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Application of monthly test-day milk yield in Murrah buffalo

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ABSTRACT

In the present study buffalo herds of Murrah breed at various centres are studied to evaluate the sires on the basis of as many daughters as possible. The data pertaining to first lactation monthly test-day milk yield (FLMTDMY) and first lactation 305-days or less milk yield (FL305DMY) of 1,105 Murrah buffalo during 1993 to 2010 at National Dairy Research Institute, Karnal (NDRI); Central Institute for Research on Buffalo, Hisar (CIRB); Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana (GADVASU) and Choudhary Charan Singh Haryana Agricultural University, Hisar (CCSHAU) were collected and adjusted against significant environmental influences. In the present study FLMTDMY and FL305DMY were significantly affected by farm. First lactation records of 832 Murrah buffalo were used for evaluating 95 sires used in 7 sets. First lactation monthly test-day 6 milk yield (FLMTD6MY) had the highest genetic (0.99 ± 0.04) and phenotypic (0.78 ± 0.02) correlation with FL305DMY in Murrah buffaloes. An attempt was being made in the present investigation to estimate and compare the estimated breeding values (EBVs) of Murrah bulls through different sire evaluation methods, viz. contemporary comparison (CC), least-squares (LS), simple regressed least-squares (SRLS) and best linear unbiased prediction (BLUP) for FLMTDMY. The rank correlations among all the 4 methods of sire evaluation were highly statistically significant. BLUP method was found to be more efficient, accurate and stable with lowest genetic variation.

Key words: Best linear unbiased prediction, Buffalo, Contemporary comparison, Least-squares, Simple regressed least-squares, Sire evaluation

India is the treasure house of world's best buffalo germplasm. The Indian buffalo contributes 17% of world milk production and 48 % of Asian milk production (Food and Agriculture Organization 2012). Keeping the importance of buffalo in India, Network Project on Buffalo Improvement was initiated to envisage and undertake progeny testing for improvement of buffalo breeds at various farms in different parts of the country. Till present study 7 sets of Murrah bulls have been evaluated through progeny testing under Network Project on Buffalo Improvement. Sire evaluation is one of the most important aspects of dairy breed improvement programme as the contribution of sire path is higher than the dam path for overall genetic improvement of a trait. The primary aim of an animal breeder is to develop appropriate methodology for sire evaluation to bring about fastest possible genetic improvement in desirable traits. There are several methods of sire evaluation, viz. contemporary comparison (CC), least-squares (LS) and simple regressed least-squares (SRLS) and best linear unbiased prediction (BLUP). The first sire index in India was proposed by Krishnan (1956), which was, however, similar to the contemporary comparison of Robertson and Rendel (1954). The CC method, in addition to adjusting for environment factors, in some cases also accounts for performance of dams of daughters. The ordinary LS and BLUP procedures have the ability to account for systematic differences among sires and to adjust for fixed effects (farm-year-season) simultaneously. However the efficiency of the methods in predicting the estimated breeding values (EBVs) of the sires varies. Hence, the present study was undertaken to study the efficiency of estimating EBVs of Murrah sires by the above 4 different methods. An attempt is being made to estimate and compare the EBVs of Murrah bulls through different sire evaluation methods.

In India test bulls are evaluated based on their daughters first lactation 305-days or less milk yield without taking into account variation in lactation days though the variation in lactation length is reflected in persistency. Genetic evaluation of dairy bulls for milk production based on individual monthly test-day yields rather than 305-days or less milk yield has a number of benefits (Jamrozik and Schaeffer 1997). Because of variability of lactation days in

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dairy animals, the use of test-day models (TDM) instead of lactation model (LM) is of more interest in genetic evaluation. Information on estimates of test-day is lacking in Murrah buffaloes and hence, the present study was carried out.

