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Research article

EVALUATION OF SIRES USING ANIMAL MODELS FOR IMPROVEMENT OF FIRST LACTATION AND LIFE TIME PRODUCTION TRAITS IN MURRAH BUFFALOES

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ABSTRACT: The data spread over the period of 25 years for the present study. Data were obtained from the history sheets of 1312 Murrah buffaloes maintained at four military dairy farms of northern India viz. Ambala, Agra, Lucknow and Bareilly. The sires were evaluated for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits. The sires have been evaluated and ranked on the basis of solutions obtained through univariate and multivariate REML using animal model and BLUP value for sire effects under model 8. Less than half of the sires were superior to the population mean under BLUP1, BLUP2 and BLUP3. The superiority of the best sire (as per cent of the raw mean) were 8 % for the reproduction traits under BLUP1 but above 15% under BLUP2 and around 10% under BLUP3, for FLMY and HLMY, this superiority was around 11, 7 and 9% respectively. The responding values under BLUP1, were 19, 15 and 15% under BLUP2, 18, 14 and 6% under BLUP3. It was observed that top ranking sire for AFC (i.e. M-140) was same under BLUP1, BLUP2 and BLUP3 for FLMY (i.e. M-143) was same in BLUP 1 and BLUP2. In BLUP2 and BLUP3, around 50% animals were superior to the population mean for reproduction and production traits. The superiority of the best animal (as per cent of the raw means was above 13% under BLUP2 and BLUP3) for reproduction traits except WFC. But there values were 31, 18 and 21% (BLUP2) and 33, 23 and 25% (BLUP3) for FLMY, HLMY and FLP respectively. Rank correlation under different methods were highly significant and ranged from 0.697 (between model 8 and multivariate animal model for first lactation period) to 0.999 (between model 8 and unuvariate animal model for first service period). Rank correlations were above 0.973 for all the traits when sires were ranked by model 8 and univariate animal model. The rank correlations among methods with in traits were though highly significant (P<0.01), yet not perfect, revealed that the ranking of sires by different methods were not similar. The rank correlations among traits within method were low than among methods within traits within the method. From these results, it was observed that the range of sire effect, per cent sire superior to population mean and superiority of best sire/animal was more under BLUP1 and BLUP3 than BLUP1. Therefore, REML using animal model could be used to evaluate the animals along with their sires and dams.

Key words: Sire evaluation, Rank correlation, animal model, best linear unbiased prediction.

INTRODUCTION

In order to make rapid genetic progress in performance through selection for traits of economic importance in buffalo genotypes, selected animals must be chosen for their superior breeding value (The genetic worth of individuals as parent) [1, 3, 7]. There are many source of information, which can provide clues about an individual's breeding value. These include individual performance, family performance and combined performance of individual and family weighted appropriately [2, 3,7] after correction for known environment effects. The Conditions under which the use of these different sources of information are appropriate and well documented in the literature [3,7]. A point worth highlighting is that when heritability is low, combining individual and family performances, appropriately weighted, provides the maximum response to selection [3]. This is because the estimated breeding value of an individual using data from different relationships is more accurate than a single estimate from the individual alone [3, 7]. In practical animal breeding, multiple traits are usually measured on each individual to collect as much information as possible about its productivity. In genetic studies, multivariate estimation of (Co) variance components and genetic values for sire evaluation has recently been received considerable attention. In most of the cases, the breeding values of sires have been estimated using single trait models. However, now-a-days, there is a constant thrust to get best linear unbiased prediction (BLUP) evaluations using a single or multi trait animal model.

As per objectives under the present study the sires have been ranked on the basis of solution obtained through univariate and multivariate REML using animal model and BLUP value for sire effects under model 8 and find out rank correlations among sires/animals on the basis of BLUP values.

MATERIALS AND METHODS

The data spread over the period of 25 years for the present study. Data were obtained from the history sheets of 1312 Murrah buffaloes maintained at four military dairy farms of northern India viz. Ambala, Agra, Lucknow and Bareilly.

The animals with known pedigree and complete records on all target traits viz. weight at first calving, age at first calving, first lactation milk yield, herd life milk yield (first three lactations milk yield), first lactation period, first dry period, first calving interval and first service period were considered for the present study. The sires with less than 4 progenies had been deleted from the analysis.

Statistical Methodology

For the estimation of parameters and (co) variance components, least-squares analysis (LSA) and derivative free restricted maximum likelihood (DFREML) methods were employed. Data were subjected to LSMLMW and MIXMDL package of Harvey [4] under different models. Two models were considered to examine the effect of genetic and non-genetic factors on various first lactation traits and herd life milk yield.

Model 2

The model 2 considered was from LSMLMW and MIXMDL package of Harvey [4] which consists one set of cross classified non-interacting random effect. All eight traits were analyzed simultaneously, the model is as follows.

$$y_{ijklm} = u_c + s_i + Fj + p_k + s_l + e_{ijklm}$$

Where,

y_{ijklm} is observation on 1st progeny of ith sire of jth farm lth season in kth year.

u_c is the over all mean,s_i is the random effect of ith sire (i = 1, 2, ……., 122),F_j is the fixed effect of the jth farm (j = 1, 2, …, 4),p_k is the fixed effect of kth period of birth (k = 1, 2, …., 5),s_l is the fixed effect of lth season of birth,e_{ijklm} is the random error which is normally and independently distributed with mean 0 and variance $\sigma^2{}_e$.

The analysis was computed with the mixed model least squares program which utilizes the method 3 of Henderson [5].

Model 8

The model 8 considered was from LSMLMW and MIXMDL package of Harvey [4], non interacting random effect. The same model was fitted on all the traits and the traits were analyzed separately. The general formulation of the mixed model fitted is as follows.

$$y_{ijklm} = u_c + s_i + F_j + p_k + s_l + e_{ijklm}$$

Where, all the abbreviations are same as described in first model. The formulation of model in matrix notation is as follows.

$$Y = l\, u_c + xb + za + e$$

Where

l is the column vector of the means, u_c is an overall mean, b is the column vector of fixed effects.

a is a column vector of random effect,z is an incidence matrix of 0's and 1' s,x is an incidence matrix of 0' s, 1' s & -1's and x-x values for the discrete effects, and,e is a column vector of the random errors.

