

Genetic Evaluation of First Lactation Traits in Sahiwal Cattle Using Restricted Maximum Likelihood Technique

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ABSTRACT : The data on 283 Sahiwal cows, sired by 16 bulls, maintained at Cattle Breeding Farm of Nagpur Veterinary College and Dairy Farm of Agricultural College, Nagpur, were considered for the estimation of genetic parameters. Variance and covariance estimates of first lactation traits were obtained using restricted maximum likelihood technique (REML). When first lactation milk yield (FLMY), first lactation length (FLL) and average daily yield (ADY) traits were considered for REML analysis, the heritabilities were 0.184 ± 0.146 , 0.132 ± 0.131 and 0.141 ± 0.133 , respectively. While, genetic and phenotypic correlations between them were medium to high except phenotypic correlations between FLL and ADY (-0.025). REML procedure considering FLMY, age at first calving (AFC) and first service period (FSP) combination exhibits heritabilities as 0.274 ± 0.173 , 0.506 ± 0.233 and 0.274 ± 0.172 , respectively. Genetic correlations were -0.120 ± 0.376 , 0.225 ± 0.423 and 0.365 ± 0.331 between FLMY and AFC, FLMY and FSP, AFC and FSP, respectively. Phenotypic correlations were 0.057, 0.289 and 0.123, respectively. Considering all five traits REML combination heritabilities estimated were 0.238 ± 0.162 , 0.160 ± 0.139 , 0.136 ± 0.132 , 0.409 ± 0.209 and 0.259 ± 0.168 for FLMY, FLL, ADY, AFC and FSP, respectively. The genetic correlations were positive except FLMY and AFC. The phenotypic correlations were also positive except FLL and ADY, ADY and FSP. Almost all estimates were associated with high standard error. (*Asian-Aust. J. Anim. Sci. 2003, Vol 16, No. 5 : 639-643*)

Key Words : REML, Convergence, Iteration, Canonical Transformation, Sahiwal Breed

INTRODUCTION

Precise and accurate knowledge of genetic parameters are of paramount importance for planning appropriate selection and breeding strategies for the genetic improvement of dairy animals. Information on first lactation traits enables the breeder to predict the later lactation performance of the animals as it is highly correlated with the future performance traits (Jairath et al., 1995). Besides, performance of first lactation traits will help in early selection of the superior animals and thus reduce the generation interval. Routinely used methods like least squares and maximum likelihood for estimating variances and covariances have their limitations. Restricted maximum likelihood (REML) method overcomes such limitations and is employed to avoid selection bias and small sample bias associated with nuisance effects (Lee and Pollak, 1997). REML estimation is the most widely used method in animal breeding because of its attractive statistical procedure (Lee, 2000). Among the 26 well-defined breeds of cattle in India,

Sahiwal is one of the best dairy cattle known for its production potential in harsh environments. The number of this animal is gradually depleting and its conservation and development is earnestly needed. Hence, the precise information on genetic parameters in this breed is utmost important for accurate evaluation of the genetic worth of the animals. Therefore, the present study was undertaken to obtain the estimates of heritability, genetic and phenotypic correlations among the first lactation traits in Sahiwal cattle using REML.

MATERIALS AND METHODS

Information on 283 Sahiwal cows was collected from Cattle Breeding Farm of Nagpur Veterinary College and Dairy Farm of Agriculture College, Nagpur. The traits under study were production traits viz. first lactation milk yield (FLMY), first lactation length (FLL), and average daily yield (ADY), and reproduction traits viz. age at first calving (AFC) and first service period (FSP). REML technique was used considering Schaeffer's (1986) approach (Method 1).