MATERIALS AND METHODS

In the present study, lactation records of 1,105 Murrah buffaloes, during 1993 to 2010, were collected from the history-cum pedigree sheets and milk yield registers maintained at the National Dairy Research Institute, Karnal (NDRI); Central Institute for Research on Buffalo, Hisar (CIRB); Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana (GADVASU) and Choudhary Charan Singh Haryana Agricultural University, Hisar (CCSHAU). The reproduction records of buffaloes showing abortion, dystocia, and other reproductive disorders were not included in the study. Data of buffaloes with a minimum of 500 kg of milk production in at least 100 days of lactation, calving and drying under normal physiological conditions were included in the analysis. First lactation monthly test-day milk yield (FLMTDMY) and first lactation 305-days or less milk yield (FL305DMY) was considered for the present study. On standardization and normalization, records of 832 Murrah buffaloes were retained for analysis. The data were adjusted for significant non-genetic factors for buffaloes calved in different farms, years and seasons of calving using fixed linear models. Since the data were non-orthogonal, the least-squares technique suggested by Harvey (1990) was used to estimate the effect of non-genetic factors, and the means were compared using Duncan's multiple range test (Kramer, 1957). The model considered was as follows:

$Y_{ijkl} = \mu + P_i + S_j + F_k + e_{ijkl}$ where, Y_{ijkl} is the l^{th} observation in K^{th} farm, j^{th} season and i^{th} year of calving; μ the overall mean; P_i the fixed effect of i^{th} year of calving; S_j the fixed effect of j^{th} season of calving; F_k the fixed effect of the k^{th} farm; and e_{ijkl}, the random error~NID $(0, \sigma^2 e)$.

The genetic and phenotypic correlations were calculated from the analysis of variance and covariance among sire groups (Becker 1975). The standard errors of phenotypic correlations were obtained by Snedecor and Cochran (1994). Genetic and phenotypic correlations between FL305DMY and different FLMTDMYs were used to select particular FLMTDMY for daily milk recording. The EBVs of Murrah buffalo bulls were estimated for FLMTDMY by 4 different methods, viz. contemporary comparison (Sundaresan *et al*. 1965), least-squares (Harvey 1979), simple regressed least-squares (Harvey 1979) and best linear unbiased prediction (Henderson 1975). The EBVs of Murrah buffalo bulls were estimated set-wise and subsequently ranked in respective set. The Spearman's rank correlation method (Steel and Torrie 1960) was used to judge the effectiveness of different methods of sire evaluation. To compare different sire evaluation methods, Spearman's rank correlations were estimated using ranks of bulls based on EBVs for FLMTDMY. Two methods (CC-LS, CC-SRLS, CC-BLUP, LS-SRLS, LS-BLUP and SRLS-BLUP) were compared at a time and significance of rank correlations was tested.

RESULTS AND DISCUSSION

The data were adjusted for significant non-genetic factors. Genetic correlation among FLMTDMYs with FLM305DMY ranged between 0.14 (test-day 10) and 0.99 (test-day 6). Phenotypic correlations of FLMTDMYs with FLM305DMY obtained as 0.21 (Test-Day1) to 0.78 (test-day 6) in Murrah buffaloes. It was observed that first lactation monthly test-day 6 milk yield (FLMTD6MY) had the highest genetic (0.99 ± 0.04) and phenotypic (0.78 ± 0.02) correlation with FL305DMY in Murrah buffaloes. Record of FLMTD6MY of daughter can be taken in 5 months only instead of 10 months with FL305DMY. It is also easy to record FLMTD6MY as compared to FL305DMY. So FLMTD6MY was used to evaluate the bulls. Kaygisiz (2013) reported that correlation between breeding values for test day and 305-day milk yield were estimated as 0.92 ($P<0.01$) for Holstein cows. Kaygisiz (2013) suggested use of TD milk yield for genetic evaluations permits researchers to gain more advantages. The high genetic correlation between test day yield and 305-days lactation yield imply that both traits could genetically be considered as expression of the same trait. Use of test day record is easier and advance than lactation record as in this case only 1 or 2 particular day (test day) record is required instead of taking all day records up to 305-days of lactation.