This model is same as first model, except the random effect may be correlated.

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In univariate analysis, all the traits under study were analyzed separately. The same model was fitted on all traits. The general formulation of the mixed model fitted is as follows.

$$y_{ijklm} = \mu + A_i + F_j + p_k + s_l + e_{ijklm}$$

Where,

Ai is random effect of ith animal and all the other abbreviations are same as described in earlier models. The formulation of general single trait animal model is matrix notation is as follows:

$$y = xf + z_a + e$$

Where,

y is a vector of Nxl records, f is a vector of fixed environmental effects of sex and year, and co variable was taken here,a is vector of breeding values for additive direct genetic effects fitted which is random, s is a N*N F design matrix for fixed effects with column ranks N*F*,z is a N* NR design matrix for random animal effects, where z = 1, and e is a vector of N random residual errors.

Multivariate model

In multivariate analysis, all the eight mentioned traits were taken simultaneously for analysis. The multi-trait animal model used to estimate parameters could be represented as follows.

$Yijklm = \mu + F_i + P_j + S_k + A_l + eijklm$

Where eijklm is the observation on the mth individual belonging to ith farm, jth period kth season and ith animal. **μ** is the overall mean ,$\mathbf{F_i}$ is the fixed effect due to ith farm (I = 1, 2, 3, 4),$\mathbf{P_j}$ is the fixed effect due to **jth** period (1, 2, 3, 4, 5),$\mathbf{S_k}$ is the fixed effect due to **kth** season (1, 2, 3, 4),$\mathbf{A_l}$ is the random effect due to animal
eijklm is the random error which is normally and independently distributed with mean 0 variance σ^2_e
The above multi trait animal model, in matrix notation, for 8 traits used, was
$Y = Xb + Zu + e$
Where,
Y is a vector of Nt* 1 of records (N number of animals with performance and t number of traits),b is the vector of fixed environmental effects of farm (1, 2, 3, 4 period (1, 2, 3, 4, 5), season (1, 2, 3, 4). No co variable was taken here .u is a vector of breeding values for additive direct genetic effects fitted which is random. e is a vector of N random residual errors, X and Z are incidence matrices relating the records to the effects of the model.

The starting values of sig a and sig e for interactions were taken from the result of model 2 analysis.
Assumptions of the model are
$E[y] = Xb$
$E[u] = E(e) = 0$
With variances
$Var(\mu) = G = A\#G_0$
$Var(e) = R = 1\# R_0$
Where,
Go is a matrix of covariances for additive genetic effect among traits.
Ro is a matrix of the residual covariance among trait.
1 represent identity matrix and # is Kronecker product

Three solutions for sire evaluation were used Best Linear Unbiased Prediction ($BLUP_1$) values of model 8 of Least squares analysis [4], univariate ($BLUP_2$) and multivariate ($BLUP_3$) solutions of REML using animal model [6], which utilized information from all the known relationship. Under univariate and multivariate and multivariate animal model no sire effect was fitted. The sire solutions was sorted out from the solution of all the animals used for comparison with BLUP values obtained under model 8. On the basis of these BLUP values sires were ranked.
Rank Correlation:
The spearman's rank correlation between BLUP values obtained by above methods was worked out [8] as follows.

$$r = \frac{1-{}^{6}\sum_i d_i^2}{(n-1)\, n\, (n+1)}$$

Where,
r is the rank correlation
n is the number of sires
d_i is the difference between rank of the sire ranked by two methods
The significance of the rank correlation was tested by students t-test as follows

$$t= r \sqrt{\ } (n-2) / (1- r^{2)} \quad \text{with n-2 degree of freedom}$$

RESULTS AND DISCUSSION

Sire evaluation under different models
Three solutions for sire evaluation were used. Best linear unbiased prediction (BLUP1), values of model 8, univariate (BLUP2) and multivariate (BLUP3) solutions of REML. All the methods were based on progeny testing; the BLUP2 and 3 were based on an animal model, which utilized information from all the known relationship. Under univariate and multivariate animal model, no sire effect was fitted. The sires were evaluated for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits.

A total of 122 sires were evaluated. The information on sire evaluation viz. per cent of sires with negative or positive sire effects, sire effect for the top and bottom ranking sires, and per cent superiority / inferiority of top bottom ranking sires under various methods are presented in Table -1-10

Weight at first calving

The estimated average WFC of 497.87 kg was used for BLUP1, BLUP2 and BLUP3. About half of the sires (50.82%) were superior to the population mean under BLUP1. The corresponding values were low under BLUP2 (49.18%) and BLUP3 (48.25%).

The range of sire effect for WFC were -4.933 to + 8.383, -16.804 to + 25.053 and -28.368 to + 34.038 respectively, under BLUP1, BLUP2 and BLUP3 (Table 1,2 and 3). The range of sire effects was much wider and higher under BLUP2 and BLUP 3 but lower and narrower in BLUP1. More than 50% animals were superior to the population mean. The superiority of the best sires (as per cent of the raw mean) were 1.68, 5.03 and 6.84, respectively under BLUP1, BLUP2, BLUP3 whereas corresponding values of inferiority of worst sire were -0.99, -3.38, and -5.70 . BLUP 3 had shown maximum value in terms of superiority and / or inferiority. The range of animal solution was -24.172 to + 24.383 and -33.177 to + 35.328 respectively, under BLUP2 and BLUP3. The superiority of the best animals (as per cent of the raw mean) were 4.90 and 7.10% respectively under BLUP2 and BLUP3 whereas corresponding values for inferiority of the worst animal were -4.86 and -6.66%. BLUP2 and BLUP3 had shown almost similar values in terms of superiority and / or inferiority of animal solutions. In BLUP2 and BLUP3, about 58% animals were superior to population mean.