Model:

$$Y_{ij} = \mu + S_i + e_{ij}$$

Where,

Y_{ij} = observation on j^{th} daughter of i^{th} sire,

μ = population mean,

S_i = random effect of i^{th} sire and

e_{ij} = random residual effect.

$$V(Y_k) = G+R$$

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Table 1. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) from three traits restricted maximum likelihood analysis

Trait	First lactation milk yield	First lactation length	Average daily yield
First lactation milk yield	0.184±0.146	0.463±0.492	0.560±0.421
First lactation length	0.675±0.044	0.132±0.131	0.437±0.551
Average daily yield	0.301±0.056	-0.025±0.059	0.141±0.133

Where,

$V(Y_k)$ = Variance-covariance matrix of Y_k

Y_k = $t \times 1$ vector of observations on k^{th} animal

t = number of traits

$k = 1, 2, \dots, N$

N = total number of animals

G = variance covariance matrix of sire effect,

R = variance covariance matrix of residual effect.

N = number of observations (animals).

Canonical transformation of Y_k is needed ($Z_k = QY_k$) where Q is the transformation matrix such that $QRQ' = I$ and $QQ' = D_g$. I is the identity matrix and D_g is the diagonal matrix. Eigenvalues and eigenvectors were estimated considering variance and covariance matrices G and R for canonical transformation. Once data is transformed genetic and residual variance and covariance matrices were constructed on original scale by using inverse transformation.

$$\hat{G} = Q^{-1} D_g Q$$

$$\hat{R} = Q^{-1} D_g Q$$

Convergence criteria was decided on the basis of convergence criteria values which must exceed 95% and genetic parameters which tallies up to two decimals in successive iterations. Convergence criteria value (CC_i) was estimated as follows.

$$CC_i = 1 - \{ \|G_i - G_{i-1}\| / \|G_i\| \}, \text{ where } i = i^{\text{th}} \text{ iteration}$$

After attaining the convergence criteria, matrices were used for estimation of genetic parameters. LOTUS 2.2 package was used for calculations.

RESULTS AND DISCUSSION

In the present study, to evaluate all the five traits simultaneously, five trait combination model has been

analysed. The estimates of genetic parameters have been reported to vary with the number of traits analysed (Lin and Lee, 1986). So to compare the estimates obtained from different combinations, two sets of three trait combinations were also considered for REML analysis.

Three traits combinations

Two different combinations of three traits were analysed. In first combination production traits (FLL and ADY) and in second combination reproduction traits (AFC and FSP) were analysed along with FLMY. Since the first lactation milk yield is the most important economic trait, it was kept common in both combinations. Genetic parameters of FLMY, FLL and ADY traits under first three trait combination are presented in Table 1. The heritability of FLMY was found to be low which was in agreement with the findings reported by Beaumont (1989) in Montbeliarde dairy cattle, Kaps and Posavi (1991) in Holstein-Friesian and Dahlin et al. (1998) in Sahiwal cattle. Van Vleck et al. (1988), Chauhan and Hayes (1991), and Albuquerque et al. (1995) all in Holstein cattle and Chauhan (1995) in Haryana cattle reported higher heritability. Low heritability estimate was observed for FLL. Raheja (1993) reported almost similar heritability in Murrah buffalo. ADY also revealed low estimate of heritability. Hossain et al. (2002) reported medium heritability estimate for this trait in Red Sindhi cattle. The low estimates of heritability of these three production traits may be due to the genetic factors regulating lesser additive gene action. The genetic correlations between production traits were significantly high and positive which indicate simultaneous improvement in other traits while selecting any one of them. The phenotypic correlation of FLMY with FLL was high and with ADY, it was medium. This might be due to higher influences of common environmental effect controlling environmental correlation. The phenotypic correlation between FLL and ADY was negative and low.

