



Estimation of Genetic Parameters of First Lactation and Life Time Traits Using Sire Model and Animal Model in Crossbred Cattle

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ABSTRACT

Data for the present investigation were collected from the history sheet of crossbred cattle maintained at the instructional dairy farm of G.B. Pant University of Agriculture and Technology, Pantnagar. The data pertained to 1029 crossbred cattle from 107 sires were distributed over a period of 49 years from 1966 to 2014. The overall least-squares mean of first lactation traits viz. AFC, FLMY, FLP, FDP, and FCI was estimated to be 1198.22 ± 9.78 days, 2857.00 ± 38.76 kg, 334.46 ± 3.05 days, 119.90 ± 3.87 days, and 488.02 ± 4.26 , respectively. The lifetime milk yield and lifetime lactation length were estimated as 10554.32 ± 244.67 kg. and 1133.79 ± 18.91 days respectively. The sire effect was significant on all the first lactation and lifetime traits, except the first lactation period. In contrast, different genetic groups were found to have no significant influence on all the traits. The season of calving was also found non-significant influence on all the traits. The period of calving was found to have a significant influence on all the traits except the first lactation period. The heritability estimates of different first lactation traits were observed from low to high. Estimates of h^2 obtained from multiple traits analysis using the animal model were higher than the sire model. The estimates of genetic and phenotypic correlations were obtained from analysis using sire and animal models, estimates obtained from both sire and animal models indicated almost the same trend.

HIGHLIGHTS

- The least-squares means and heritability of first lactation traits and life time traits were estimated
- Estimates of h^2 obtained from multiple traits analysis using the animal model were higher than the sire model.

Keywords: Crossbred Cattle, First Lactation Milk Yield, Life Time Traits, Animal model, sire model, Heritability

The improvement in indigenous cattle breeds for milk production through the selection and grading up has not been effective up to the desired levels. Considering the need for the large and rapid increase in milk production, crossbreeding of local cattle with exotic dairy breeds was therefore thought to be the only option. The potential for genetic improvement in a trait largely depends upon genetic variation existing in a population of interest. The variability for a particular trait in a population is measured by heritability estimates of traits under given environmental conditions. Variance and covariance are of prime importance to the breeder for estimating the genetic parameters and then utilizing these estimates for the selection of animals. The selection of dairy bulls

using conventional methods (such as the contemporary comparison of sire evaluation) has long been carried out under Indian conditions. These methods of sire evaluation do not take into account the relationships between the individuals of the population on which observations have been made (Sun *et al.*, 2010). Therefore, the use of advanced linear models needs to be carried out for accurate estimation of breeding values (BVs) giving emphasis to

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the relationship between the individuals of the population. Both the sire and animal models include the numerator relationship matrix (NRM), which takes into account the relationship and the inbreeding coefficient of the individuals of the population. However, in the sire model, it is assumed that the mates are of equal merit which could result in biased estimates of BVs (Mrode, 2005). Estimates of genetic parameters are needed for the prediction of breeding values and planning of selection strategies for desired genetic advancement with this object in view, the present investigation was conducted for estimating the genetic and phenotypic parameters of first lactation and lifetime performance traits.

MATERIALS AND METHODS

The data for the present study were collected from history sheets of crossbred cattle maintained at Instructional dairy farm, Nagla, G.B. Pant University of Agriculture and Technology, Pantnagar. The data pertained to 1029 crossbred cattle from 107 sires were distributed over a period of 49 years from 1966-2014. Cows with abnormal and incomplete records were excluded from the study. Cows with abnormal and incomplete records were excluded from the study. Only the sires having records on at least 5 daughters were included in the present study. The records of only those animals with known pedigree and normal lactation were considered. The lactation records of less than 150 days were considered abnormal and were not included in the analysis. The total duration of the present study was divided into 10 periods out of which 9 periods are of five years each and period 10 is of 4 years. Each year was divided into three seasons namely winter (November-February), summer (March-June), and rainy (July – October). In order to classify the data for different genetic groups, periods and seasons of calving were considered for all the traits. The traits considered in the present study were age at first calving, first lactation period, first dry period, first calving interval, first lactation milk yield, lifetime milk yield, and lifetime lactation yield.