The upper limit of sire effects for WFC was increased from 8.383 kg in the BULP1 solution to 25.053 kg in BLUP2 and 34.038 kg in BLUP 3 whereas the lower limits were reduced from -4.933 kg in BLUP1 to -16.084 kg in BLUP2 and 28.368 kg in BLUP3. The upper and lower limit of sire effects under BLUP 1 was almost 1/3 and 1/4, respectively of the BLUP2 and BLUP3 methods.

Age at first calving (AFC)

The estimated average AFC of 1276.05 days was used for BLUP1, BLUP2 and BLUP3 were found superior to the population mean under BLUP1. The corresponding values were low under BLUP2 (58.20%) and BLUP3 (57.03%).

The range of sire effect for AFC were -114.489 to + 245.649, -194.941 to + 396.116 and 210.376 to + 398.276 respectively under BLUP1, BLUP2 and BLUP3 (Table 1, 2 and 3). The range of sire effects was almost the same under BLUP2 and BLUP3 but low in BLUP1. More than 59% animals were superior to the population mean. The superiority of the best sire (as present of the raw mean) were -8.97, -15.28 and -16.49, respectively under BLUP1, BLUP2 and BLUP3, whereas corresponding values of inferiority of worst sire were 19.25, 31.04 and 31.21. BLUP 3 had shown maximum value in terms of superiority and /or inferiority. The range of animal solution was ± 564.472 to -177.676 and + 456.137 to -258.632 respectively under BLUP2 and BLUP3 (Table 8 and 10). The superiority of the best animal (as per cent of the raw mean) were -13.92% and -20.27% respectively under BLUP2 and BLUP 3, whereas corresponding values for inferiority of the worst animals were 44.24% and 35.75% BLUP3 had shown higher values in terms of superiority whereas BLUP2 had shown higher value in terms of inferiority of animals solutions. In BLUP2 and BLUP3, about 60% animals were superior to population mean (less AFC being desirable).

The upper limit of sire effects of AFC was decreased from -114.489 days in the BLUP1 solution to -194.941 days in BLUP2 and -210.376 days in BLUP3 whereas the lower limits were increased from 245.649 days in BLUP1 to 396.116 days in BLUP2 and 398.276 days in BLUP3. The upper and lower limit of sire effects under BLUP1 was almost 3/5 of BLUP2 and BLUP3 methods.

First lactation period (FLP)

The estimated average FLP of 306.74 days was used for BLUP1, BLUP2 and BLUP3. Less than half of the sires (48.36%) were superior to the population mean under BLUP1. The corresponding value were low under BLUP2 (42.62%) but observed higher under BLUP3 (62.30%).

The range of sire effect for FLP were -13.069 to + 27.463, -72.138 to + 47.835 and -9.649 to + 17.104 respectively under BLUP1, BLUP2 and BLUP3 (Table 1, 2 and 3). The range of sire effects was higher under BLUP2 and low BLUP1 and BLUP3. The superiority of the best sire (as per cent of the raw mean) were 8.95, 15.59 and 5.58 respectively under BLUP1, BLUP2 and BLUP3, whereas corresponding values of inferiority of worst sire were -4.26, -23.52 and -3.15, BLUP2 had shown maximum value in terms of superiority and / or inferiority. The range of animal solution was –69.0192 + 64.451 and -78.238 to -77.725 respectively, under BLUP2 and BLUP3.

The superiority of the best animal (as per cent of the raw mean) were 21.11% and 25.34% respectively under BLUP2 and BLUP3, whereas corresponding values for inferiority of the worst animal were 22.50% and 25.51%. BLUP2 and BLUP 3 had shown almost similar values in terms of superiority and / or inferiority of animal solution. In BLUP2 and BLUP3 about 45% animals were superior to population mean.

The upper limit of sire effects for FLP was observed to have increased from 27.463 days in the BLUP1 solution to 47.835 days in BLUP2 and 17.104 days in BLUP3, whereas the lower limits decreased from 13.069 days in BLUP1 to 72.138 days in BLUP2 and 9.649 days in BLUP3.

First dry period (FDP)

The estimated average FDP of 177.09 days was used for BLUP1, BLUP2 and BLUp3. Above half of sire (55.74%) were superior to the population mean under BLUP1. The corresponding values were almost similar under BLUP2 (54.10%) and higher under BLUP3 (60.66%). The range of sire effects for FDP was -19.694 to + 25.050, -32.449 to + 39.928 and -24.225 to + 73.702, under BLUP1, BLUP2 and BLUP3, respectively (Table 1,2 and 3). The range of sire effects was lowest under BLUP1 and highest under BLUP3. The superiority of the best sire (as per cent of the raw mean) -11.12, -18.32 and -13.68, respectively under BLUP1, BLUP2 and BLUP3 whereas corresponding values of inferiority of worst sire were +14.15, + 22.53 and + 4.62. BLUP2 showed maximum value in terms of superiority and / or inferiority. The range of animal solution was -29.016 to + 42.719 and -35.621 to 31.621 under BLUP2 and BLUP3 respectively (Table 8 and 10). The superiority of the best animal (as per cent of the mean) was -16.38% and -20.11%, respectively under BLUP2 and BLUP3 whereas corresponding values for inferiority of the worst animal were + 24.12% and + 17.86%. BLUP3 showed higher values in terms of superiority whereas BLUP 2 showed higher in terms of inferiority of animal solutions. The upper limits of sire effect for FDP was decreased from -19.694 days in BLUP1 solution to -32.449 days in BLUP2 and -24.225 days in the BLUP3 solution. Whereas the lower limits were increased from 25.050 days in BLUP1 to 39.928 days in BLUP2 and 73.072 days in BLUP3. The upper and lower limit of sire effects under BLUP1 was lowest than the BLUP2 and BLUP3 method.

