Research Article

Estimation of Genetic Parameters for Economic Traits in Frieswal Cattle at MF Ambala

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Abstract
A total number of 3005 lactation records of 1147 Frieswal cows, sired by 64 sires born and reared at Military Dairy Farm, Ambala. The period of study were divided into 5 periods of 3 years each (1993 to 2007). The average performances of production traits, effect of genetic factors were analyzed and estimation of genetic parameters of production traits were estimated. The heritability estimates were low for almost all the traits under study. The heritability estimates for total lactation milk yield, 300 days milk yield, peak yield, lactation length was 0.14 ± 0.03, 0.13 ± 0.04, 0.13 ± 0.03, 0.074 ± 0.028, respectively. Total lactation milk yield had very high and positive genetic correlation with peak yield (0.93 ± 0.04) and medium and positive (0.35 ± 0.19) with lactation length. Genetic correlation between peak yield and lactation length was found positives but very low (0.29 ± 0.22). The phenotypic correlation of total lactation milk yield was high (0.726) with peak yield and low (0.425) with lactation length. The peak yield had very low phenotypic correlation (0.026) with lactation length.

Introduction

In India, contribution of dairy cattle to total milk production is about 43.38% of the milk production, out of which crossbred cattle contribute around 51.28% [1]. As per 18th Indian livestock census, cattle population in India increased by about 7.5% and population of exotic and crossbred cattle increased by 35%. The total share of crossbreds in the cattle population showed an increase of 16.6%. Moreover, higher productive and reproductive efficiency of crossbred cattle in comparison to indigenous cattle, make them more profitable. Over the years various strains of crossbred cattle have been developed in country, as a result of different crossbreeding projects that were undertaken in different institute herds to increase the productivity of indigenous breeds of dairy cattle. Most of the research on the estimation of genetic parameters of production and fertility traits, in Indian crossbred cattle, was done mainly by analysis of variance and on the basis of first lactation records. The analysis of variance (ANOVA) used for the estimation of covariance components is more applicable under controlled breeding experiments [2, 3]. Estimation of genetic and phenotypic parameters for productive traits is an important tool for the definition and evaluation of selection programs. Results from various studies analyzed that research should be intensified to identify and utilize animals with greater genetic potential. The performance traits like milk yield is considerably affected by environmental factors, which, in addition to genetic differences, are responsible for the marked variation between breeds, herds and animals within the same breed. It is therefore fundamentally important to identify factors that affect crossbred cow productivity so that breeding programs may be planned and implemented properly in order to obtain a balance between genetics and environment according to [4].

Estimation of genetic and phenotypic parameters for productive and reproductive traits is an important tool for the definition and evaluation of selection programs. Results from various studies analysed that research should be intensified to identify and utilize animals with greater genetic potential. The performance traits like milk yield is considerably affected by environmental factors, which, in addition to genetic differences, are responsible for the marked variation between breeds, herds and animals within the same breed. It is therefore fundamentally important to identify factors that affect crossbred cow productivity so that breeding programs may be planned and implemented

properly in order to obtain a balance between genetics and environment. Major environmental factors that affect performance and evaluation of individual animals and populations are herd, year and calving season, age at calving and management [5, 6]. In view of the above facts the present study was conducted on the Frieswal cows maintained at Military Farm, Ambala.

Materials and Methods

The data on production traits, total lactation milk yield, 300 days milk yield, peak yield, lactation length. pertained to 1147 Frieswal cattle progeny of 64 Sires, over a period of 15 years (1993 to 2007).The total years were classified into five periods taking into three seasons winter (Nov-Feb), Summer (Mar-Jun), Rainy (Jul-Oct) in accordance with agro climatic condition of the study centre. The least squares means, heritability, genetic and phenotypic correlation and effects of genetic and non-genetic factors were estimated by using Mixed Model Least Squares and Maximum Likelihood programme as suggested, [7].

