Genetic Parameters and Sire Evaluation Based on Fat Based Energy Corrected Milk Yield in Sahiwal Cattle

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ABSTRACT

A total of 531 first lactation records of daughters of 28 sires, having 5 or more progeny were evaluated by 4 methods viz., least-squares (LS), best linear unbiased prediction (BLUP), best linear unbiased prediction-sire model (BLUP-SM) and Animal Model. Heritabilities, genetic and phenotypic correlations between the two traits were analysed using univariate and bivariate linear animal models. The h^2 estimates for 305 days or less milk yield (305MY) and Fat based energy corrected milk yield (ECMY) were 0.24 and 0.37. The Animal Model was most stable, efficient and accurate method. There was a remarkable 97-100 percent level of similarity on comparison of ranks of the sires based on 305MY and ECMY by all methods. The genetic evaluation of Sahiwal bulls based on ECMY has the advantage of being a composite trait, and with high heritability and high genetic and phenotypic correlations (0.99) with 305MY can help in mitigating the nutritional insecurity of the country in the long run.

Keywords: BLUP, energy corrected milk yield, genetic parameters, sahiwal cattle, sire evaluation

Milk as a major source of dietary energy, protein and fat, contributing on an average 134 kcal of energy, 8 g of protein and 7.3 g of fat/capita/day (FAOSTAT 2012) has the immense potential of fighting the demons of nutritional insecurity in the largely vegetarian India. Breed improvement programme effectiveness depends on sire evaluation process as contribution of sire path is higher than the dam path for the overall genetic improvement for a trait. In India, though the production of milk has increased many folds in last few decades, the relative contribution of milk and other dairy products towards the dietary energy is very less. To produce milk and grow while reproducing and staying healthy cows require sufficient energy intake (Banos *et al.,* 2006). Energy balance should be included into future breeding programs (Huttmann *et al.,* 2009). The present study considered ECMY exclusively based on fat%. As the heritability of fat% is higher and fat is solely

contributing to the ECMY. Therefore there is a possibility of inheritance of ECMY more than the inheritance of milk yield. Till date no report is available on genetic parameter estimates and sire evaluation based on fat based energy corrected milk yield. Keeping in view the importance present investigation has been planned.

MATERIALS AND METHODS

Data structure

Under the Indian conditions the average dairy animal holding through in rural households varies from 2-3. In single organised herd of Sahiwal cattle the breedable population size varies from 250-300 where, a set of 8-10 bulls are used. Data on records of 531 Sahiwal cows from

28 sires, spread over a period of 25 years (1989-2013), maintained at ICAR-National Dairy Research Institute, Karnal were analyzed for First lactation 305-day milk yield (305MY- kg) and Fat based energy corrected milk yield (ECMY- kcal). The opportunity of mating randomly in breedable population under organised conditions and considering the accurate estimate of genetic parameters the average number of sires per progeny considered was more than five. The study has relevance for the evaluation of Sahiwal bulls considering more than five progenies in single organised herd.

However, the accuracy of progeny testing increases with the number of progenies which is possible when either a very large Sahiwal herd is considered or Sahiwal bulls are evaluated based on the use in Multiple herds. The records of Karan-Fries cows of known pedigree and with normal lactation were included in the present study. The normal lactation was considered as a period of milk production by a cow for at least 100 days, the milk production in lactation was recorded a minimum of 500 kg and the cows calved and dried under normal physiological conditions. Out 531 Sahiwal cows, Information of 193 Sahiwal cows were not considered for this study due to various reasons like abortion, still birth and other reproductive problems. The study was classified into eight periods viz; 1(1989-1991); 2(1992-1994); 3(1995-1997); 4(1998-2000); 5(2001-2003); 6(2004-2006); 7(2007-2009) and 8(2010-2013). The basis of classifying the period used in the analysis was 3 years as Sahiwal animals were under progeny testing programme. A set of Sahiwal bulls as per technical programme used 3-4 years for A.I. under the programme. Each year was sub-classified into four seasons, depending on prevalent meteorological factors, feed and fodder availability as recorded in CSSRI, Karnal Singh (1983). Age at first calving of Sahiwal cows was classified into three age groups using mean and one standard deviation after normalizing the distribution of AFC in the population as 1{≤ 972 (52)}; 2{972-1264 (248)} and 3{≥ 1264 (37)}. First lactation energy corrected milk yield was estimated by using standard practices as suggested by Overmann and Sanmann (1926) as follows: Fat based energy per kg (cal) (FBE/kg) = (ATDFP × 9.23) × 1000 /103 where, the value 9.23 is the calories of heat evolved by the complete combustion of one gram butter fat. Fat based energy corrected milk yield (kcal) (ECMY) = (FBE/kg) × (305MY).