In the second three trait combination, FLMY, AFC, and FSP were analyzed and the heritability and genetic and phenotypic correlation obtained were presented in Table 2. The heritability of FLMY was medium. The result was in consonance with the findings of Van Vleck et al. (1988) and

Table 2. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) from three traits restricted maximum likelihood analysis

Trait	First lactation milk yield	Age at first calving	First service period
First lactation milk yield	0.274±0.173	-0.120±0.376	0.225±0.423
Age at first calving	0.057±0.059	0.506±0.233	0.365±0.331
First service period	0.289±0.057	0.123±0.059	0.274±0.172

Chauhan and Hayes (1991) in Holstein cattle. The estimate of heritability for AFC was high, suggesting that sufficient variability is available in this trait for improvement through individual selection. Estimate reported by Chauhan and Naraian (1993) in Haryana cattle was higher than the present estimate. The estimate of heritability for FSP was medium. Mantysaari (1989) reported low, while, Jain and Sadana (2000) reported near to zero heritability estimate for FSP in Finnish Ayrshire cattle and in Murrah buffalo, respectively. Low and negative genetic correlation was observed between FLMY and AFC. Raheja (1994) also reported similar findings in Friesian×Haryana and Friesian×Sahiwal crossbred cattle, while, high genetic correlation was reported in Holstein cattle (Ertuqrul et al., 2002). However, the result suggests that the selection of animals for decreasing the age at first calving will improve milk yield in first lactation. The genetic correlation between FLMY and FSP was medium. Jain and Sadana (2000) reported negligible genetic correlation between the two traits in Murrah buffalo. Genetic correlation between the two reproduction traits (AFC and FSP) was positive and high. On the contrary negligible genetic correlation between these two traits, considering three trait model, was reported by Jain and Sadana (2000) in Murrah buffalo. There was very low phenotypic correlation between FLMY and AFC. The result was in agreement with the findings of Ertuqrul et al. (2002) in Holstein cattle. On the contrary, Chauhan and Naraian (1993) reported high estimate in Haryana cattle. The phenotypic correlation between FLMY and FSP was medium. Jain and Sadana (2000) reported negligible phenotypic correlation between the two traits.

Five traits combination

The REML technique was applied to analyse all five traits simultaneously. For evaluation of all the five traits, five trait model was more efficient in terms of computer time than the analysis of two sets of three trait combinations. Heritability of FLMY was medium and is in agreement with the findings reported by Van Vleck et al. (1988) and Chauhan and Hayes (1991) both in Holstein cattle, while Chauhan and Narain (1993) reported high estimate of heritability for FLMY in Haryana cattle. The heritability estimate for FLL was found to be low. Raheja (2000) reported almost similar heritability in Murrah buffalo with the six trait REML analysis. The ADY revealed low heritability suggesting its improvement through accurate recording of the daily milk yield and improvised managerial practices. Medium heritability estimate was reported by Hossain et al. (2002) in Red Sindhi cattle. High estimate of heritability was found for AFC. The result suggests that there is lot of scope for improvement of this

(1993), in Haryana cattle, reported higher than the present heritability estimate, while, low heritability estimate was reported by Jain and Sadana (2000) and Raheja et al. (2000) in Murrah buffalo. The heritability of FSP was medium. Montysaari (1989) reported low estimate of heritability in Finnish Ayrshire cattle.