Estimation of Genetic Parameters
Estimation of Heritability

The estimates of heritability were obtained by paternal half-sib correlation method. The analysis of variance for half-sib data with unequal number of progeny under different sires assumed the following form.

S.V.	D.F.	M.S.	E.M.S.
Between sire	S-1	MSs	$\sigma^2 e + k\sigma^2 s$
Error	N-S	MSe	$\sigma^2 e$
Total	N-1		

Where, S = Number of sires, N = Total number of cows.

$$\sigma^2 s = \frac{MS_s - MS_e}{K}, \qquad K = \frac{1}{S-1}\left[N.. - \frac{\sum_{i=1}^{S} n_i}{N..} \right]$$

$$\sigma^2 e = MS_e$$

n_i = Number of daughters (Progeny) of the ith sire.

The intra class correlation 't' among paternal half-sub was estimated as:

$$t = \frac{\sigma^2 s}{\sigma^2 s + \sigma^2 e}$$

Then heritability was estimated by the following formula.

$$h^2 = \frac{4x\sigma^2 s}{\sigma^2 s + \sigma^2 e} = 4xt$$

Where, $\sigma^2 s$ = component of sire variance, $\sigma^2 e$ = Error variance.

The standard error of heritability was calculated by using the formula given by Swiger *et al.* (1964).

$$S.E.(h^2) = \sqrt[4]{\frac{2(N-1)(1-t)^2[1+(k-1)t]^2}{k^2(N-1)(S-1)}}$$

Where, N= total number of daughters, S= total number of sires, t= Intra-class correlation among paternal half sibs and k= Average number of progeny per sire and was estimated by the formula given above.

Genetic and Phenotypic correlation

The genetic and phenotypic correlations among different traits were estimated by the analysis of variance and covariance technique according to Becker (1975).

The genetic correlation between x and y

$$r_g(xy) = \frac{Cov_s\,(xy)}{\sqrt{\sigma_s{}^2(x).\sigma_s{}^2(y)}}$$

Where, x & y = Two different traits for same individual, Cov_s (xy) = sire component of co-variance between trait x and y, $\sigma_s{}^2$ (x) & $\sigma_s{}^2$ (y) = sire component of variance for trait x and y respectively.

The standard error of genetic correlation (r_g) was estimated by using the following formula given by Robertson (1959)

$$S.E.\,(r_g) = \frac{1-r_g^2}{\sqrt{2}} \times \frac{\sqrt{S.E.(h_y^2)S.E.(h_x^2)}}{\sqrt{h_x^2 h_y^2}}$$

Where, $h^2{}_x$ and $h^2{}_y$ are the h^2 estimates of trait x and y respectively, S.E. = Standard error, and r_g=Genetic correlation,

The phenotypic correlation (r_p) between traits x and y was estimated as

$$r_p(xy) = \frac{Cov_s(xy) + Cov_e(xy)}{\sqrt{[\sigma_s{}^2(x) + \sigma_e{}^2(x)]\,[\sigma_s{}^2(y) + \sigma_e{}^2(y)]}}$$

The standard error of phenotypic correlation was estimated by the formula given by Panse and Sukhatme (1967) as.

$$S.E. = \frac{\sqrt{1 - r_{P\,(xy)}^2}}{\sqrt{N-2}}$$

$r_{p(xy)}$ =The phenotype correlation between trait x and y, N = Total number of observations, N-2 = Degree of freedom

Results and Discussion
Total lactation Milk yield

The heritability estimate for total lactation milk yield was very low (0.14±0.039). The similar h^2 estimates 0.10, 0.10±00, 0.116±0.012, were reported by [8], [9] and [10] respectively. [11] in FXS, [12] in FXS and BSXS, [13] in FXS, in cross bred reported higher heritability estimates than the present findings. However, comparatively low h^2 estimates were reported by [14] in JXS, and [15] in HFXS.