Model

Sires having five or more progeny were evaluated by 4 methods viz.

Least squares (LS)

The following fixed effect least squares model of Harvey (1990) was employed to estimate the breeding value of sires:

$$Y_{ijklm} + \mu + p_i + S_j + M_K + A_l + e_{ijklm}$$

Where, Y_{ijklm} is observation on m^{th} the progeny in l^{th} age group, k^{th} season, j^{th} sire and i^{th} period.

μ is overall mean

P_i is fixed effect of ith period

S_j is random effect of jth sire which is NID (0, σ_s^2)

M_K is fixed effect of kth season

A_l is fixed effect of lth age group

e_{ijklm} is the random error associated with each record which is NID (0, σ_e^2)

The index of ith sires were estimated by following formula:

$$I = \mu + S_j$$

Where, I = Index of jth sire

μ = Population mean

S_j = Least squares constant of jth sire

Best linear unbiased prediction (BLUP)

The breeding values of sires using BLUP method were estimated using model 08 of Harvey (1990). The season of calving, period of calving and age groups were taken as fixed effects and sire as random effect for 305MY and ECMY traits. The numerator relationship matrix is not considered under this model.

The following mixed model was used:

$$Y = Xb + Zu + e$$

where, Y is the vector of observations for traits under study

b is the vector of observations of unknown fixed effects

u is a vector of observations of unknown random effects

X and Z are the incidence matrices pertaining for fixed and random animal effect respectively.

$$E(Y) - Xb; E(u) = 0; E(e)0$$

$$Var(u) = G = G_0$$

$$Var(e) = R = I * R_0$$

The mixed model equation is:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} X'R^{-1}Y \\ Z'R^{-1}Y \end{bmatrix}$$

By solving the mixed model equations, the BLUP breeding values of the random effects (sires) and estimation of fixed effects were obtained.

Best linear unbiased prediction - sire model (BLUP-SM)

Restricted maximum likelihood (REML) method was applied on data of 305MY and ECMY traits to predict the breeding values of sires and to estimate fixed effects using WOMBAT software (Meyer, 2007). Restricted maximum likelihood method (REML) is a maximum likelihood method that accounts for the loss of degrees of freedom due to fitting fixed effects.

The aim in REML is to find the sets of parameters which maximize the likelihood of the data. Sire model take account of relationship between sires (of pedigree) only through numerator relationship matrix. The following sire model of analysis fitted the season of calving, period of calving and age groups as fixed effect and sires as random effect for the above traits.

The following model was considered:

$$Y_{ijk} = Xb_i + Zu_j + e_{ijk}$$

Where, Y_{ijk}, b_i, u_j and e_{ijk} denotes the vector of observations, fixed effects, random effects and residual error respectively and X and Z are incidence matrices pertaining to b and u.

$$E(Y) = Xb; E(u) = 0; E(e) = 0 \;\; and$$

$$Var(u) = G = A * G_0$$

$$Var(e) = R = I * R_0$$

where, A is a numerator relationship matrix

G_0 is the genetic (co)variances matrix between traits of sires only

R_0 is the residual (co)variances matrix, and

The mixed model equation was:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} X'R^{-1}Y \\ Z'R^{-1}Y \end{bmatrix}$$

By solving the mixed model equations, the BLUP breeding values of the random effects (sires) was obtained.

Animal model

Animal model fitting restricted maximum likelihood method (REML) was applied on data of 305MY and ECMY traits to predict the breeding value of sires using WOMBAT software (Meyer, 2007). The animal model takes account of relationship between all animals (sires and dams) of pedigree only through numerator relationship matrix. The animal model of analysis fitted the season of calving, period of calving and age groups as fixed effect and sires as random effect for all milk yield traits. By solving the mixed model equations, the BLUP breeding value of the random effects (sires) were obtained.