Statistical analysis

Records on various first lactation and lifetime traits of crossbred cattle being in non-orthogonal nature were analyzed by the GLM procedure of the SAS program

(version 9.1, 2003) was used to determine the fixed factors affecting the studied traits according to the following model:

$$Y_{ijklm} = m + S_i + P_j + G_k + M_l + e_{ijklm} \quad (\text{Model 1})$$

where,

Y_{ijklm} = the observation of m^{th} progeny of i^{th} sire of the j^{th} period of the k^{th} season and l^{th} genetic group, m = population mean; S_i = random effect of i^{th} sire ($i = 1, 2, \dots, 107$); P_j = fixed effect of period of calving ($j = 1, 2, \dots, 10$); G_k = fixed effect of season of calving ($k = 1, 2, 3$); M_l = fixed effect of genetic group ($l = 1, 2, \dots, 9$); e_{ijklm} = random error NID (0, error)

The SAS statistical package (SAS 1985) and the method of unequal subclass analysis of variance were used to test the significance of the fixed effects and random effects.

Multiple traits analyses using animal and sire models were used to estimate heritability, and genetic and phenotypic correlation coefficients by (MTDFREML) proposed by Boldman *et al.*, (1995). The following linear animal model was used for the studied traits.

$$Y = X\beta + Za + e \quad (\text{Model 2})$$

Where,

Y = is a vector of observations for the studied traits; X = is the incidence matrix for the fixed effects; β = is the vector including the overall mean and the fixed effects; Z = is the incidence matrix for random effects; a = is the vector of the direct genetic effect of the animal where $\text{Var}(a) = A\sigma^2a$ where A is the numerator of the relationship matrix of animals, and e = is a vector of random residuals normally and independently distributed with zero mean and variance $I\sigma^2e$.

The following linear sire model was used for the studied traits.

$$Y = X\beta + Zs + e \quad (\text{Model 3})$$

Where,

s = is the vector of the direct genetic effect of sire and other terms in the model are defined as in model 2.

RESULTS AND DISCUSSION

Mean and standard errors for first lactation and lifetime traits are presented in Table 1. The overall least-squares mean of first lactation traits viz. AFC, FLMY, FLP, FDP, and FCI, were estimated to be 1198.22 ± 9.78 days, 2857.00 ± 38.76 kg, 334.46 ± 3.05 days, 119.90 ± 3.87 days, and 488.02 ± 4.26, respectively. These estimates are in close agreement with those reported by Lodhi *et al.*, (2016) and Girimal *et al.*, (2020). The lifetime milk yield and lifetime

lactation length were estimated as 10554.32 ± 244.67 kg, and 1133.79 ± 18.91 days respectively. Various researchers have also reported similar results in crossbred cattle (Lodhi *et al.*, 2016; Ambhore *et al.*, 2017; Salem and Hammoud, 2019; Girimal *et al.*, 2020).

The least-squares analysis of variance to estimate different non genetic effects are presented in Table 2. The least-squares analysis of variance showed a significant effect of sire on AFC, FLMY, FDP, FCI, and LTMY and LTL

Table 1: Least Squares Means with S.E. For First Lactation and lifetime Production traits