300-d milk yield

The heritability estimate of 300 days milk yield was low 90.13±0.049. Higher estimates than the present finding were reported by [16] and [17] in cross breed cattle.

Peak Yield

The heritability estimate of peak yield was low (0.13±0.038). Almost similar heritability estimates of peak yield were reported by [18] in SXHF, [9] in SXJ. Lower heritability estimate in compression of present finding were reported by [14] in SXJ and SXRD, and [15] HFXS. Higher estimates than the present finding were also reported by [14] in SXHF, [19] in JXH, BSXH and HFXH.

Lactation Length

The estimates of heritability for lactation length in Freiswal were relatively very low ranging from (0.074±0.028) (**Table 1**). [11, 20-22] in FXS, and [15] in HFXS. However, moderate to high estimates of (0.26±0.05 to 0.44±0.27) for Sahiwal breed has also been reported by some workers [14] in JXS, [9] in JXS, [23] crossbred, [12] in FXS, [13] in FXS, [24] and [25] in cross bred. A very wide range of heritability estimates exist for Tharparkar, Hariana, Red Sindhi, Cholistani breeds, Sahiwal crossbreds and Friesian cattle in hot climate. Method of analysis and models contribute to the differences apart from actual breed differences and environmental variation.

Table 1 Heritability estimate of different production and reproduction traits in Frieswal cows

Sr. N.	Trait	Heritability ($h^2 \pm SE$)
1.	Total lactation milk yield	0.14±0.039
2.	Milk yield 300 Days	0.13±0.049
3.	Peak yield	0.13±0.038
4.	Lactation length	0.074±0.028

The present study pertains to estimation of genotypic and phenotypic correlations among different production traits with a view to investigate whether any association exists between the productive traits in Freiswal cattle maintained at Military Dairy farm Ambala. The correlation between two traits was estimated by the method of analysis of variance and covariance by paternal half sib analysis. The genetic correlation between two characters arises due to the pleiotropic effect of gene and some linkage among genes. However, in a large population under random mating, the effect of linkage in quantitative genes is expected to be negligible. Phenotypic correlations between two traits are a function of genetic and environmental correlations between them with the assumption that there is no covariance between genotype and environment. The genetic and phenotypic correlation coefficient among various productive traits.

Total lactation milk yield had very high and positive genetic correlation with peak yield (0.93±0.04) and medium and positive genetic correlation (0.35±0.19) with lactation length. Genetic correlation between peak yield and lactation length was found positives but very low (0.29±0.22) (**Table 2**). [24] reported high genetic correlation (0.65±0.10) between lactation milk yield and lactation length. [21] reported that lactation length has moderate genetic correlation (0.40) with lactation milk yield. However, [25] reported low (0.12±0.03) genetic correlation between milk yield and lactation length. Phenotypic correlation total lactation milk yield was found high (0.726) with peak yield and low (0.425) with lactation length, whereas lactation length was found to have very low (0.02) phenotypic correlation with peak yield (Table 2). [24] also reported high phenotypic correlation between total lactation milk yield and lactation length while [25] reported medium phenotypic correlation (0.45±0.32) between these two traits.

Table 2 Genetic (above diagonal) and Phenotypic (below diagonal) correlations among Total lactation milk yield, peak yield and lactation length of Frieswal cows

Traits	Total Lactation milk yield	Peak yield	Lactation length
Total Lactation milk Yield	-	0.93±0.045	0.359±0.199
Peak yield	0.726	-	0.297±0.227
Lactation length	0.425	0.026	-

Conclusion

It may be concluded that the effect of sire was found non-significant on all traits, Low heritability estimate for lactation milk yield indicate that there is a very little additive genetic variance in these traits and individual selection will not be helpful for improving them. High genetic correlation between lactation milk yield and peak yield indicated that selection for peak yield may bring reasonable genetic improvement in milk yield of Frieswal cows.

Acknowledgments

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