In the present study, EBVs of sires based on first lactation monthly test-day 6 milk yields (FLMTD6MY) were estimated by 4 different methods and they were ranked subsequently. The estimated EBVs of sires by CC method for FLMTD6MY was 6.80 kg. There were 53 (55.79%) sires whose breeding values were above the average and 42

Table 1. Average breeding value estimates for first lactation monthly test-day 6 milk yield by different methods of estimation

Trait	Sire evaluation method	Average breeding value	Minimum breeding value (% below average)	Maximum breeding value (% below average)	Number of sires over average breeding value (% of sires)	Number of sires below average breeding value (% of sires)
FLMTD6MY[1]	CC[2]	6.80 kg	6.04 kg	7.57 kg	53 (55.79%)	42 (44.21 %)
	LS[3]	6.82 kg	4.68 kg	7.66 kg	51 (53.68%)	44 (46.32%)
	SRLS[4]	6.83 kg	5.40 kg	7.02 kg	51 (53.68%)	44 (46.32%)
	BLUP[5]	6.80 kg	5.75 kg	7.06 kg	44 (46.32%)	51 (53.68%)

Table 2. Rank of sires on the basis of estimated breeding values for first lactation monthly test-day 6 milk yield by 4 different sire evaluation (CC, LS, SRLS and BLUP) methods

Set 1	Rank*				Set 2	Rank				Set 3	Rank				Set 4	Rank				Set 5	Rank				Set 6	Rank				Set 7	Rank			
	A	B	C	D		A	B	C	D		A	B	C	D		A	B	C	D		A	B	C	D		A	B	C	D		A	B	C	D
392	4	4	3	3	93	7	7	7	5	993	6	10	10	9	1319	9	9	9	9	1485	15	14	14	15	1135	9	9	9	16	1419	5	3	2	6
896	5	5	6	4	759	6	6	6	6	1023	2	1	2	1	1341	6	2	2	3	1491	7	10	10	10	1153	1	5	3	3	1727	8	8	8	11
3098	3	1	2	2	761	4	3	2	2	1061	11	8	8	7	1360	5	6	6	6	1524	13	13	13	14	1667	8	8	8	8	1746	12	10	11	8
3108	2	3	1	1	829	9	9	9	8	1084	15	14	15	14	1363	14	14	14	14	1536	10	12	11	12	1706	12	16	14	15	1749	3	5	7	9
3117	6	6	5	7	1241	5	1	3	7	1131	7	3	3	3	1434	12	13	13	13	1555	5	5	5	6	1713	13	13	12	9	1796	1	1	1	1
3125	11	10	11	11	1253	3	4	5	4	1153	1	2	1	2	1437	7	7	7	7	1573	11	7	7	7	1717	2	2	4	4	2121	11	11	10	10
3127	10	8	9	9	1290	11	12	12	12	1165	3	4	4	6	1446	8	11	11	11	1641	4	4	4	4	1836	5	7	7	7	2133	9	12	12	12
3206	1	2	4	5	3551	2	5	4	3	1171	13	15	14	13	1451	4	3	3	1	1666	8	9	9	9	1922	11	10	10	10	2184	6	6	6	5
3294	8	9	8	8	3638	1	2	1	1	1315	8	6	7	4	1506	1	1	1	2	1749	14	15	15	13	1933	4	6	5	6	2331	2	2	3	2
3462	9	11	10	10	3689	8	8	8	9	1354	5	5	5	5	1538	13	12	12	12	1798	2	1	1	2	1944	14	12	13	13	2363	10	9	9	7
3567	7	7	7	6	3736	12	11	11	11	3865	14	13	13	12	4071	2	5	5	5	4244	9	8	8	8	2028	16	15	16	14	4807	7	4	5	4
					3750	10	10	10	10	3924	9	11	12	11	4090	10	10	10	8	4245	12	11	12	11	4506	3	1	1	1	4915	4	7	4	3
										3930	4	7	6	10	4124	11	8	8	10	4371	1	3	2	1	4523	6	3	2	2					
										3949	10	12	11	15	4188	3	4	4	4	4393	3	2	3	3	4619	7	4	6	5					
										3966	12	9	9	8						4395	6	6	6	5	4637	10	11	11	12					
																									4640	15	14	15	11					

*A, B, C and D showing ranks by CC, LS, SRLS and BLUP method respectively.