Source	n	AFC Mean±SE	FLMY Mean±SE	FLP Mean±SE	FDP Mean±SE	FCI Mean±SE	LTMY Mean±SE	LTL Mean±SE
Overall mean	1029	1198.22 ± 9.78	2857.00 ± 38.76	334.11 ± 3.05	119.90 ± 3.87	448.02 ± 4.26	10554.32 ± 244.67	1130.79 ± 18.91
GENETIC GROUP								
G ₁ (J × S)	184	1159.48 ± 22.19	2661.72 ± 87.97	334.59 ± 6.93	122.09 ± 8.78	450.61 ± 9.66	9287.21 ± 555.31	1063.78 ± 1147.99
G ₂ (HF × S)	47	1185.33 ± 32.73	3223.66 ± 129.72	354.41 ± 10.22	127.26 ± 12.94	475.63 ± 14.24	12054.57 ± 818.86	1190.95 ± 1315.13
G ₃ (RD × S)	45	1208.02 ± 33.52	2939.13 ± 132.85	316.11 ± 10.47	96.49 ± 13.23	406.44 ± 14.59	11663.74 ± 838.64	1158.09 ± 1285.27
G ₄ (J × R)	64	1135.65 ± 30.89	2550.58 ± 122.42	322.12 ± 9.64	108.59 ± 12.21	425.27 ± 13.44	9554.94 ± 772.79	1123.55 ± 1240.75
G ₅ (HF × RD × S)	128	1199.22 ± 18.84	2923.40 ± 74.68	344.885 ± 5.88	136.86 ± 7.45	475.77 ± 8.20	9945.63 ± 471.44	1069.36 ± 1140.85
G ₆ (HF × J × R)	113	1206.41 ± 20.60	2934.57 ± 81.63	333.634 ± 6.43	127.61 ± 8.14	455.18 ± 8.96	10384.46 ± 515.31	1089.43 ± 1167.58
G ₇ (RD × J × R)	84	1236.20 ± 25.44	2643.59 ± 100.85	321.49 ± 7.94	116.29 ± 10.06	431.63 ± 11.07	9627.70 ± 636.62	1154.12 ± 1250.66
G ₈ (HR × RD × J × S)	113	1196.63 ± 25.39	2851.19 ± 100.65	339.89 ± 7.93	108.51 ± 10.04	442.52 ± 11.05	14023.32 ± 635.33	1404.74 ± 1501.09
G ₉ (RD × J × F × S)	251	1257.013 ± 16.74	2985.16 ± 66.35	339.84 ± 5.23	135.37 ± 6.62	469.14 ± 7.29	8447.34 ± 418.82	923.12 ± 986.64
SEASON								
S ₁ (Rainy)	346	1204.72 ± 13.03	2861.37 ± 51.65	330.08 ± 4.07	119.17 ± 5.15	443.72 ± 5.67	10220.013 ± 326.01	1123.93 ± 25.19
S ₂ (Winter)	387	1190.95 ± 12.62	2804.71 ± 50.04	336.667 ± 3.94	126.06 ± 4.99	457.46 ± 5.49	10714.65 ± 315.88	1122.47 ± 24.41
S ₃ (Summer)	296	1199.00 ± 14.27	2904.91 ± 56.56	335.58 ± 4.46	114.46 ± 5.64	442.88 ± 6.21	10728.31 ± 357.01	1145.98 ± 27.59
PERIOD								
P ₁ (1966-1970)	59	1087.61 ± 30.41	2864.38 ± 120.54	300.87 ± 9.50	103.48 ± 12.03	404.35 ± 13.24	13191.43 ± 760.93	1287.34 ± 58.81
P ₂ (1971-1975)	226	1162.86 ± 17.71	2807.20 ± 70.21	318.55 ± 5.53	119.80 ± 7.01	438.52 ± 7.71	11354.68 ± 443.20	1233.79 ± 34.251
P ₃ (1976-1980)	158	1156.27 ± 17.03	2582.01 ± 67.49	328.50 ± 5.32	144.41 ± 6.73	472.95 ± 7.41	8299.57 ± 426.06	949.14 ± 32.93

P ₄ (1981-1985)	65	1308.27 ±26.57	2634.26 ±105.33	330.16 ±8.30	122.38 ±10.51	452.34 ±11.57	7900.31 ±664.89	1021.08 ±51.38
P ₅ (1986-1990)	53	1364.11 ±28.71	2241.54 ±113.78	333.30 ±8.96	111.84 ±11.35	444.92 ±12.49	10676.07 ±718.24	1420.03 ±55.51
P ₆ (1991-1995)	119	1331.08 ±22.06	2583.34 ±87.44	344.46 ±6.89	147.31 ±8.72	491.68 ±9.60	12172.43 ±551.97	1344.52 ±42.66
P ₇ (1996-2000)	122	1303.92 ±23.55	2966.60 ±93.35	341.35 ±7.35	145.56 ±9.31	487.15 ±10.25	11819.44 ±589.27	1151.98 ±45.54
P ₈ (2001-2005)	116	1059.94 ±25.06	2901.87 ±99.83	314.78 ±7.82	104.22 ±9.91	418.74 ±10.91	10248.09 ±629.96	1020.89 ±48.45
P ₉ (2005-2010)	66	1450.97 ±33.51	3140.28 ±132.83	344.63 ±10.46	92.17 ±13.25	436.57 ±14.58	8894.17 ±838.51	800.23 ±64.80
P ₁₀ (2011-2014)	45	1110.18 ±36.27	3848.51 ±143.78	384.48 ±11.33	107.80 ±14.35	432.99 ±15.79	10987.06 ±907.63	1078.94 ±70.14