First calving interval (FCI)

The estimated average FCI of 481.87 days was used for BLUP1, BLUP2 and BLUP3. More than half of the sire (52.46%) were superior to the population mean under BLUP1. The corresponding values were high under BLUP2 (54.92%) and low under BLUP3 (43.44%). The range of sire effect for FCI were -40-571 to + 42.701, -74.891 to + 83.599 and -203.010 to + 259.640 under BLUP1, BLUP2 and BLUP3, respectively (Table 4.15, 4.17 and 4.19). The range of sire effect was very high under BLUP3, but low in BLUP1 and BLUP2. The superiority of the best sire (as per cent of mean) were -8.42, -15.54 and -42.13 respectively under BLUP1, BLUP2 and BLUP3 whereas corresponding values of inferiority of worst sire were + 8.86, + 17.35 and + 53.88 BLUP had shown maximum value in terms of superiority and / or inferiority. The range of animal solution was -85.177 to +105.465 and -95.136 to + 111.527, respectively, under BLUP2 and BLUP3 (Table 4.21 and 4.23). The superiority of best animal (as per cent of raw mean) was -17.68% and -19.74% respectively under BLUP2 and BLUP3 whereas corresponding values for inferiority of the worst animal were 21.89% and 23.14%. BLUP2 and BLUP3 had shown almost similar values in terms of superiority and/or inferiority of animal solution. In BLUP2 and BLUP3 about 51% animals were superior to population mean.

The upper limit of sire effect of FCI decreased from -40.571 days in the BLUP1 solution to -74.891 days in BLUP2 and -203.010 days in BLUP3, whereas the lower limit increased from 42.701 days in BLUP1 to 83.599 days in BLUP2 and 259.640 days in BLUP3 solution.

First service period (FSP)

The estimated range of FSP, 179.55 days was used for BLUP1, BLUP2 and BLUP3. A little more than 50% of the sires (52.46%) were superior to the population mean under BLUP1. The corresponding values were almost similar under BLUP2 (53.28%) and lower under BLUP3 (44.26%). The range of sire effects for FSP were -30.989 to + 30.803, -39.007 to + 40.424 and -11.18 to ± 14.270 respectively, under BLUP1, BLUP2 and BLUP3 (Table 1,2 and 3). The range of sire effects was narrowest under BLUP3 and broadest under BLUP2. The superiority of best sires (as per cent of raw mean) were -17.26, -21.72 and -6.23, respectively under BLUP1, BLUP2 and BLUP3, whereas corresponding values of inferiority of worst sire were +17.16, + 22.51 and + 7.95. BLUP2 had shown maximum value in terms of superiority and or inferiority. The range of animals solution was -33.308 to + 56.872 and -38.328 to + 57.256 respectively, under BLUP2 and BLUP3. The superiority of the best animal (as per cent of the raw mean) were -18.55% and+ 31.67% respectively under BLUP2 and BLUP3, whereas corresponding values for inferiority of the worst animal were +31.67% and + 31.89%. BLUP3 had shown higher values in terms of superiority whereas BLUP2 and BLUP3 had shown almost similar values in terms of inferiority of animal solution. In BLUP2 and BLUP3 about 53% animals were superior to population mean.

The upper limit of sire effects for FSP was decreased from -30.989 days in the BLUP1 solution to -39.007 days in BLUP2 and -11.18 days in BLUP2 and 14.270 days in BLUP3. The upper and lower limits of sire effects under BLUP3 was lower than the BLUP1 and BLUP2 methods.

First lactation milk yield (FLMY)

The estimated average FLMY of 1761.57 kg was used for BLUP1, BLUP2 and BLUP3. Half of the sires (50.82%) were superior to the population mean under BLUP1. The corresponding values were lower under BLUP2 (49.18%) and BLUP3 (46.72%). The range of sire effect for FLMY were -312.369 to +195.035, -548.992 to + 337.595 and -373.579 to+ 329.507 respectively under BLUP1, BLUP2 and BLUP3 (Table 1,2 and 3). The range of sire was high under BLUP2, but low in BLUP1. The superiority of the best sire (as per cent of raw mean) were 11.07, 19.16 and 18.71 respectively under BLUP1, BLUP2 and BLUP3, whereas corresponding values of inferiority of worst sire were 17.73, 31.16 and 21.21. BLUP1 had shown minimum and BLUP2 maximum value in terms of superiority and/or inferiority. The range of animal solution was -506.762 to 553.254 and -365.237 to + 587.019, respectively under BLUP2 and BLUP3 (Table 7 and 9). The superiority of best animal (as per cent of raw mean) was 31.41% and 33.32% respectively under BLUP2 and BLUP3. Whereas corresponding values for inferiority of the worst animal were -28.77% and -20.73%. BLUP2 and BLUP3 had shown almost similar values in terms of superiority and BLUP3 had shown lower values in terms of inferiority of animal solution.

The upper limit of sire effects of FLMY was increased from 195.035 kg in the BLUP1 solution to 337.595 kg in BLUP2 and 329.507 kg in BLUP3, whereas the lower limit were decreased from -312.369 kg in the BLUP1 to -548.992 kg in BLUP2 and -373.579 kg in BLUP3 solution.

