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Genetic Divergence and Cluster Analysis on Production Traits among Gir and Its Crosses

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Abstract The objective of the present study was to estimate the genetic divergence among various genetic groups of Gir crossbreds viz. PG (50% HF × 50% Gir cow), IFG (FG × FG *Interse*), FJG (50% HF + 25% Jersey + 25% Gir), IFJG (FJG ×FJG *Interse*), R (JR 50% Jersey × 50% Red Sindhi) maintained by using Mahalanobis D^2 statistic technique. The traits used in this study were first lactation production traits such as age at first conception (AFConcp) age at first calving (AFC), calving interval (CI), lactation length (LL), lactation milk yield (LMY), lactation milk yield/days of lactation length (ML) and lactation milk yield/days of calving interval (MI). All possible combinations of genetic groups showed significant difference except IFH and R. Out of total D^2 (31.727) the highest contribution for genetic divergence was observed due to AFConcp (65.423%) followed by DMY 300 (20.233%) and FLMY (10.004%). Tocher's method showed that FG and FJG were grouped in one cluster while IFG, JFJG and R were remained in another cluser. The variation in Gir inheritance showed significant differences among groups and it was suggested that more inter-se mating may be stabilize herd performance.

Keywords Genetic divergence, Gir cross breed, Mahalanobis D^2, Cluster analysis.

Introduction

Crossbreeding program are mainly focused towards improvement of breeds and increasing productive and reproductive performance. The superior genetic groups are being proposed to be used as a base for developing new high yielding strains/breeds of crossbreed cattle. The percent inheritance of exotic breeds influences the many productive and reproductive characters which show genetic divergence among the various genetic groups. Genetic diversity is the raw material in which breeder has scope to select highly diverse parents through application of considering many traits simultaneously. It may be used to evaluate the superiority of some genotypes over others and to identify divergent genotypes that may be used as parents in breeding programs.

Mahalonobis D^2 statistic [1] is the rational criterion for studying and identifying diverse parents for crosses. It has been widely used in Psychometry, Antropometry and biology for classificatory purpose

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[2, 3] clustering analysis is also important criteria to identify divergent genotype. This technique divides genetic groups into number of clusters according to intra and inters cluster distances between groups. The Tocher's method is the most used among the optimization methods used in cluster analysis.

The genotypes belonging to different clusters are having maximum divergence and can be successfully utilized in hybridization program to get desirable transgressive segregants. It is assumed that maximum amount of heterosis will be mainfested in cross combinations involving the parents belonging to most divergent clusters [4]. Mahalanobis's D^2 statistic, a tool for quantifying the degree of divergence and Tocher's method were utilized for grouping the genotypes into different clusters [5].

Further, the studies on estimation of genetic divergence among the crossbreds provide guidelines to formulate or update an appropriate breeding policy. It also increases the availability of informatics resources towards strategies for improvement program. Therefore, the aim of the present study was to estimate the genetic divergence among different genetic grades of Gir crossbreds using Mahalanobis D^2 statistic and cluster analysis.

Materials and Methods

Data collection

The data records used in this study was obtained from the registers maintained at Research cum Development Project (RCDP) on Cattle, Mahatma Phule Krishi Vidyaapeeth Rahuri (Maharashtra State) for 37 years (1977 to 2013).

Total five different genetic groups of cattle were maintained at the project as follows: FG (50% HF ×50% Gir), IFG (FG × FG *Interse*), FJG (50% HF +25% Jersey + 25% Gir), IFJG (FJG × FJG *Interse*) and R (JR 50% Jersey × 50% Red Sindhi) with corresponding sample size included in the study were 158, 212, 107, 324 and 71, respectively.

The variables studied were age at first conception (AFConcp), age at first calving (AFC), calving interval (CI), lactation length (LL), lactation milk yield (LMY), lactation milk yield/days of lactation length (ML) and lactation milk yield/days of calving interval (MI).

