Original Research

Genetic Divergence Analysis of Gir Crossbred Cattle Based On Some Important Parameters

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Rec. Date:	Jul 09, 2018 09:43
Accept Date:	Feb 01, 2019 14:36
DOI	10.5455/ijlr.20180709094307

Abstract

The study was undertaken to estimate the genetic divergence using Mahalanobis D^2 statistics. Data were collected from 1972 to 2015 on FG (50% HF+50% Gir), IFG (FG Interse), FJG (50% HF+25% Jersey+25% Gir), IFJG (FJG Interse) and R (50% HF+12.50% Jersey+37.50% Gir) crosses of Gir on the basis of age at first conception, age at first calving, lactation milk yield, 300 days milk yield, lactation milk yield per day of lactation length. The genetic groups influence was significant ($P<0.01$) for all traits separately and simultaneously (V test) based on five traits. The Mahalanobis distance values among all the genetic groups combinations, were significant except IFG with R genetic group combination. The total D^2 values for AFCon, AFC, LMY, 300DMY and LMY/LL were 18.86, 0.07, 3.12, 6.42 and 0.78 respectively. The contribution of reproductive trait age at first conception was maximum as 64.47 per cent. The dendogram showed that there are two clusters; cluster one includes IFG, IFJG and R genetic groups and cluster two FG and FJG genetic groups. The magnitude of inter-cluster distance was greater than intra-cluster distance.

Key words: Clusters, Canonical Discriminant Analysis, D^2 Value, Genetic Divergence, Multivariate Analysis

How to cite: Mote, M., Bhoite, U., Fulpagare, Y., Nimbalkar, C., & Bangar, Y. (2019). Genetic Divergence Analysis of Gir Crossbred Cattle Based on Some Important Parameters. International Journal of Livestock Research, 9(3), 84-90. doi: 10.5455/ijlr.20180709094307

Introduction

Livestock sector plays an important role in the national economy and in the socio-economic development of the country. The contribution of livestock sector to the national economy in terms of gross domestic product is 3.9 per cent at current prices (BAHFS, 2013). Still, identification and stabilization of the optimum level of exotic inheritance is moot point in the crossbreeding programme. It is very difficult to predict which cross will give high economic returns when raised under the local environment conditions as one character of the crossbred may be improved, while simultaneously the other may deteriorate. Univariate statistical analysis, analyzes each variable separately and do not explain how the populations under investigations differ when all traits are considered simultaneously (Dossa *et al.*, 2007 and Yakubu *et al.*, 2010). Multifactorial discriminant analyses have been found to be more suitable in assessing variation within a population and can discriminate different population types when all traits are considered jointly (Pundir *et al*., 2015). Therefore, it is essential to use some sound of multivariate analysis technique which would take into consideration maximum number of economically important traits for comparative evaluation of performance of different crossbreds. Hence, an attempt was made for genetic group differentiation using D^2 statistics by combining information on important characters and to know the divergence through relative contribution of characters.

Materials and Methods

Data on age at first conception, age at first calving, lactation milk yield, 300 days milk yield, lactation milk yield per day of lactation length of FG (50% HF+50% Gir), IFG (FG *Interse*), FJG (50% HF+25% Jersey+25% Gir), IFJG (FJG *Interse*) and R (50% HF+12.50% Jersey+37.50% Gir) crosses of Gir were collected from Research Cum Development Project on Cattle, MPKV, Rahuri, for the period of 44 years from 1972 to 2015.

Data Structure

The data pertaining to 161 FG, 237 IFG, 114 FJG, 364 IFJG and 80 R crosses of Gir were collected for the study.

Standardization of Data

Records of abnormal cases like abortion, dystocia, and still-births were not included in the study. Similarly, halfbreds, Triple cross and 5/8 Gir crossbred cows which yielded less than 1500 kg milk in lactation or a lactation less than 200 days were not considered.

Statistical Methods

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 studied and for all the genetic groups. The significance of dispersion was tested by using V-statistics test, where Wilk's criterion was used as described by Rao (1952).

$$\mathbf{V-Stat} = -\ \mathbf{m}\ \mathbf{log_e}\ \Delta$$

Where,

DOI 10.5455/ijlr.20180709094307

$$m = n - \frac{p + q + 1}{2}$$

$$n = \left(n_1 + n_2 + \ldots\ldots\ldots\ldots\ldots + n_k\right) - 1$$

p = number of characters under consideration for respective sets
q = the degrees of freedom for between genetic groups
k = number of genetic groups and

$$\Delta = \left|\frac{W}{X}\right| = \frac{Determination\ of\ matrix\ W_{ij}}{Determination\ of\ total\ matrix\ S_{ij}}$$

The V-Statistics is distributed as χ^2 with pq degree of freedom. The original mean values of the character were transformed to uncorrelated variables by using pivotal condensation method (Rao, 1952). The diversities between different genetic groups based on various characters were estimated by using Mahalanobis (1928) D^2 Statistics. The test of significance of D^2 values was done for any two out of five genetic groups by using statistics suggested by Rao (1952). The percentage contribution of each character to overall diversity was calculated on the basis of D^2 values and rank basis. For grouping of the genetic groups into various clusters, Tocher's method (Singh and Choudhary, 1985) was used. Clustering pattern was verified by canonical analysis (Rao, 1948).