Four different criterias for convergence of matrix are as under: The first two are simple changes, available for all maximisation algorithms i.e., increase in log likelihood values between subsequent iterates and change in the vector of parameter estimates from the last iterate. The other two are norm of the gradient vector and newton decrement which are obtained from the AI algorithm. The default thresholds for convergence criteria algorithm criterion AI are as follows:

Change in log L should be $< 5 * 10^{-4}$; Change in parameters should be $< 10^{-8}$ and Norm of gradient vector should be $< 10^{-3}$. The results of the study were in conformity with the above parameters. The effectiveness of different sire evaluation methods was judged by using the various criteria like within sire variance or error variance,

coefficient of determination (%), coefficient of variation (%) and rank correlations. The most efficient method had the lowest error variance. Higher the coefficients of determination (R²-Value) for fitting a model, higher the accuracy. The sire evaluation method, which retains the coefficient of variation (CV %) of the population near to the CV (%) unadjusted data was the most stable method. Higher (near to unity) rank correlation amongst the sires from different sire evaluation methods revealed higher degree of similarity of ranking for the two traits.

RESULTS AND DISCUSSION

Heritability, Genetic and Phenotypic correlation of first lactation traits

The heritability for 305MY and ECMY was medium to high i.e. 0.24 and 0.38 thus indicates sufficient additive genetic variance for affecting the selection to improve the traits genetically. The present h² estimate was higher than report

of Divya (2012) and lower than (Singh 2013, Singh 2014) who reported values of 0.20, 0.34 and 0.35, respectively. The ECMY had positive genetic and phenotypic correlations (0.99) with 305MY. Very high correlations also indicate that sires can be evaluated on ECMY as it accounts for both yield and constituent traits. Navid Ghavi Hossein-Zadeh (2012) reported heritabilities from 0.14 to 0.21 for ECM and greatest genetic correlations were between ECM2 and ECM3 (0.96), greatest phenotypic correlations were between ECM1 and ECM2 (0.57) and ECM2 and ECM3 (0.57). Huttmann *et al.* (2009) reported the average heritability of 0.23 for daily ECM in the first lactation Holstein cows and Liinamo *et al.* (2010) reported the average heritability of 0.25 for daily ECM in Nordic Red dairy cattle. Estimates of genetic and phenotypic correlations are important in genetic improvement programmes since they indicate the extent to which one trait will genetically and phenotypically change if a correlated trait is improved. The high and positive genetic correlations between ECMY and 305MY are evidence for

Table 1: Average breeding values (BV) estimates of sires for and by different methods

Methods	Average BV	First lactation 305 days or less milk yield				
		Number of sires above average BV	Number of sires below average BV	Maximum BV	Minimum BV	Difference
LS	1738.14	17	11	2200.60 (26.61)	875.45 (49.63)	1325.15
BLUP	1770.23	15	13	1799.03 (1.63)	1741.87 (1.60)	57.16
BLUP-SM	1780.28	15	13	2213.34 (24.33)	1229.47 (30.94)	913.87
Animal Model	1761.53	15	13	2009.65 (14.09)	1607.77 (8.73)	401.88
Fat based energy corrected milk yield						
LS	747.40	16	12	959.68 (28.40)	382.24 (48.86)	577.43
BLUP	767.42	13	15	779.92 (1.63)	756.56 (1.42)	23.36
BLUP-SM	769.19	15	13	945.89 (22.97)	540.86 (29.68)	405.04
Animal Model	761.78	15	13	835.34 (9.66)	716.20 (5.98)	119.13

Figures in the parentheses indicate percent above and below the average breeding value. LS=Least square, BLUP=Best linear unbiased prediction, BLUP-SM=Best linear unbiased prediction-Sire model and Animal model

common genetic and physiological mechanism controlling these traits.

Least square

The overall least squares population mean for first lactation 305 days milk yield and fat based energy corrected milk yield was 1738.14 ± 90.66 kg and 747.40± 39.70 kcal, respectively. The average breeding value of sires from different methods for 305MY ranged from 1,738.14 kg (LS) to 1,770.23 kg (BLUP) and 747.40 kcal (LS) to 767.42 kcal (BLUP) for ECMY. By least squares method (LS), the average breeding value of sires for first lactation 305 days or less milk yield was 1,738.14 kg and for ECMY was 747.40kcal (Table 1). Out of 28 sires seventeen sires (60.71%) for 305MY and sixteen sires (57.14%) for ECMY had breeding value above average breeding value. The highest breeding value for 305MY was observed as 2,200.60 kg, which was 26.61 percent higher than the average breeding value, whereas in ECMY was observed as 959.68 kcal, which was 28.40 percent higher than the average breeding value. Out of total 28 sires, six (10.7%) for 305MY and three (21.43%) for ECMY had breeding value 20 percent and above than the overall average breeding value (Table 2).

