Prediction of Breeding Value Using Bivariate Animal Model for Repeated and Single Records

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ABSTRACT

The present investigation was carried out on Karan Fries cows maintained at National Dairy Research Institute (NDRI), Karnal, Haryana. Data were collected on fertility and production performance spread over a period of 34 years (1978 to 2012). Breeding values estimated by univariate animal model were compared with univariate animal repeatability model on the basis of spearman's rank correlation estimate. The rank correlation estimates ranged between 0.39 to 0.47 indicating that sires rankings on first lactation basis had moderate correlation with the rankings on the basis of breeding values estimated by repeatability model. Further the bivariate animal repeatability models *viz*. SP & 305MY, CI & 305MY and DPR & 305MY had lower error standard deviation 251.85, 254.92 and 249.93 kgs in comparison to bivariate animal model for single records for which the error standard deviation estimates were 281.84, 279.81 and 278.99 kgs, respectively. The error standard deviation estimates of SP & TMY, CI & TMY, DPR & TMY were 284.99, 294.35 and 285.47 kgs in comparison to bivariate animal model for single records for which the error standard deviation estimates were 272.01, 315.30 and 298.22 kgs, respectively. Results of the present study indicated that the repeatability model was superior in comparison to the animal model for single records and thus repeated records should be used for breeding value prediction in dairy cattle.

Keywords: Animal model, breeding value, bivariate, repeatability, fertility.

Sire and dam contribute equally to the inheritance of productive and functional characters of progeny. During selection more emphasis is given to sire than dam, as a bull can be bred to a more number of cows, therefore greater selection intensity can be applied to bulls (Schaeffer, 2006). In India animal breeders are mostly interested in prediction of breeding values using conventional approaches *viz*. contemporary comparison method, least-squares approach and simplified regressed least-squares. Prediction of breeding values in dairy cattle breeding using repeatability animal model is becoming more common as such model accounts for repeated performance of an animal with respect to any trait (Suzuki and Van Vleck, 1994). There is a need to consider repeated records obtained for fertility traits in addition to production traits in multi-trait selection. The use of repeated records increases the accuracy of

breeding value as the repeatability animal model used for prediction partitions the variance effectively into genetic, permanent and residual environmental effects (Afifi *et al.,* 1989). Further, multi-trait selection has been advocated under Indian conditions due to small number of daughters per sire; as such selection will improve the accuracy and efficiency of sire evaluation (Sahana and Gurnani, 1999). Multi-trait selection slows down the rate of improvement in productivity of dairy cattle, however such reduction can be more than compensated by simultaneous improvement in fertility traits. Information regarding comparative efficiency of univariate and multivariate repeatability animal model with animal model for single records for breeding value prediction in Indian conditions is scanty. The present investigation was undertaken with the objective of prediction of breeding values in Karan Fries

cattle using univariate and bivariate animal models for repeated records and to study which model (univariate or bivariate) would be more appropriate under Indian conditions.

MATERIALS AND METHODS

The present investigation was carried out on Karan Fries cows maintained at National Dairy Research Institute (NDRI), Karnal, Haryana. The Karan Fries crossbred dairy cattle was developed as a result of crossbreeding project started in 1971, at N.D.R.I., Karnal, wherein it was finally declared as a specific strain in 1982 (Singh and Gurnani, 2004).

Table 1. Rank correlations (r_s) of Estimated Breeding Values (EBVs) by univariate animal repeatability model and univariate animal model for single records.

First lactation trait	All lactation trait	Spearman's Rank Correlations
FSP	SP	0.45**
FCI	CI	0.43**
FDPR	DPR	0.47**
F305MY	305MY	0.46**
FTMY	TMY	0.39**

**indicates highly significant at p<0.01.

Data Collection and Traits studied

Data collected on fertility and production performance were spread over a period of 34 years (1978 to 2012) and a total of 1988 first lactation and 5878 all lactation records were collected for all the traits under the present study. The cows completing at least one normal lactation (i.e. ≥500 kg lactation yield and ≥100 days lactation length) were considered in the study. A total of 5878 lactation records on 1988 Karan Fries cows, sired by 186 bulls, were utilized for the present study. The all lactation fertility traits considered for analysis included service period (SP), calving interval (CI), calving to first service (CFS), daughter pregnancy rate (DPR) and the production traits included lactation length (LL), 305 day or less milk yield (305MY), total milk yield (TMY), milk yield per day of lactation length (MY/LL) and milk yield per day of calving interval (MY/CI).