The CANDISC (SAS 2013) procedure was used to perform multivariate analysis that calculated the Mahalanobis distance between the five genetic groups and to compute canonical discriminant analysis to derive canonical functions. Based on the Mahalanobis distance dendogram was created using PROC CLUSTER (SAS, 2013).

Results and Discussion

The analysis of variance indicated that the genetic group differences were significant ($P<0.01$) for each trait separately. The V-statistics indicated that the genetic groups had significant ($P<0.01$) effect on all the five traits considered together (Table 1). The significant genetic group difference for AFCon and AFC was also reported by Saha *et al*. (1989) and Saha *et al*. (1988) in Gir crosses when four and ten characters were studied, respectively.

DOI 10.5455/ijlr.20180709094307

Table 1: Analysis of variance for reproduction and production traits as affected by genetic group

Source of Variation	d. f.	MS				
		Age at First Conception	Age at First Calving	LMY	300DMY	LMY/LL
Between genetic groups	4	2368865.00**	2363591.25**	10766853.38**	15751690.22**	180.32**
Within genetic groups	951	17755.05	17871.49	575333.33	339762.77	3.21
Simultaneous test of significance for the above three traits						
Wilk's criterion			0.000158			
V-statistic			8315.08**			

$** = P < 0.01$

Total D^2 Values and Character-Wise D^2 Values with Ranks

The differences between inter-genetic D^2 values were significant ($P<0.01$) from each other in all combinations except between IFG with R (Table 2).

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

GG Combination	1st Lactation					
	Total D^2	AFCon	AFC	LMY	300 DMY	LMY/LL
FG-IFG	5.95**	3.04 (1)	0.00 (5)	0.92 (3)	1.82 (2)	0.17 (4)
FG-FJG	0.91**	0.00 (5)	0.01 (4)	0.48 (1)	0.32 (2)	0.10 (3)
FG-IFJG	4.55**	1.99 (1)	0.01 (5)	0.70 (3)	1.61 (2)	0.24 (4)
FG-R	6.36**	4.10 (1)	0.00 (5)	0.86 (3)	1.20 (2)	0.20 (4)
IFG-FJG	3.75**	3.05 (1)	0.01 (4)	0.07 (3)	0.61 (2)	0.01 (5)
IFG-IFJG	0.15**	0.11 (1)	0.01 (4)	0.01 (2)	0.01 (5)	0.01 (3)
IFG-R	0.14	0.08 (1)	0.00 (5)	0.00 (4)	0.06 (2)	0.00 (3)
FJG-IFJG	2.54**	2.00 (1)	0.00 (5)	0.02 (4)	0.49 (2)	0.03 (3)
FJG-R	4.48**	4.11 (1)	0.02 (4)	0.05 (3)	0.28 (2)	0.02 (5)
IFJG-R	0.42**	0.38 (1)	0.01 (3)	0.01 (4)	0.02 (2)	0.00 (5)
Total D^2	29.25	18.86	0.07	3.12	6.42	0.78
Rank total		14	44	30	23	39

$** = P < 0.01$

Maximum squared distance values were observed between FG and R group as 6.36. Maximum D^2 values between two groups showed higher differences in performance of the traits studied. The maximum D^2 values among FG-R genetic groups might be due to the fact that cows of FG group conceived in early age than cows of R group and also due to higher lactation milk yield in FG than R group. The higher performance of FG (F_1) might be due to heterotic effect. The inter-genetic D^2 value between IFG and R group was least (0.14). The minimum D^2 value among these groups indicates similarity in performance between these groups for the traits studied.

Among all combinations maximum D^2 value of age at first conception was between FJG and R genetic group combination. The highest D^2 value 4.11 of AFCon among these groups indicates maximum difference

DOI 10.5455/ijlr.20180709094307

in AFCon in both groups. This might be due to higher Gir inheritance in R crossbred (37.50%) than FJG crossbred (25.00%). The minimum D^2 value for AFCon was noticed between FG with FJG genetic group combination. The total D^2 value contributed by all five traits was 29.25 (Table 2). The rank total indicated that AFC had higher rank, whereas, AFCon had the lowest rank. This indicates minimum per cent contribution of AFC and maximum per cent contribution of AFCon in overall divergence. The per cent contribution of AFCon was maximum as 64.47, whereas, AFC contributed minimum as 0.24 in total diversity (Table 3). This indicates that the effect of AFC was masked by AFCon as gestation period is the constant factor between these two traits. Sangwan and Singh (1995) studied on five traits and reported contribution of LMY and LMY/LL as 70 and 10 per cent, respectively.