Table 1: Range of solution (LSC) of sire effect of WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under model 8

Traits	Best			Worst sire			% of sire with	
	Value	% of mean	Sire code	Value	% of mean	Sire code	+ve sire effect	-ve sire effect
WFC	8.383	1.68	Du-295	-4.933	-0.99	L-135	50.82	49.18
AFC	-114.489	-8.97	M-140	245.649	19.25	WL-818	40.98	59.02
FDP	-19.694	- 1.12	N-371	25.050	14.15	K-840	44.26	55.74
FCI	-40.571	- 8.42	H-58	42.701	8.86	SA-310	47.54	52.46
FSP	-30.989	- 7.26	H-58	30.803	17.16	M-143	47.54	52.46
FLMY	195.035	11.07	M-143	-312.369	-17.73	H-58	50.82	49.18
HLMY	399.829	7.10	SA-304	-443.946	-7.89	H-58	50.00	50.00
FLP	27.463	8.95	L-121	-13.069	-4.26	M-142	48.36	51.64

Table 2: Sire effect of ten top ranking sires for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under model 8

Rank	WFC		AFC		FDP		FCI	
1	2	3	4	5	6	7	8	9
1	Du-295	8.383	M-140	-114.489	N-371	-19.694	H-58	-40.571
2	NE-377	6.110	H-59	-86.664	M-138	-16.051	N-371	-31.976
3	M-142	5.144	Du-295	-80.830	M-142	-15.423	M-138	-31.849
4	SA-309	4.816	D-271	-77.994	D-271	-13.532	N-374	-31.384
5	M-145	4.368	NE-377	-77.557	N-374	-13.487	M-142	-29.031
6	A-103	4.151	N-371	-75.948	M-142	-13.475	D-27	-28.701
7	H-60	6.541	FL-54	-75.216	DL-285	-13.220	AS-105	-24.737
8	M-158	3.130	B-155	-65.082	F-52	-12.074	M-148	-23.213
9	M-146	2.977	H-58	-63.822	N-381	-11.179	F-52	-22.306
10	C-171	2.789	B-151	-63.079	J-72	-10.74	L-735	-22.054

Rank	FSP		FLMY		HLMY		FLP	
10	11	12	13	14	15	16	17	18
1	H-58	-30.989	M-143	195.035	NK-625	399.829	L-121	27.463
2	N-371	-29.325	L-137	177.059	NK-249	366.363	M-171	21.761
3	M-138	-24.205	L-122	157.681	CG-885	358.952	T-322	21.488
4	AS-105	-21.043	DL-272	157.456	T-322	354.573	L-135	18.579
5	F-52	-17.374	SH-311	152.996	M-171	351.840	NK-58	17.005
6	M-142	-16.976	S-306	152.313	DL-272	300.778	CG-885	16.807
7	BA-154	-16.125	NK-249	150.262	L-137	226.223	M-149	15.860
8	NK-65	-15.708	P-356	144.257	M-141	218.719	NK-249	15.798
9	MO-152	-15.296	CG-885	135.406	WL-818	218.026	G-55	15.263
10	B-155	-15.078	WL-818	134.181	M-146	217.210	WL_818	15.259

Table 3: Range of solution (LSC) of sire effect for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under univariate REML animal model

Traits	Best			Worst sire			% of sire with	
	Value	% of mean	Sire code	Value	% of mean	Sire code	+ve sire effect	-ve sire effect
WFC	25.053	5.03	Du-295	-16.804	-3.38	L-135	49.18	50.82
AFC	-194.941	-15.283	M-140	396.116	31.04	WL-818	41.80	58.20
FDP	-32.449	-18.32	N-371	39.928	22.53	N-371	45.90	54.10
FCI	-74.891	-15.54	H-58	83.599	17.35	SA-310	45.08	54.92
FSP	-39.007	-21.72	H-58	40.424	22.51	M-143	46.72	53.28
FLMY	337.595	19.16	M-143	-548.992	-31.16	H-59	49.18	50.82
HLMY	815.804	14.49	NK-625	-962.316	-17.09	H-58	50.00	50.00
FLP	47.835	15.59	L-121	-72.138	-23.52	H-58	42.62	57.38

Table 4 : Sire effect of ten top ranking sires for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under univariate REML animal model

Rank	WFC		AFC		FDP		FCI	
1	2	3	4	5	6	7	8	9
1	Du-295	25.053	M-140	-194.941	N-371	-32.449	H-58	-74.891
2	NE-377	21.346	Du-295	-148.207	M-142	-27.987	N-371	-61.789
3	SA-310	16.441	H-59	-133.238	M-138	-26.167	M-138	-60.987
4	M-142	14.954	D-271	-126.230	DL-285	-21.564	M-142	-59.023
5	M-145	14.129	NE-377	-122.829	D-271	-21.520	N-374	-57.303
6	A-103	14.047	FL-54	-121.182	N-374	-21.134	D-271	-54.292
7	H-60	12.023	N-371	-117.412	M-148	-20.254	AS-105	-46.281
8	M-146	10.936	B-151	-108.891	F-52	-19.453	F-52	-42.697
9	M-158	10.704	H-58	-104.108	N-381	-17.767	M-148	-39.097
10	J-71	9.581	BH-153	-102.066	J-72	-17.552	L-735	-37.839

Rank	**FSP**		**FLMY**		**HLMY**		**FLP**	
10	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**
1	N-371	-39.07	M-143	337.595	NK-625	815.804	L-121	47.835
2	H-58	-38.947	L-137	323.619	M-171	773.102	T-322	37.495
3	M-138	-32.264	DL-272	285.295	NK-249	760.436	M-171	35.912
4	AS-105	-27.349	L-122	266.194	CG-885	757.742	CG-885	30.401
5	M-142	-27.048	CG-885	266.021	T-322	747.606	L-135	30.189
6	BA-154	-23.896	S-306	260.738	DL-272	647.538	M-149	27.534
7	F-52	-21.987	SH-311	260.281	L-137	593.689	NK-58	26.887
8	A-103	-20.904	P-366	256.597	WL-818	472.583	NK-249	26.877
9	NK-65	-20.379	NK-249	256.356	P-356	462.101	G-55	24.622
10	MO-152	-19.202	M-171	230.993	M-141	456.832	WL-818	23.929

Table 5 : Range of solution (LSC) of sire effect for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under multivariate REML animal model