(44.21%) sires with below average values (Table 1). The estimated average breeding value of sires by LS method for FLMTD6MY was 6.82 kg. Out of 95 sires, 51 (53.68%) had EBVs above the overall average, and 44 (46.32%) sires had below the average breeding value (Table 1). The average breeding value for FLMTD6MY using SRLS was 6.83 kg. Of the 95 sires, 51 (53.68%) had EBVs above the average, while 44 (46.32%) were having values below the average breeding value (Table 1). The average breeding value for FLMTD6MY using BLUP was 6.80 kg. Out of 95 sires, 44 (46.32%) had EBVs above the average, while 51 (53.68%) were having values below the average breeding value (Table 1).

Sires were ranked separately based on EBVs for the 4 sire evaluation methods (Table 2). Accuracy of the methods of sire evaluation was determined by comparing the spearman's rank correlations between ranks of sires estimated by various sire evaluation methods. Rank correlations between ranks of sires by various methods are presented in Table 3. The rank correlations among sires using FLMTD6MY from different methods ranged from 0.678 (in set 7 between CC and BLUP) to 1.000 (in set 4 between LS and SRLS). The rank correlations among all the 4 methods of sire evaluation were highly statistically significant indicating that all the methods of sire evaluation were equally effective to discriminate amongst sires based on FLMTD6MY.

In the present study, the EBVs of sire for first lactation milk yield by BLUP showed less genetic variation than CC, LS and SRLS methods (Table 1) and therefore BLUP was considered as the most efficient method out of all 4 methods of sire evaluation. Bajetha (2006), Dubey *et al.* (2006) and Singh and Singh (2011) also reported BLUP as the best sire evaluation method when compared with other procedures of sire evaluation.

In general EBVs for sires did not show any systematic trend of FLMTD6MY. The estimated breeding values of sires for first lactation yield showed large variation between estimated breeding values of sires, which revealed more genetic variation in the herd. Large genetic variation was also observed between the estimated breeding values of sires by Banik and Gandhi (2006) and Mukherjee *et al.* (2007) in Sahiwal cattle. This might be due to the fact that these herds had number of genetic groups and animals with low production might have not been culled from the herd.

Sires ranked on the basis of first lactation milk yield revealed that all sires would not rank same for all the methods. However, the rank of sires for different sire evaluation methods revealed that 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) and Moges *et al.* (2009). The rank correlation coefficients amongst ranks of sires by different methods of sire evaluation showed a reasonably high degree of agreement in the ranking of sires. In comparison of these methods of sire evaluation BLUP method was found to be more efficient, accurate and stable with lowest genetic variation.

Table 3. Spearman's rank correlations for first lactation monthly test-day6 milk yield among different sire evaluation methods

Method 1	Method 2	Set 1	Set 2	Set 3	Set 4	Set 5	Set 6	Set 7
CC	LS	0.927**	0.895**	0.857**	0.895**	0.929**	0.897**	0.860**
CC	SRLS	0.927**	0.937**	0.879**	0.895**	0.943**	0.938**	0.853**
CC	BLUP	0.891**	0.937**	0.725**	0.899**	0.936**	0.794**	0.678*
LS	SRLS	0.927**	0.972**	0.986**	1.000**	0.993**	0.968**	0.937**
LS	BLUP	0.900**	0.832**	0.939**	0.969**	0.975**	0.871**	0.790**
SRLS	BLUP	0.955**	0.916**	0.904**	0.969**	0.979**	0.879**	0.839**

* Significant at $P < 0.05$; ** significant at $P < 0.01$.

In conclusion, the high genetic correlation between test-day yield and 305-days lactation yield imply that both traits could genetically be considered as expression of the same trait. Estimation of breeding value based on test-day milk yield would offer a solution to handle complex situation like lack of necessary infrastructure for daily milk recording and hence cost of recording could be reduced substantially.

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