Table 3: Per cent contribution of different traits in divergence

Traits	Per cent Contribution
AFCon	64.47
AFC	0.24
LMY	10.67
300 DMY	21.95
LMY/LL	2.67
Total	100

Rank Wise Contribution of Each Character to Overall Genetic Divergence

The rank wise contribution to genetic divergence of AFCon, AFC, LMY, 300 DMY and LMY/LL was in the range of 90 to zero per cent (Table 4).

Table 4: Rank wise contribution of each character to the divergence

Characters	AFCon	AFC	LMY	300 DMY	LMY/LL	Total
Number of times appearing in first ranking	9	0	1	0	0	10
Per cent contribution	90	0	10	0	0	100

The D^2 values of AFC, 300 DMY and LMY/LL did not appeared first in ranking for any of the genetic group combinations hence their contribution was zero. It indicates that reproductive trait age at first conception played an important role than productive traits like LMY, 300 DMY and LMY/LL.

Cluster Formation

The clusters were formed on the basis of D^2 values as IFG, IFJG and R formed one cluster, whereas, FG and FJG formed second cluster (Figs. 1 and 2). Jagtap *et al*. (1989) observed similar clustering pattern in Gir crossbreds where FG, FJG and JFG genetic groups formed one cluster. Singh and Parekh (1989) in Gir crossbreds noticed that FG and FJG formed common cluster due to minimum genetic divergence between

DOI 10.5455/ijlr.20180709094307

them. The dendogram showed that there are two clusters; cluster one includes Manipur and Mizoram cows and cluster two Tripura cows those are clearly separated from cluster one (Pundir *et al.*, 2015).

Intra and Inter-Cluster Distance

The magnitude of inter-cluster distance was greater than intra-cluster distance (Fig. 1). This shows distinct difference between grades belonging to two clusters. The inter-cluster distance value between cluster I and cluster II was 2.14.

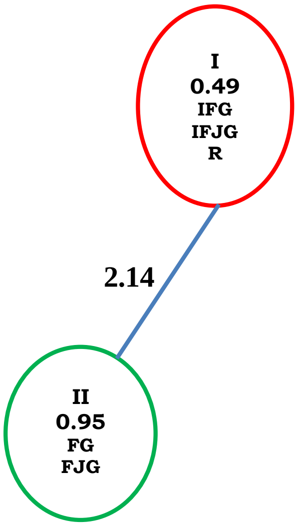

Fig. 1: Cluster and their interrelationship

Canonical Analysis

This method is used to plot the various grades into two dimensional picture (Fig. 2) by considering the mean values of the canonical variants (Z_1 and Z_2). The nearness observed between these grades on the basis of Z_1 and Z_2 values were more appropriate than distance observed on the basis of D^2 values. It's due to the fact that the first two roots explained 98.91 per cent of variability.

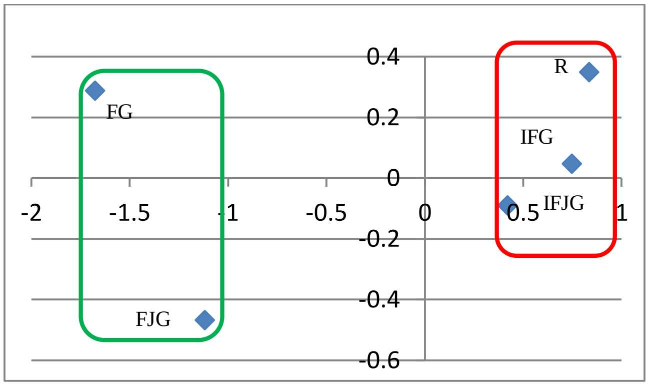

Fig. 2: Clustering pattern plotted with 2-dimensional diagram

DOI 10.5455/ijlr.20180709094307

Conclusion

The D^2 statistics indicated that reproductive trait age at first conception played an important role in discriminatory analysis than all other traits studied. The IFG, IFJG and R crosses formed one cluster, whereas, FG and FJG formed second cluster with higher intra cluster distance. Therefore, to select parents for future breeding from different crossbreds, it is dependent on choice of breeder to improve intentional traits. The due weightage should be given to higher inter-cluster distances, higher cluster means and contribution of trait to overall productivity.

Acknowledgement

The authors extend their sincere thanks to MPKV, Rahuri for providing the facilities for conducting the present investigation.

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DOI 10.5455/ijlr.20180709094307