Statistical analysis

The genetic divergence between five genetic groups of Gir crossbred was undertaken by Mahalanobis ´D^2 Statistic [6]

Mahalnobis D^2 statistic is defined by the formula

$$D^2_p = b_1d_1 + b_2d_2 + \ldots b_pd_p$$

Here, b_1 values are to be estimated such that the ratio of variance between populations to the variance within the populations is maximized. In term of variance and covariances the D^2 value is

$$D^2_p = W^{ij} (\overline{x^1_i} - \overline{x^2_i}) (\overline{x^1_j} - \overline{x^2_j})$$

Where, W^{ij} is the inverse of estimated variance covariance matrix.

The D^2 values were tested on the basis of significance by F-distribution [4] as follows.

$$F = \frac{N_1N_2\,(N_1 + N_2 - P-1)}{P\,(N_1 + N_2)(N_1 + N_2 - 2)}\,D^2 \quad .$$

Where N_1 and N_2 are number of observations in group 1 and group 2, respectively. P represent the number of traits.

The contribution of each trait to overall divergence was obtained by ranking the traits according to D^2 values. The Tocher's method was used for the formation of clusters of genetic groups [7] and canonical variate analysis was carried out to verify the clustering pattern [3].

Results and Discussion

The genetic divergence between 5 genetic groups (FG, IFG, FJG, IFJG and R) revealed 10 pairwise combination of genetic groups. The D^2 values for each traits along with its ranking due to each pairwise combina-

Table 1. Percent contribution and D^2 values with ranks of each character. Value in parentheses are ranks of D^2 values,**-significant at1%.

Genetic group combination	AFConcp	AFC	FLMY	DMY300	LL	CI	LMY_CI	LMY_LL	Total D^2
FG, IFG	3.2963 (1)	0.0000 (8)	0.8884 (3)	1.8923 (2)	0.0626 (5)	0.0003 (7)	0.0179 (6)	0.1804 (4)	6.3382**
FG, FJG	0.0000 (8)	0.0109 (7)	0.4598 (1)	0.3165 (2)	0.0474 (5)	0.0101(6)	0.0135 (4)	0.1113 (3)	0.9696**
FG, IFJG	2.1360 (1)	0.0085 (8)	0.7195 (3)	1.5820 (2)	0.1857 (4)	0.0140 (6)	0.0031 (7)	0.1363 (5)	4.7852**
FG, R	4.5720 (1)	0.0000 (8)	0.9107 (3)	1.0821 (2)	0.1054 (5)	0.0027 (7)	0.0389 (6)	0.1861 (4)	6.8974**
IFG, FJG	3.3170 (1)	0.0117 (4)	0.0699 (3)	0.6611 (2)	0.0011 (7)	0.0069 (6)	0.0003 (8)	0.0083 (5)	4.0761**
IFG, IFJG	01250 (2)	0.0092 (5)	0.0089 (6)	0.0139 (3)	0.0327 (2)	0.0102 (4)	0.0061 (7)	0.0031 (8)	0.2093**
IFG,R	0.1040 (2)	0.0000 (8)	0.0001 (6)	0.1125 (1)	0.0055 (3)	0.0012 (5)	0.0040 (4)	0.0000 (7)	0.2274
FJG, IFJG	2.1530 (1)	0.0002 (8)	0.0289 (4)	0.4833 (2)	0.0455 (3)	0.0003 (7)	0.0037 (5)	0.0013 (6)	2.7159**
FJG,R	4.5960 (1)	0.0120 (4)	0.0763 (3)	0.2282 (2)	0.0114 (5)	0.0024 (8)	0.0065 (7)	0.0096 (6)	4.9421**
IFJG,R	0.4580 (1)	0.0095 (6)	0.0113 (5)	0.0473 (2)	0.0113 (4)	0.0044 (7)	0.0200 (3)	0.0039 (4)	0.5654**
Total D^2	20.757	0.0619	3.1739	6.4191	0.5086	0.0523	0.1140	0.6402	31.7266
Rank total	18	66	37	20	43	63	57	56	
% contribution	65.423	0.1951	10.0038	20.2326	1.6031	0.1648	0.3594	2.0180	

tions are given in Table 1. It was observed that total D^2 for each combinations was significant except IFG and R combination was found to be non-significant.