Traits	Best			Worst sire			% of sire with	
	Value	% of mean	Sire code	Value	% of mean	Sire code	+ve sire effect	-ve sire effect
WFC	34.038	6.84	Du-295	-28.368	-5.70	L-135	48.25	51.75
AFC	-210.376	-16.49	M-140	398.276	31.21	WL-818	42.97	57.03
FDP	-24.225	-13.68	S-307	73.702	4.62	L-135	39.34	60.66
FCI	-203.010	-42.13	H-58	259.640	53.88	L-135	56.56	43.44
FSP	-11.18	-6.23	H-58	14.270	7.95	N-378	55.74	44.26
FLMY	329.507	18.71	SA-304	-373.579	-21.21	P-355	46.72	53.28
HLMY	758.536	13.47	K-85	-658.293	-11.69	B-151	50.00	50.00
FLP	17.104	5.58	M-171	-9.649	-3.15	H-58	62.30	37.70

Table 6: Sire effect of ten top ranking for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under REML multivariate animal model

Rank	WFC		AFC		FDP		FCI	
1	2	3	8	5	6	7	8	9
1	Du-295	34.038	M-140	-210.376	S-307	-24.225	H-58	-203.01
2	NE-377	31.327	H-58	-196.258	M-820	-23.554	N-374	-170.26
3	M-145	29.241	D-271	-165.231	PA-354	-22.988	N-371	-152.33
4	A-103	16.354	Du-295	-161.032	M-171	-21.185	F-52	-150.70
5	M-158	16.213	FL-54	-157.923	N-372	-17.271	L-735	-135.52
6	SA-310	16.107	N-371	-142.325	N-375	-16.279	EMT-38	-135.38
7	M-142	16.002	B-151	-139.236	P-353	-16.106	B-155	-127.17
8	H-60	12.704	B-155	-131.359	M-158	-15.942	D-271	-119.20
9	C-171	12.696	BH-153	-124.568	S-306	-15.597	MO-152	-117.56
10	J-11	11.379	H-59	-113.358	G-55	-15.479	M-138	-110.89

Rank	FSP		FLMY		HLMY		FLP	
10	11	12	13	14	15	16	17	18
1	H-58	-11.18	SA-304	329.507	K-85	758.536	M-171	17.104
2	N-374	-9.39	CG-885	296.829	AR-106	742.781	N-378	12.338
3	N-388	-8.44	AR-106	255.982	M-171	703.972	SA-310	10.323
4	F-52	-8.28	S-306	227.672	EC-111	645.039	K-840	9.923
5	L-735	-7.51	J-73	224.905	CG-885	630.230	M-147	9.104
6	EMT-38	-7.47	K-85	224.037	J-73	615.762	M-141	8.488
7	B-155	-7.05	M-145	218.875	SA-304	540.652	SH-311	7.409
8	D-271	-6.52	SH-311	210.577	F-52	530.413	P-357	7.157
9	MO-152	-6.49	J-71	200.187	DL-272	458.976	CK-173	7.016
10	M-138	-6.06	NK-203	199.625	P-356	315.169	NKG-12	6.770

Table 7: Range of solution (LSC) for animal effect for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under univariate animal model

Traits	Best			Worst sire			% of sire with	
	Value	% of mean	Sire code	Value	% of mean	Sire code	+ve sire effect	-ve sire effect
WFC	24.383	4.90	M-40	-24.172	-4.86	L-260	56.10	43.90
AFC	-177.676	-13.92	WK-164	564.472	44.24	L-991	40.09	59.91
FDP	-29.016	-16.38	WK-147	42.719	24.12	L-94	45.50	54.50
FCI	-85.177	-17.68	WK-21	105.465	21.89	WK-633	44.44	55.56
FSP	-33.308	-18.55	WK-880	56.872	31.67	WK-551	46.27	53.73
FLMY	553.254	31.41	WK-537	-506.763	-28.77	CLK-67	46.34	53.66
HLMY	1032.604	18.34	WK-749	-1250.400	-22.21	CA-880	48.93	51.07
FLP	64.751	21.11	WK-45	-69.019	-22.50	CLK-67	44.89	55.11

Table 8 : Animal effect of ten tops ranking animal for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under univariate animal

Rank	WFC		AFC		FDP		FCI	
1	2	3	4	5	6	7	8	9
	Animal	Soln	Animal	Soln	Animal	Soln	Animal	Soln
1	M-40	24.383	WK-164	-177.676	WK-147	-29.016	WK-21	-85.177
2	WK-100	22.857	WK-175	-175.479	WK-281	-24.695	CA-882	-65.967
3	WK-304	22.546	WK-275	-167.601	L-737	-24.276	CA-904	-62.622
4	WK-119	21.394	WK-372	-164.741	L-218	-24.203	CA-880	-61.931
5	WK_265	21.026	WK-209	-162.887	CB-70	-24.028	WK-147	-61.341
6	WK-342	20.777	WK-223	-160.032	CA-882	-23.101	CJH-600	-57.011
7	WK-794	19.596	WK-35	159.734	WK-5	-22.445	CA-986	-55.393
8	WK-950	19.437	WK-30	-157.823	CJ-303	-22.302	CJ-986	-55.199
9	WK-951	19.267	WK-76	-153.886	SJ-857	-21.733	L_822	-54.543
10	WK-201	18.691	WK-176	-152.497	TO-400	-21.446	CMJ-270	-53.922

Rank	**FSP**		**FLMY**		**HLMY**		**FLP**	
10	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**
	Animal	**Soln**	**Animal**	**Soln**	**Animal**	**Soln**	**Animal**	**Soln**
1	CA-880	-33.308	WK-537	553.254	WK-749	1032.604	WK-45	64.751
2	CA-986	-29.421	WK-749	525.502	L-461	1014.892	L-161	59.325
3	L-966	-28.966	WK-762	515.617	WK-636	927.408	M-890	48.939
4	CJ-986	-28.812	L-161	398.723	WK-375	922.401	391/D37	48.112
5	CMJ-270	-28.654	WK-196	393.616	WK-726	893.329	M-890	46.032
6	CLK-239	-28.248	L-261	383.008	WK-762	858.703	361/D16	45.836
7	CA-904	-28.148	L-151	381.152	WK-733	833.056	276/D38	41.866
8	SJ-857	-27.845	EMT-742	377.311	L-474	820.034	L-167	41.413
9	WK-95	-27.535	WK-726	376.529	WK-680	802.423	L-153	40.676
10	WK-815	-26.869	WK-551	376.339	WK-462	801.174	276/D33	40.098