Animal Model and (Co) variance Component Estimation

(Co) variance components were estimated using average information restricted maximum likelihood (AIREML) (Meyer, 1989). The linear model used for describing animal model for single records was $y = Xb + Za + e$. This animal model for single records in mixed model equation form is expressed as;

Table 2. Error variance, standard deviation (S.D.) and mean sire breeding values for 305MY estimated by bivariate animal model for repeated records and bivariate animal model single records

Bivariate Model	Error Variance		SD		Mean Sire BV (kg)	
	Repeated records	Single Records	Repeated records	Single Records	Repeated records	Single Records
SP & 305MY	650450.00	421315.00	251.85	281.84	3407.21	3057.63
CI & 305MY	650020.00	423082.00	254.92	279.81	3407.32	3056.87
DPR & 305MY	651340.00	423798.00	249.93	278.99	3406.10	3063.15

Table 3. Error variance, standard deviation (S.D.) and mean sire breeding values for TMY estimated by bivariate animal model for repeated records and bivariate animal model for single records

Bivariate Model	Error Variance		SD		Mean Sire BV (kg)	
	Repeated records	Single records	Repeated records	Single records	Repeated records	Single records
SP & TMY	1137900.00	1350430.00	284.99	272.01	3680.67	3393.93
CI & TMY	1135800.00	1311260.00	294.35	315.30	3679.51	3398.12
DPR & TMY	1140600.00	1323070.00	285.47	298.22	3678.98	3394.20

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\alpha \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

Where, $\alpha = \sigma^2_e / \sigma^2_a$ and A is the numerator relationship matrix of all the animals, which has nonzero off-diagonals only for the animal's parents, progeny, and mates. The elements of A can contain additive genetic effects, non-additive genetic effects, maternal effects, and permanent environmental effects (Henderson, 1988).

Repeatability Animal Model

The univariate animal repeatability model was also run using WOMBAT for genetic evaluation of all lactation data. When there are more than one records on an animal for a trait, then the genetic evaluation and breeding value prediction can be done by the repeatability model. The repeatability model not only estimates the breeding value of an animal but also derives its permanent environmental effects. The repeatability model can be written as $y = Xb + Za + Wpe + e$. Where, pe = vector of permanent environmental effects and non-genetic effects; W = incidence matrix relating records to permanent environmental effects. The permanent environmental effects and residual effects are assumed to be normally independently distributed with means zero and variance σ^2_{pe} and σ^2_e, respectively. Therefore,

$$var \begin{bmatrix} pe \\ e \\ a \end{bmatrix} = \begin{bmatrix} I\sigma^2_{pe} & 0 & 0 \\ 0 & I\sigma^2_e & 0 \\ 0 & 0 & A\sigma^2_a \end{bmatrix}$$

Where, $var(e) = I\sigma^2_e = R$ and $var(y) = ZAZ'\sigma^2_a + WI$ $I\sigma^2_{pe}W' + R$. The mixed model equation for repeatability

mode takes the following form;

$$\begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{pe} \end{bmatrix} = \begin{bmatrix} \acute{X}R^{-1}X & \acute{X}R^{-1}Z & \acute{X}R^{-1}W \\ \acute{Z}R^{-1}X & \acute{Z}R^{-1}Z + A^{-1}1/\sigma^2_a & \acute{Z}R^{-1}W \\ \acute{W}R^{-1}X & \acute{W}R^{-1}Z & \acute{W}R^{-1}W + I(1/\sigma^2_{pe}) \end{bmatrix}^{-1} \begin{bmatrix} \acute{X}R^{-1}y \\ \acute{Z}R^{-1}y \\ \acute{W}R^{-1}y \end{bmatrix}$$