Out of all combinations of all combinations, total D^2 was maximum between FG-R (6.8974) followed by FG-IFG (6.3382), FJG-R (4.9421), FG-IFJG (4. 7852), IFG-FJG (4.0761) while it was lowest between IFG-IFJG (0.2093) followed by IFG-R (0.2274), IFJG-R (0.5654), FG-FJG (0.9696) and FJG-IFJG (2.7159). Highest D^2 value was observed between FG and R might be due to half breeds calved at earlier age.

The D^2 values contributed by all the (eight) traits taken into consideration was 31.727. This distance was chiefly contributed due to AFConception (20.757), DMY 300 (6.4191) and FLMY (3.1739). The percent contribution due to AFConception, DMY 300 and FLMY were 65.423%, 10.004% and 20.233%, respectively. The cumulative D^2 values due to these three traits was 95.659%. It indicates the importance of these traits in genetic divergence between five groups. The rank total was observed in order (lowest first) as AFConcep-DMY300-FLMY-LL-LMY_LL-LMY_CI- CI-AFC. The LMY_LL, LMY_CI, CI and AFC had little contribution in genetic divergence. It was concluded that different genetic groups showed maximum genetic divergence to Age at first Conception (AF Conception). Maximum genetic divergence in Gir and its crosses due to age at first calving. The clustering was done on the basis of distance between genetic groups using canonical variate analysis method and two groups were formed according to intra and inter cluster distances (Table 2). The group-

Table 2. Average inter and intra cluster distances among five genetic groups of cattle.

Clusters	I	II
I	0.722	2.135
II		0.694

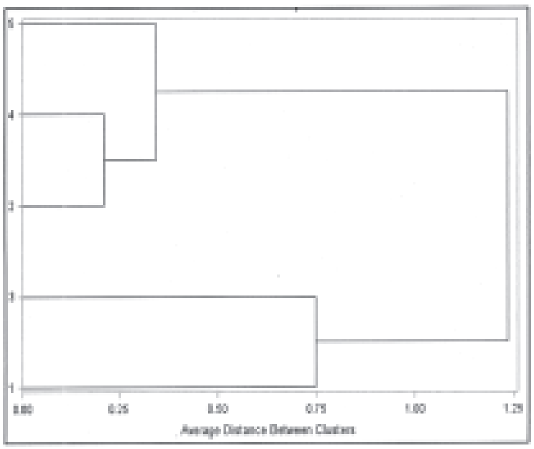

Fig. 1. Cluster analysis.

ing of genetic groups in two clusters due to Tocher's method are shown in dendogram (Fig. 1). FG and FJG were grouped in one cluster while IFG, IFJG and R were remained in another cluster. The maximum intra cluster distance was found within cluster I (0.72) which indicated that genetic group of cluster I might varied genetic architecture. The significant difference between FG and FJG ($D^2 = 0.9696$) within Cluster I might be due reduction of 25% Gir and inclusion of 25% Jersey inheritance. The inter cluster distance were greater than the intra cluster distance revealing that considerable amount of genetic diversity existed among the accession. The highest inter-cluster distance between cluster I and II was 2.135. The replacement of HF by Red Sindhi with Gir i.e. FG and R showed maximum divergence among the all combinations. Athough inter-se mating grouped into same cluster, the significant difference ($D^2 = 0.2093$) may be due to addition of Jersey inheritance. It is suggested that adopting more inter-se mating can lead to more stabilized herd performance.

Conclusion

Highest D^2 value (6.8974) was observed between FG and R might be due to half breeds calved at earlier age. D^2 values contributed by eight traits taken into consideration was 31.727. Out of total D^2, the highest contribution for genetic divergence was observed due to AFConcp (65.423%) followed by DMY 300 (20.233%) and FLMY (10.004%). Different genetic groups showed maximum genetic divergence to Age at first Conception (AFConception). The maximum intra cluster distance was found within cluster I (0.72) which indicated that genetic group of cluster I might varied genetic architecture. FG and R showed maximum divergence among the all combinations. It is suggested that adopting more inter-semating can lead to more stabilized herd performance.

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