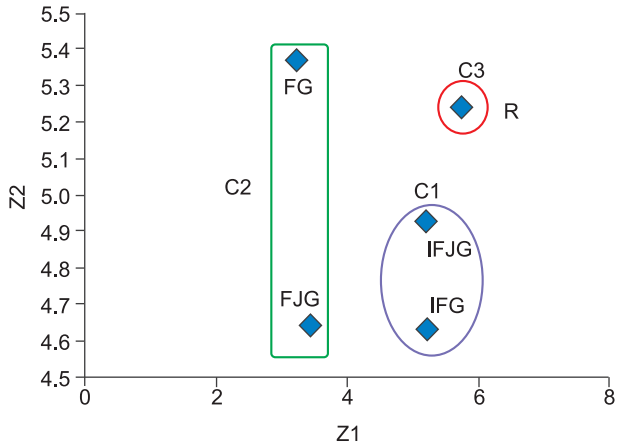

Fig. 3B. Clustering pattern plotted with 2-dimensional diagram of third subset.

in cluster 2 (FG and FJG) were maximum for first (0.90), second (0.58) and third lactation (0.76), respectively. These results indicated maximum distance between FG and FJG groups whereas, IFG and IFJG were close to each other.

Canonical variate analysis confirmed the clustering pattern obtained by Tocher's method. The nearness observed between these grades on the basis of Z_1 and Z_2 values were considered as more appropriate than distance observed on the basis of D^2 values (Figs 1B, 2B and 3B). Boujenane (2015) reported that canonical discriminant analysis confirmed the squared Mahalanobis distance between Oulmes-zaer and Tidili cattle breeds.

The Mahalanobis D^2 statistics was used to differentiate Gir crossbreds by combining information of important traits

and to know the contribution of each trait in total divergence. The reproductive trait (age at first conception) played an important role than productive traits (LL and 300 DMY) in discriminatory analysis. The contribution of AFCon was higher in total diversity among three traits combination in all three lactations. The FG halfbred and FJG triple cross formed one cluster in all three subsets. Though the FG and FJG genetic groups were in one cluster, the intra cluster distance were higher in all subsets. The performance of FG halfberd and FJG triple cross was better over other Gir crossbreds.

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