Table 2: Least square analysis of variance for first lactation and lifetime traits

Source of Variance	d.f.	Mean Sum of Square (MS Value)						
		AFC	FLMY	FLP	FDP	FCI	LTMY	LTL
Sire	70	73365.08*	1155825.03**	4011.84	8681.10*	12014.57**	62792964.56**	331703.92**
Genetic group	8	91669.84	490528.29	4119.49	3422.99	9904.97	17928894.78	181654.56
Season	2	8245.69	229227.02	5903.68	6233.03	21067.96	26315248.46	110105.87
Period	9	117984.49*	1291697.53*	4988.51	15034.79*	26781.94**	145291843.42**	653693.05**
Error	857	53394.44	602681.23	3904.69	6327.39	7474.91	22165453.95	131532.66

**P<0.01, *P<0.05.

AFC = Age at First Calving; FLMY = First Lactation Milk Yield; FLP = First Lactation Period, FCI = First Calving Interval; FDP = First dry period, LTMY = Lifetime Milk Yield; LTL = Lifetime Lactation length.

traits revealed that superior sire could be used effectively for the improvement of all these traits. While the non significant effect was observed on FLP.

In the present study, the different genetic group was found to have no significant influence on all the traits under study. The result indicates that there is no statistically significant difference among the different crosses under the study. These findings were in close agreement with the various other reports (Lodhi *et al.*, 2016; Ambhore *et al.*, 2017; Salem and Hammoud, 2019; Girimal *et al.*, 2020).

The effect of season was found to have a non-significant influence on all the first lactation and lifetime Production traits. A similar non-significant effect of season of calving, results were also reported by was reported by other researchers (Lodhi *et al.*, 2016; Ambhore *et al.*, 2017; Salem and Hammoud, 2019; Girimal *et al.*, 2020).

The period of calving significantly influenced all first lactation and lifetime production traits. The present

results are in close agreement with the reports. The mean performance of age at first calving was observed lowest in the first period P₈ and highest in period P₉. The mean performance of the first lactation milk yield was observed highest in period P₁₀ and it was lowest in period P₅ of calving. The mean performance of the first lactation period was observed highest in period P₁₀ and it was lowest in the period P₁ of calving. The mean performance of the first dry period was observed highest in the period P₆ and it was lowest in the period P₉ of calving. The mean value of the first calving interval was observed highest for the sixth period and it was lowest in the period P₁ of calving. These results are in close agreement with the findings of Mandal and Sachdeva (2001) and Lodhi *et al.*, (2016).

The mean value of lifetime milk yield was observed highest for the first period. The mean value of total lactation length was observed highest for the fifth period. However, no consistent trend was found, fluctuations being observed over the period of calving. The variability in all the traits

over the periods might be due to differences in management practices followed during different periods of time. These results are in close agreement with the findings of other workers (Lodhi *et al.*, 2016; Ambhore *et al.*, 2017; Salem and Hammoud, 2019; Girimal *et al.*, 2020).

The heritability estimates for AFC, FLMY, FLP, FDP, FCI, LTMY and LTLL were observed as 0.088 ± 0.066 , 0.290 ± 0.072 , 0.070 ± 0.070 , 0.129 ± 0.074 , 0.204 ± 0.080 , 0.349 ± 0.014 and 0.327 ± 0.014 , respectively by Animal Model. The heritability estimates by Sire Model for AFC, FLMY, FLP, FDP, FCI, LTMY and LTLL were observed as 0.011 ± 0.013 , 0.151 ± 0.023 , 0.101 ± 0.039 , 0.037 ± 0.020 , 0.059 ± 0.023 , 0.218 ± 0.019 and 0.256 ± 0.009 , respectively.