Table 9 : Range of solution for animal effect for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under multivariate animal model

Traits	Best			Worst animal			% of sire with	
	Value	% of mean	Animal code	Value	% of mean	Animal code	+ve animal effect	-ve animal effect
WFC	35.328	7.10	M-40	-33.177	-6.66	L-260	58.25	41.75
AFC	-258.632	-20.27	WK-164	456.137	35.75	L-991	40.32	59.68
FDP	-35.621	-20.11	WK-147	31.621	17.86	L-94	47.25	52.75
FCI	-95.136	-19.74	WK 21	111.527	23.14	WK-633	49.27	50.73
FSP	-38.328	-21.35	CA-880	57.256	31.89	WK-551	46.89	53.11
FLMY	587.019	33.32	WK-537	-365.237	-20.73	WK-304	48.89	51.11
HLMY	1306.416	23.20	M-451	-1295.30	-23.01	WK-475	50.13	49.87
FLP	77.725	25.34	WK-45	-78.238	-25.51	CLK-67	46.78	53.22

Herd life milk yield (HLMY)

The estimated average HLMY of 5630.00 kg was used for BLUP1, BLUP2 and BLUP3. Exactly half of the sires (50.00%) were superior to the population mean under BLUP1. The corresponding values were similar under BLUP2 and BLUP3.

The range of sire effect for HLMY was -443.946 to ± 399.829, -962.316 to + 815.804 and -658.293 to + 758.536 respectively under BLUP1, BLUP2 and BLUP3 (Table 1, 2 and 3). The range of sire was highest under BLUP2 and lowest under BLUP. The superiority of the best sire (as per cent of raw mean) were 7.10, 14.49 and 13.47 respectively under BLUP1, BLUP2 and BLUP3, whereas corresponding value of inferiority of worst sire were -7.89%, -17.09 and -11.69%. BLUP2 had shown maximum value in terms of superiority and or inferiority. The range of animal solution was -1250.400 to + 1032.604 and -1295.367 to + 1306.416, respectively under BLUP2 and BLUP3 (Table 7 and 9), the superiority of best animal (as per cent raw mean) were 18.34% and 23.20% respectively under BLUP2 and BLUP3.

Whereas corresponding values for inferiority of the worst animal were -22.21% and -23.01%. BLUP3 had shown higher values in terms of superiority and/or inferiority of animal solution. In BLUP2 and BLUP3 about 49% animals were superior to population mean.

The upper limit of sire effects of HLMY was increased from 399.829 kg in the BLUP1 solution to 815.804 kg in BLUP2 and 758.536 kg in BLUP3 solution. Whereas the lower limit were decreased from -443.946 kg in BLUP1 to -962.316 kg in BLUP2 and -658.293 kg in BLUP3 solution. The upper and lower limit of sires effects under BLUP2 was observed to be higher than the BLUP1 and BLUP 3 methods.

Rank correlation

All the 122 sires were ranked on the basis of the solutions obtained under model 8 and univariate and multivariate REML using animal models for WFC, AFC, FLP, FDP, FCI, FSP, FLMY and HLMY. The rank correlation coefficients among methods within traits and among traits within method are presented in Table 11. Rank correlations for the traits under all methods were highly significant, ranging from 0.697 (between model 8 and multivariate for FLP) to 0.999 (between model 8 and univariate for FSP). Rank correlations were above 0.973 for all the traits when sires were ranked by model 8 and univariate animal model. Therefore, the ranking by these two models was almost same. Rank correlations of models were almost same. Rank correlations of model 8 with univariate and multivariate animal models were higher than univariate with multivariate animal model.

Table 10 : Animal effect of ten tops ranking animal for WFC, AFC, FDP, FCI, FSP, FLMY, HLMY and FLP traits under multivariate animal model

Rank	WFC		AFC		FDP		FCI	
1	2	3	4	5	6	7	8	9
	Animal	Soln	Animal	Soln	Animal	Soln	Animal	Soln
1	M-40	35.328	WK-164	-258.632	WK-147	-35.621	WK-21	-95.136
2	WK-794	32.859	WK-265	-239.567	LB-70	-35.016	CA-986	-81.289
3	WK-265	27.027	WK-275	-195.321	WK-5	-29.521	CA-880	-79.935
4	WK-304	24.832	WK-175	-179.696	CJ-303	-24.785	WK-147	-65.256
5	WK-119	22.556	WK-372	-176.489	SJ-857	-24.286	CJH- 600	-65.023
6	WK-372	21.379	WK-35	-169.608	L-218	-24.209	L-822	-58.238
7	WK-950	19.597	WK-30	-167.883	L-737	-24.032	CA-904	-56.007
8	WK-951	19.235	WK-76	-162.527	WK-281	-23.951	CA-882	55.823
9	WK-35	19.137	WK-175	-160.823	CA-882	-23.752	L-966	55.549
10	WK-201	19.017	WK-176	-157.358	JO-400	-22.378	CMJ-270	54.327

Rank	**FSP**		**FLMY**		**HLMY**		**FLP**	
10	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**
	Animal	**Soln**	**Animal**	**Soln**	**Animal**	**Soln**	**Animal**	**Soln**
1	CA-880	-38.328	WK-537	587.019	M-451	1306.416	WK-45	77.725
2	L-966	-36.305	WK-749	460.095	EMT-742	1301.527	391/D37	77.018
3	CMJ-270	-33.951	M-451	456.635	M-425	1271.311	L-167	67.526
4	CLK-230	-31.361	WK_762	449.700	M-69	1265.346	276/D32	63.113
5	CA-904	-29.892	WK-737	363.003	WK-485	1215.373	M-890	59.365
6	SJ-857	-29.008	WK_740	347.813	WK-762	1215.315	391/D37	57.839
7	CJH-600	-28.976	WK-808	346.287	WK-749	1209.368	L-161	57.132
8	CA-986	-28.732	WK-443	343.156	WK-537	1197.368	361/D16	52.939
9	L-882	-28.325	WK-726	332.492	WK-506	1197.020	WK-201	48.273
10	WK-815	-27.567	M-160	321.103	WK-949	1145.376	276/D33	41.836

