

Estimation of Breeding Values by Different Animal Models for Selection of Sires in Crossbred Cattle

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ABSTRACT: Performance records of 1085 crossbred cattle daughters of 57 sires maintained during 1974-2004 at Instructional Dairy Farm of G. B. Pant University of Agriculture & Technology, Pantnagar were used to evaluate sires for first lactation and life time performance traits. The data were analyzed to estimate the breeding values of sires using least squares methods (LSM), best linear unbiased prediction (BLUP) and derivative free restricted maximum likelihood (DFREML) method. The average breeding values of sires estimated by all three methods were similar and estimated for AFC, FLP, FDP and FCI as 1359.95 days, 356.56 days, 177.58 days and 534.15 days respectively and for HL, TLL and LTM as 1641.30 days, 1320.20 days and 9110.30 kg respectively.

Keywords: BLUP; DFREML; breeding value

Introduction

In India, most of the progeny testing is limited to organized farms with small herd size and this is a limiting factor in assessing the sires breeding values. Today, the need for sire evaluation for the additive genetic value (breeding value or transmitting ability) to its progeny has been recognized. Therefore, accurate, efficient and early evaluation of breeding value of sires is of prime importance. In recent past the best linear unbiased prediction (BLUP) procedure has been widely used as standard method of sire evaluation. However, Henderson (1984) opined that analysis of variance and covariance may give biased components of variance from selected population by BLUP method; whereas restricted maximum likelihood (REML) can give bias free estimate. Hence, the sire evaluation using advanced statistical techniques based on derivative free restricted maximum likelihood methods were also used to judge the effectiveness of different methods.

Hence in this paper an attempt is made to compare effectiveness of different methods of sire evaluation for first lactation and lifetime traits milk production in crossbred cattle.

Materials and Methods

Data. The data for the present study were obtained from the performance records of 1085 crossbred daughters of 57 sires maintained at Instructional Dairy Farm of Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, U.S.Nagar, India during 1974-2004.

Statistical Analyses. Breeding value of sires for first lactation traits were estimated by least squares method (LSM) as described by Harvey (1990), best linear unbiased prediction (BLUP) by Henderson (1975) and DFREML version 3.0 – β by Meyer (1998). The effectiveness of different sire evaluation methods was judged by the estimated breeding value of sires taken as twice the sire genetic group solution plus sire solution within sire genetic group for that trait. After estimation of breeding value of sire, the sires were given ranks as per their genetic merit. The product moment and rank correlation among sire's estimated breeding values of different traits was calculated according to Steel and Torrie (1980).

Results and Discussion

Estimated Breeding Value. The estimated overall average breeding values of sires by LSM, DFREML and BLUP methods for age at first calving, first lactation period, first dry period and first calving interval were 1359.95 days, 356.56 days, 177.58 days and 534.15 days respectively. The EBV'S for AFC, ranged from 1296.20 to 1414.70 days, for FLP 330.70 to 399.80 days for FDP 171.40 to 188.90 days and for FCI 509.50 to 562.00 days respectively. By DFREML method the estimated breeding value for AFL ranged from 1162.00 to 1522.20 days, for FLP 305.90 to 449.70 days, for FDP 137.80 to 254.60 days for FCI 470.20 to 616.20 days respectively. By BLUP method the estimated breeding value for AFC ranged from 1204.40 to 1512.70 days, for FLP 302.80 to 447.70 days, for first dry period 151.00 to 226.20 days and for FCI 469.30 to 610.60 days respectively (Table 1.). These estimates showed large genetic differences between sires for first lactation traits. The estimated over all average breeding values of sires by LSM, DFREML and BLUP methods for herd life, total lactation length and lifetime milk yield were 1641.30 days, 1320.20 days and 9110.30 kg respectively.

The estimated breeding values by LSM ranged from 1514.90 to 1736.90 days for herd life, 1186.90 to 1486.40 days for total lactation length and 8535.30 to 9735.00 kg for lifetime milk yield. By DFREML method the estimated breeding value ranged from 1373.00 to 1846.60 days for herd life, 1053.30 to 1570.80 day for total lactation length and 7477.20 to 10878.80 kg for lifetime milk yield.

In the present investigation the estimated breeding values of sires for first of sires for first lactation traits and

lifetime performance traits showed large variation between EBV'S of sires.

Table 1. Average breeding value estimates for first lactation milk yield by different methods of estimation. Sire Evaluation Method (SEM), Average breeding value (ABV), Minimum breeding value (Min. BV), Maximum breeding value (Max. BV), Number of sires over average (No. SOA), Number of sires below average breeding value (No. SBABV)

Trait	SEM	ABV	Min. BV (% below average)	Max. BV (% below average)	No. SOA (% of sires)	No.SBABV (% of sires)
First lactation milk yield	LSM	3050	2829.20 (7.26)	3291.70 (7.89)	33.00 (57.89)	24.00 (42.11)
	DFREML	3050	2464.70 (19.21)	3784.60 (24.05)	30.00 (52.63)	27.00 (47.37)
	BLUP	3050	2484.30 (18.57)	3643.90 (19.44)	30.00 (52.63)	27.00 (47.37)

LSM – Least squares method; DFREML – Derivative free restricted maximum likelihood; BLUP – Best linear unbiased prediction

The estimated breeding values of sires estimated for first lactation and lifetime traits by LSM method showed small genetic variation in comparison to BLUP and DFREML methods. The BLUP method was considered to be second more appropriate than the DFREML method. The results obtained in the present study are in conformation to the reports of Kumar (2003) and Mukharjee (2005). However, Dhaka and Raheja (2000), Dahia (2003), Bajeeetha (2006) and Dubey et al. (2006) reported BLUP as best procedure in comparison to other procedures of sire evaluation.

The rank and product moment correlation. The simple correlations and rank correlations among all the three methods of sire evaluation were very high and significant. The product moment correlations among least squares method and DFREML and BLUP methods of sire evaluation ranging from 0.974 to 1.00 were as the rank correlations breeding value os sires ranged from 0.994 to 0.998 for first lactation traits.

The product moment correlates between EBV'S of sires for lifetime traits ranged from 0.996 to 1.00 where as the rank correlations between the EBV'S of sires for lifetime traits ranged from 0.984 to 0.998 (Table 2.). All the estimates of simple and rank correlations were highly significant. The top 10 sires ranked on the basis of first lactation and lifetime performance traits revealed that all sires would

not rank same for all the methods. However, the rank of sires for different sire evaluation methods revealed that 4-5% top sires almost had similar rank for all the methods. Similar results were also reported by Dalal et al. (1999), Bajetha (2006), Dubey et al. (2006), Moges et al. (2009) and Singh and Singh (2011).

Table 2. Spearman's rank (below diagonal) and product moment correlations (above diagonal) for first lactation traits among different sire evaluation methods of first lactation milk yield.

Method	Method		
	LSM	DFREML	BLUP
LSM	-	0.997	0.998
DFREML	0.987	-	0.998
BLUP	0.992	0.994	-

Conclusion

The estimated breeding values (EBV'S) of sires had very high and significant product moment correlations and rank correlations among all first lactation and lifetime traits estimated by all three methods. These estimates indicating that there was higher degree of similarity (about 85-90%) in ranking of sires by different methods. However, the ranks of sires for different traits revealed that 4-5% top sires had similar rank for first lactation and life time traits. The results revealed that estimated breeding values of sires estimated for first lactation and life time traits by LSM method showed small genetic variation in comparison to BLUP and DFREML methods.

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