Dropping R^{-1} from both sides of the equation, the MME can be written as:

$$\begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{pe} \end{bmatrix} = \begin{bmatrix} \acute{X}X & \acute{X}Z & \acute{X}W \\ \acute{Z}X & \acute{Z}Z + A^{-1}\alpha_1 & \acute{Z}W \\ \acute{W}X & \acute{W}Z & \acute{W}W + I\alpha_2 \end{bmatrix}^{-1} \begin{bmatrix} \acute{X}y \\ \acute{Z}y \\ \acute{W}y \end{bmatrix}$$

Where, $\alpha_1 = \sigma^2_e / \sigma^2_a$ and $\alpha_2 = \sigma^2_e / \sigma^2_{pe}$ (Mrode, 2005).

RESULTS AND DISCUSSION

Spearman's Rank Correlation of Repeatability Animal Model with Univariate Animal Model for Single Records

The sire rankings were compared with that of first lactation rankings and Spearman's rank correlation was estimated (Table 1). All the estimates of Spearman's rank correlation's were highly significant and the rank correlations for most of the traits indicated that ranking of sires on first lactation basis had moderate (0.39 to 0.47) correlation with the sire rankings done on the basis breeding values estimated by animal model for traits with repeated records. The moderate correlation estimate indicated that the sire rankings on the basis of repeated records differed significantly in comparison with sire ranking based on single first lactation record for the same traits.

Comparison between Bivariate Animal Models for Repeated and Single Records

The comparison of bivariate repeatability animal model with similar model for single records was carried out on the basis of error variance and standard deviation (SD) of estimated breeding values. The results indicated that in case of the model in which total milk yield (TMY) was considered as the production trait bivariate repeatability model was superior to bivariate model for single records as the error variance was lower. However, contrasting results were obtained with respect to the error variance when 305MY was considered as the production trait in the model. The standard deviation (S.D.) was higher for the model for single records indicating that bivariate animal model for single records had greater differentiating ability, this observation was made when the production trait in the bivariate model was 305MY or TMY (Table 2 and 3). The results of the present study were similar to the findings of Kadarmideen *et al.* (2003) who reported that the genetic parameters estimated by multi-trait animal model were superior in comparison to the single trait animal model in twenty-three thousand UK and Ireland Holstein cattle. Carvalheira *et al.* (2002) studied fifteen thousand test-day records of first three lactations in US Holsteins and reported that the repeated records allowed accurate estimation of genetic parameters. Weller and Ezra (2004) concluded that multi trait heritability estimates for individual parities were greater than the heritability estimates from the repeatability animal model. Suzuki and Van Vleck (1994) used yield records of first three lactations and divided the data into 10 files by herd within region, each with records of about twenty-four thousand cows and suggested that animal repeatability model should be used for estimation of genetic parameters in Japanese Holstein cattle. Espinoza *et al.* (2007) used 15415 lactation records of 9382 Cuban Holstein cows and did not observe any major difference between the heritability estimates by repeatability and multivariate animal models.

Overview of the results of analysis by univariate or bivariate animal repeatability model indicated that the repeatability model was superior in comparison to single record univariate animal model. There was moderate correlation in sire rankings in case of production and fertility traits, based on the breeding values estimated by univariate animal model for single and repeated records, which indicates that the rankings of the sire based on first lactation performance varied greatly in comparison to the sire rankings based on repeated daughter records. The bivariate animal repeatability model was superior in comparison to the univariate repeatability model as the correlation between the traits was accounted for by the bivariate animal repeatability model. Comparative analysis of breeding value estimation by both the bivariate models i.e. based on first lactation and overall lactations indicated that the bivariate repeatability model was superior to bivariate single records animal model as it accounted for the effect of permanent environment on the phenotypic performance of animal. Further, the bivariate repeatability model used for estimating breeding value for TMY had lower error variance and greater standard deviation of breeding values.

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