In general, the heritability estimated for the first lactation and lifetime lactation traits under the present study was observed low, which revealed less additive genetic variability is existing and traits can be improved through better environmental and management practices for particular traits. The genetic and phenotypic correlations

among all the first lactation and lifetime production traits were observed below to high. These estimates are in close agreement with those reported by Lodhi *et al.*, (2016) in crossbred cattle. Higher estimates of heritability than the present study were reported by Shahi *et al.*, (2010), Chaudhary *et al.*, (2013), Kumar *et al.*, (2016) and Kumar *et al.*, (2017).

In Animal Model, the age at first calving had positive genetic correlations with FLP, LTMY, and LTLL While, negative genetic correlation of AFC with FLMY, FDP, and FCI. The negative genetic correlation indicated that higher AFC will lead to lower FLMY, FDP, and FCI. The AFC had a positive and very low phenotypic correlation with FLMY. While negative phenotypic correlations of AFC were observed with FLP, FCI, FDP, LTMY, and LTLL, which indicate that higher AFC will lead to lower FLP, FCI, FDP, LTMY, and LTLL on the phenotypic scale. FLMY had a positive genetic correlation with all traits except LTLL. FLMY had positive phenotypic correlations with FLP, FCI, LTMY, and LTLL. Negative phenotypic correlations of FLMY with FDP indicate that higher

Table 3: Estimation of Heritability by Animal Model and Sire Model of First Lactation and Lifetime Production traits in Crossbred Cattle

Sl. No.	Traits	Animal Model	Sire Model
		Heritability ($h^2 \pm S.E$)	Heritability ($h^2 \pm S.E$)
1	AFC	0.088 ± 0.066	0.011 ± 0.013
2	FLMY	0.290 ± 0.072	0.151 ± 0.023
3	FLP	0.070 ± 0.070	0.101 ± 0.039
4	FDP	0.129 ± 0.074	0.037 ± 0.020
5	FCI	0.204 ± 0.080	0.059 ± 0.023
6	LTMY	0.349 ± 0.014	0.218 ± 0.019
7	LTLL	0.327 ± 0.014	0.256 ± 0.009

Table 4: Genetic Correlations (below diagonal) and Phenotypic Correlations (above diagonal) among Various First lactation and life time Production Traits Estimated by Animal Model in Crossbred Cattle

Sl. No.	Traits	AFC	FLMY	FLP	FDP	FCI	LTMY	LTLL
1	AFC	—	0.038 ± 0.030	-0.035 ± 0.032	$-0.005 \pm 0.032^{**}$	$-0.020 \pm 0.032^{**}$	$-0.082 \pm 0.032^*$	$-0.121 \pm 0.031^{**}$
2	FLMY	$-0.112 \pm 0.043^*$	—	$0.670 \pm 0.017^{**}$	$-0.087 \pm 0.032^{**}$	$0.302 \pm 0.029^{**}$	$0.281 \pm 0.024^{**}$	0.102 ± 0.025
3	FLP	0.202 ± 0.530	0.284 ± 0.273	—	$-0.091 \pm 0.032^*$	$0.502 \pm 0.024^{**}$	$0.149 \pm 0.029^{**}$	$0.154 \pm 0.029^{**}$
4	FDP	-0.410 ± 0.468	0.210 ± 0.325	0.237 ± 0.564	—	$0.674 \pm 0.018^{**}$	$-0.088 \pm 0.032^{**}$	$-0.118 \pm 0.032^{**}$
5	FCI	-0.135 ± 0.387	0.319 ± 0.233	$0.797 \pm 0.297^*$	$0.757 \pm 0.186^{**}$	—	0.034 ± 0.032	0.011 ± 0.032
6	LLMY	0.555 ± 0.349	0.137 ± 0.080	-0.163 ± 0.319	0.065 ± 0.287	-0.109 ± 0.225	—	$0.770 \pm 0.012^{**}$
7	LTLL	0.590 ± 0.347	-0.120 ± 0.00	-0.031 ± 0.297	0.024 ± 0.283	-0.038 ± 0.222	$0.930 \pm 0.047^{**}$	—