Table 2: Number of sires with 20, 15, 10 and 5 percent and higher breeding value than the average breeding value

Methods	First lactation 305 days or less milk yield			
	20%	15%	10%	5%
LS	6(21.43)	7(25)	9(32.14)	13(46.43)
BLUP	0	0	0	0
BLUP-SM	0	0	1(3.5)	4(14.2)
Animal Model	2(7.14)	4(14.2)	9(32.14)	10(35.7)
Fat based energy corrected milk yield				
LS	3(10.7)	9(32.14)	9(32.14)	12(42.8)
BLUP	0	0	0	0
BLUP-SM	0	0	0	1(3.57)
Animal Model	2(7.14)	3(10.7)	9(32.14)	10(35.7)
LS	3(10.7)	9(32.14)	9(32.14)	12(42.8)

Figures in the parentheses indicate the percentage.

Banik and Gandhi (2006) reported lower estimates of average breeding value of sires for first lactation 305 days or less milk yield in Sahiwal cattle. The difference between upper and lower estimates breeding values was highest for 305MY and ECMY as 1,325.15 kg and 577.43 kcal, respectively indicating that this method discriminated amongst bulls to the highest extent as compared to other methods.

BLUP

Under best linear unbiased prediction (BLUP), the average breeding value of sires for 305MY and ECMY was 1,770.23 kg and 767.42 kcal, respectively. No sire out of a total of 28 sires was having breeding value 20, 15, 10 and 5 percent and above in both the traits (Table 2). The highest estimate of breeding value for 305MY and ECMY was 1,799.03 kg and 779.92 kcal, which was 1.63 percent higher than the average breeding value. Banik and Gandhi (2006) reported lower average breeding value for 305MY in Sahiwal cattle than that of the present study.

BLUP-SM

The evaluation of breeding value of sires by blup sire model (BLUP-SM) method for both the traits gave the average breeding value as 1,780.28 kg and 769.19 kcal, respectively (Table 1). Out of 28 sires fifteen (53.57%) sires for 305MY and ECMY had breeding value above average breeding value whereas, 13(46.43%) sires had breeding value below the average. The difference between the maximum and minimum breeding value was 913.87 kg and 405.04 kcal, respectively for both traits which indicated it discriminated bulls to maximum after LS method.

Animal Model

The average breeding value under Animal Model for both traits was 1761.53 kg and 761.78 kcal, respectively (Table 1). Fifteen (53.57%) out of 28 sires showed higher breeding values whereas, 13 (46.43%) sires showed lower breeding values than the average breeding value for both traits. The highest breeding value was estimated as 2009.65 kg and 835.34 kcal which was 14.09 and 9.66 percent higher than the average breeding value. The difference between highest and lowest breeding values was 401.88 kg and

119.13 kcal, respectively. Two sires (7.14%) showed breeding value over and above 20 percent as compared to overall average breeding value for both the traits (Table 2).

Error variance and coefficient of determination

The within sire variance or error variance of Animal Model was lowest ($258490kg^2$ and 51876 kcal^2) therefore, was the most efficient out of all the four sire evaluation methods (Table 3). The least-squares method was second best efficient method after Animal Model based on this criterion. BLUP method was found to be least efficient due to maximum error variance for both traits (423198 kg^2 and 80073 kcal^2). The result agreed with Banik and Gandhi (2006) who observed similar results in Sahiwal cattle except that Animal Model sire evaluation method was not used. However, Tajane and Rai (1990) and Deb *et al.* (1998) observed LS method to be more efficient than BLUP. Banik and Gandhi (2006) found DFREML more efficient than LS and BLUP. The relative efficiency (%) of LS, BLUP and BLUP-SM in comparison with Animal Model for 305MY were 63.16%, 60.53% and 63.16%, respectively (Table 3). For ECMY relative efficiencies were 65.10%, 64.58% and 65.10%, respectively in comparison with Animal Model method (Table 3). In contrary higher relative efficiency of LS and BLUP as 78.11% and 75.91% in comparison to DFREML method was reported by Banik and Gandhi (2006). The highest

coefficient of determination for both traits (41.8% and 38.01%) by Animal Model as compared to other methods showed that it was the most accurate method (Table 3). LS (30%) was found to be second best accurate method. Gandhi and Gurnani (1998) observed LS method as the most accurate (15.34% R^2-square value) followed by BLUP method. Banik and Gandhi (2006) reported lower coefficient of determination (11.07%) in LS method and (33.39%) in DFREML method.