The rank correlations among traits within method were lower than among methods within trait. Among traits within method, the ranking of the sires changed resulting into decreased rank correlation coefficients. The change in ranking of sires with different reproductive and productive traits of their daughters might be due to non unity in genetic correlations between different traits. Within the method, the rank correlation ranged from -0.986 (between FLP and FCI in multivariate animal model) to 0.987 (between FSP and FCI in multivariate model). The rank correlation coefficients of WFC with AFC, FLP, FLMY, HLMY were positive and non significant, while with FDP, FCI, and FSP were significant and negative under model 8.

Table 11: Rank correlation coefficient

	Trait	**Model 8**						
		AFC	**FLP**	**FDP**	**FCI**	**FSP**	**FLMY**	**HLMY**
Model 8	WFC	0.101	0.047	-0.129**	-0.103**	-0.030**	0.073	0.120
	AFC		-0.083**	0.022	0.123	0.146**	0.258**	-0.004**
	FLP			-0.366**	-0.754**	0.666**	0.602**	0.556**
	FDP				0.840**	0.684**	-0.258**	-0.303**
	FCI					0.810**	-0.540**	-0.481**
	FSP						-0.362**	-0.359**
	FLMY							0.764**
	HLMY							

	Trait	Univariate							
		WFC	AFC	FLP	FDP	FCI	FSP	FLMY	HLMY
Model 8	WFC	0.998**							
	AFC		0.990**						
	FLP			0.996**					
	FDP				0.999**				
	FCI					0.996**			
	FSP						0.999**		
	FLMY							0.994**	
	HLMY								0.973**
Univariate	WFC		0.101	0.054	-0.102**	-0.130**	-0.008**	0.177*	0.157*
	AFC			-0.160**	0.042	0.112	0.140*	0.040	0.016**
	FLP				-0.357**	0.060	-0.684**	0.622**	0.413**
	FDP					0.836**	-0.664**	0.233**	-0.255**
	FCI						-0.820**	0.467**	-0.446**
	FSP							-0.400**	-0.125**
	FLMY								0.758**
	HLMY								

	Trait	Multivariate							
		WFC	AFC	FLP	FDP	FCI	FSP	FLMY	HLMY
Model 8	WFC	0.968**							
	AFC		0.879*						
	FLP			0.697*					
	FDP				0.925**				
	FCI					0.912**			
	FSP						0.832**		
	FLMY							0.939**	
	HLMY								0.967**
Univariate	WFC	0.958**							
	AFC		0.997**						
	FLP			0.704**					
	FDP				0.963**				
	FCI					0.932**			
	FSP						0.828**		
	FLMY							0.924**	
	HLMY								0.976**
Multivariate	WFC		0.101	0.057	-0.117**	-0.142**	-0.009**	0.131	0.159*
	AFC			-0.119**	0.039	0.109	0.146*	0.046	0.019**
	FLP				-0.104**	-0.986**	-0.957**	0.625**	0.513**
	FDP					0.823**	0.637**	-0.252**	-0.237**
	FCI						0.987**	-0.457**	-0.436**
	FSP							-0.398**	-0.215**
	FLMY								0.769**
	HLMY								

*** ($P < 0.05$)** **** ($P<0.01$)**

The rank correlation coefficients of WFC with AFC and FLP were positive and non significant but positive and significant with FLMY and HLMY. However, negative and significant rank correlation coefficients of WFC were found with FDP, FCI, FSP under univariate animal model. The rank correlation coefficients of WFC with AFC, FLP and FLMY were positive and non significant, while with FDP, FCI and FSP were significant and negative. However, positive and significant rank correlation of WFC was found with HLMY under multivariate animal model.

The rank correlation coefficients of AFC with FDP and FCI were positive and non significant, and with FSP and FLMY positive and significant, while with FLP and HLMY were significant and negative under model 8. The rank correlation coefficients of AFC with FDP, FCI, and FLMY were positive and non significant but positive and significant with FSP and HLMY.

However, negative and significant rank correlation coefficient of AFC with FLP was obtained under univariate animal model. The rank correlation coefficient of AFC with FDP, FCI and FLMY were positive and non significant but positive and significant with FSP and HLMY. However, negative and significant rank correlation coefficient of AFC was found with FSLP under multivariate animal model. The rank correlation coefficients of FLP with FSP, FLMY and HLMY were positive and significant while with FDP and FCI were significant and negative under model 8. The rank correlation coefficients of FLP with FLMY and HLMY were positive and significant but positive and non significant with FCI. However, negative and significant rank correlation coefficients of FLP were found with FDP and FSP under univariate animal model. The rank correlation coefficients of FLP with FLMY and HLMY were positive and significant while with FDP, FCI and FSP were significant and negative under multivariate animal model. The rank correlation coefficients of FDP with FCI and FSP were positive and significant, but negative and significant with FLMY and HLMY under model 8, univariate and multivariate animal model. The rank correlation coefficients of FCI with FLMY and HLMY were negative and significant while with FSP positive and significant under model 8, univariate and multivariate animal models.

The rank correlation coefficient of FSP with FLMY and HLMY were negative and significant under model 8, univariate and multivariate animal models. The rank correlation coefficients of FLMY with HLMY were positive and significant under model 8, univariate and multivariate animal models. In general, FCI had highest rank correlation with FSP in all methods, ranging from 0.810 models 8 to 0.987 in multivariate animal model. This high rank correlation might be due to high genetic correlations between FCI and FSP.

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