Table 5: Genetic Correlations (below diagonal) and Phenotypic Correlations (above diagonal) among Various First lactation and life time Production Traits Estimated by Sire Model in Crossbred Cattle

Sl. No.	Traits	AFC	FLMY	FLP	FDP	FCI	LTMY	LTLL
1	AFC	—	0.061 ±0.033	-0.028 ±0.033	-0.002 ±0.032**	-0.011 ±0.032**	-0.072 ±0.032*	-0.108 ±0.034**
2	FLMY	0.639±0.474	—	0.620±0.028**	-0.096 ±0.034**	0.286 ±0.031**	0.352±0.023**	0.141 ±0.025
3	FLP	0.327±0.557	0.157±0.211	—	-0.110 ±0.034*	0.491 ±0.027**	0.217±0.034**	0.218 ±0.037**
4	FDP	-0.341±0.624	-0.008±0.301	-0.131±0.345	—	0.682 ±0.018**	-0.065±0.034**	-0.085 ±0.036**
5	FCI	0.065±0.528	0.279±0.227	0.382±0.250	0.550±0.241*	—	0.079 ±0.034	0.051 ±0.036
6	LLMY	0.658±0.494	0.544±0.043**	0.546±0.157**	0.169±0.274	0.397±0.197*	—	0.787±0.011**
7	LTLL	0.536±0.470	0.287±0.000	0.573±0.161**	0.196±0.273	0.364±0.204	0.960±0.017**	—

Significant** P<0.01,*P<0.05.

FLMY leads to lower FDP. The genetic correlations of FLP with lifetime production traits were found to be negative. The FLP had positive phenotypic correlations with all traits except FDP. The first dry period had positive genetic correlations with FCI with higher magnitude, LTMY, and LTLL with lower magnitude, while negative phenotypic correlations with LTMY and LTLL. The FCI had negative genetic and positive phenotypic correlations with LTMY and LTLL. Lifetime milk yield had highly positive genetic and phenotypic correlations with LTLL.

In the Sire Model, the age at first calving had positive genetic correlations with all traits except FDP. The AFC had negative and very low phenotypic correlations with all traits except FLMY. This indicates that higher AFC will lead to higher FLMY on the phenotypic scale. FLMY had a positive phenotypic and genetic correlation with all traits except FDP. The genetic and phenotypic correlation FLP with all traits was found positive except FDP. The first dry period had positive genetic correlations with all traits. The FDP had positive phenotypic correlations with FCI, while LTMY and LTLL had a negative phenotypic correlation. The FCI had positive phenotypic and genetic correlations with LTMY and LTLL. Lifetime milk yield had highly positive genetic and phenotypic correlations with LTLL.

These correlations indicated that selection on the basis of AFC on the genotypic scale would bring desirable improvement in LTMY and LTLL. Since very genetic and phenotypic correlations were positive with a higher magnitude between lifetime traits, so the selection of cows for lifetime traits is desirable. It is, therefore, necessary to apply selection pressure on sire for bringing genetic improvement in a lifetime performance. It is also suggested that for improving the lifetime performance, sire should be selected on the basis of the age at first calving

(AFC) of their daughters. Similar trends of genotypic and phenotypic correlations were reported by Akhtar (1998), and Chaudhary *et al.*, (2013). Bajetha and Singh (2011) and Lodhi *et al.*, (2016).

CONCLUSION

The study concluded that the data presented in this paper identify not only the models of choice to be used in the analysis of first lactation and lifetime production traits of crossbred cattle but also showed the influence of fixed and random effects on the estimation of (co)variance components. Values of heritabilities for the traits are shown and their variation among models was important to define the most adequate animal model. Regarding the magnitude of genetic and phenotypic correlations, estimates obtained from both sire and animal models indicated almost the same trend in which these estimates were slightly higher using the sire model compared with that of the animal model. The results are shown here have to be verified in other populations of crossbreds, raised in other environments.

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