Genetic correlations between production traits (FLMY, FLL and ADY) were high and positive. This indicates increase in first lactation length and average daily yield will definitely increase first lactation milk yield. The genetic correlation between FLMY and FLL in Holstein cattle reported by Ertuqrul et al. (2002) was low. FLMY had low and negative genetic correlation with AFC. The result was in agreement with the findings of Raheja (1994) in Friesian ×Haryana and Friesian×Sahiwal crossbred cattle, while, high genetic correlation between the two traits was reported by Ertuqrul et al. (2002) in Holstein cattle. Very low genetic correlation was found between FLMY and FSP, which was in consonance with the findings of Jain and Sadana (2000) in Murrah buffalo. The genetic correlation of FLL with ADY was high, while, with AFC it was low. Ertuqrul et al. (2002) reported low correlation between FLL and AFC, in Holstein cattle, which was in agreement with the present finding. FLL showed high genetic correlation with the FSP. ADY showed low genetic correlation with AFC and high with the FSP. The genetic correlation of AFC with FSP was low and was in agreement with the findings of Jain and Sadana (2000) in Murrah buffalo. Phenotypic correlation of FLMY and FLL was high and positive suggesting that higher FLMY was due to higher FLL. Almost similar findings was reported by Dahlin et al. (1998) in Sahiwal cattle, while, Raheja (1993) reported little lower estimate in Murrah buffalo. The phenotypic correlation of FLMY with ADY was medium. FLMY was lowly correlated with AFC. The result was in agreement with the findings of Ertuqrul et al. (2002) in Holstein cattle, while, Chauhan and Naraian (1993) reported high estimate of phenotypic correlation in Haryana cattle. The phenotypic correlation between FLMY and FSP was medium. Jain and Sadana (2000) reported negligible phenotypic correlation between the two traits in Murrah buffalo. Low and negative estimate of phenotypic correlation was found between FLL and ADY, while low and positive estimate was detected between FLL and AFC. High phenotypic correlation was observed between FLL and FSP. This may be due to the fact that some variation in milk is due to the variation in service period. ADY revealed negligible correlation with AFC, while low and negative phenotypic correlation was observed with FSP. The estimate of phenotypic correlation between the traits AFC and FSP was low. Jain and Sadana (2000) reported negligible phenotypic correlation between the two traits.

trait through individual selection. Chauhan and Naraian

Table 3. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) from five traits restricted maximum likelihood analysis

Trait	First lactation milk yield	First lactation length	Average daily yield	Age at first calving	First service period
First lactation milk yield	0.238±0.162	0.722±0.260	0.571±0.387	-0.034±0.417	0.042±0.469
First lactation length	0.674±0.044	0.160±0.139	0.540±0.459	0.046±0.470	0.382±0.454
Average daily yield	0.302±0.056	-0.024±0.059	0.136±0.132	0.095±0.493	0.336±0.498
Age at first calving	0.061±0.059	0.124±0.059	0.0007±0.059	0.409±0.209	0.094±0.404
First service period	0.286±0.057	0.518±0.051	-0.058±0.059	0.124±0.059	0.259±0.168

Comparison between three traits and five traits combinations

The estimate of heritability of FLMY was found to be different in all the combinations, which was highest in the second three trait combination. The result indicated that the heritability estimate may vary under models with different sets of combinations of traits depending upon the magnitude of association among the traits being considered. Heritability estimate of FLL was found to be high for five trait combination. There was little change in the estimate of heritability of ADY, being higher for three trait combination. For AFC, the estimate of three trait combination was higher than five trait combination, both combinations revealed high heritability estimate. The estimate of heritability of FSP was medium in both combinations, being little higher in five traits combination. The genotypic correlation between FLMY and FLL was higher in five traits combination. There was a vast difference in the estimates of genotypic correlation between FLMY and FSP in both the combinations. It was medium for three trait combination and low for five trait combination. Same trend of result was observed for genotypic correlation between AFC and FSP. The results suggest that REML analysis account for all inter-relationship among all the traits in estimating genetic parameters. This result supports the findings of Raheja et al. (2000) and Jain and Sadana (2000). On the contrary to the estimates of heritability and genotypic correlation, negligible changes were observed in the estimates of phenotypic correlation among the traits under three and five traits combination. Raheja et al. (2000) reported variation in the estimates of phenotypic correlation due to different combinations of traits. The result thus indicated that the estimates of heritability and genetic correlation varied depending upon the combination of traits included in a multi-trait model analysis. Therefore depending upon the goal of a breeding programme, model with appropriate traits combination should be used. In sire evaluation programmes, traits included in the multi-trait analysis should correspond to the traits of interest in the breeding goals. The estimates from different analysis leads to the conclusion that selection for improving first lactation milk yield would also increase the first lactation length and

average daily yield and reduce the age at first calving. Efforts must be made to improve managerial practices for obtaining maximum yield. There are high prospects of improvement of reproduction traits through genetic and non-genetic means.

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