Coefficient of variation and rank correlations

The alteration of CV for both traits with respect to unadjusted data was lowest and similar for Animal model and BLUP-SM (39.33% and 40.74%) and (39.29% and 40.6%). The results depict Animal Model and BLUP-SM method as the most stable method. Gandhi and Gurnani (1998) reported BLUP method as the least stable method however, in contrary Banik and Gandhi (2006) observed BLUP as most stable method of sire evaluation in Sahiwal cattle. The rank correlations of breeding value of sires estimated for 305MY from different methods of sire evaluation ranged from 0.585 (LS with BLUP-SM) to 0.904 (BLUP with Animal Model) and were statistically highly significant (p<0.01). For ECMY rank correlations of sires varied from 0.523 (LS with BLUP-SM) to 0.861 (BLUP with Animal Model) and were statistically highly significant (p<0.01). BLUP method had a highly significant

Table 3: Relative efficiency, coefficient of determination (R^2-value) and coefficient of variation (CV) of different methods of sire evaluation

Methods	Error Variance (kg)^2	First lactation 305 days or less milk yield			
		Coefficient of determination (%)	Coefficient of variation (%)	Efficiency	*Relative efficiency
LS	416013	30	37.01	0.0000024	0.631579
BLUP	423198	16.4	36.83	0.0000023	0.605263
BLUP-SM	417490	2.7	39.29	0.0000024	0.631579
Animal Model	258490	41.8	39.29	0.0000038	1
Fat based energy corrected milk yield					
LS	79781	29.9	37.01	0.0000125	0.651042
BLUP	80073	21	37.08	0.0000124	0.645833
BLUP-SM	79832	1.29	40.6	0.0000125	0.651042
Animal Model	51876	38.01	40.6	0.0000192	1

* Relative efficiency with respect to most efficient Animal Model method.

(p<0.01) rank correlation (0.861) and (0.904) for both traits with Animal Model method whereas, LS with Animal Model had rank correlation of (0.819 and 0.810) for both traits. Banik and Gandhi (2006) found rank correlations of breeding value of sires very high ranging from 0.7979 (BLUP with DFREML) to 0.9568 (LS with DFREML) and were statistically highly significant (p<0.01). Singh and Singh (1999) and Gaur *et al.* (2001) found higher rank correlations 0.815 and 0.96 between LS and BLUP methods whereas much higher rank correlation (0.9846) between these two methods was reported by Gandhi and Gurnani (1998). The similarity of ranking of sires based on 305MY and ECMY by LS, BLUP, BLUP-SM and Animal Model was 97.5-100%. Animal Model being the best method of sire evaluation for the present study had a highly significant (p<0.01) rank correlation (0.999) based on the two traits. Navid Ghavi Hossein-Zadeh (2012) higher potential exists for selecting animals for ECM based on their first parity records. This is an advantage due to reduced generation interval and increased genetic progress in selection programs.

CONCLUSION

The comparison of different methods of sire evaluation based on multi trait (first lactation 305 days or less milk yield and fat based energy corrected milk yield) showed that the Animal Model was most accurate, efficient and stable method to estimate the breeding value of sires with highest coefficient of determination and lowest error variance. The ranks of sires by different methods of sire evaluation exhibited a notable degree of similarity (59-91%) for 305MY and (53-87%). The ranks of sires when compared between the traits exhibited 97.5-100% similarity by LS, BLUP, BLUP-SM and Animal Model. There was a statistically highly significant (p<0.01) rank correlations (0.999) between the two traits by Animal Model, it is recommended that in the light of the nutritional security of the country, genetic evaluation of Sahiwal bulls should be done based on fat based energy corrected milk yield, as it accounts for both milk production and constituent traits.

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