Application of test-day model of sire evaluation in Murrah buffalo

Vijay Kumar, AK Chakravarty, CS Patil, Ankit Magotra and PR Shivahre

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Abstract  Buffalo is a triple purpose animal, being suitable for milk, meat and draught. Indian buffalo holds the greatest promise and potential for production. Indian buffalo contributes 17% of world milk production and 48% of Asian milk production (Food and Agriculture Organization, 2012). Among the various buffalo breeds available in India, the Murrah buffalo is the cynosure for dairy type. Murrah buffalo produces good quantity of milk and it is now well established that it represents a unique breed in terms of feed conversion ability with low grade feeds, ability to sustain under adverse climatic conditions, resistance to diseases and production of high value milk containing a higher fat percent. Keeping the importance of buffalo in India, Network Project on Buffalo Improvement was initiated in 1993 with the objective to envisage and undertake progeny testing for improvement of buffalo breeds at various farms in different parts of the country.

Key words: Lactation model, least-squares, Murrah buffalo, test-day model

In general, the lactation length of buffaloes is shorter than in comparison to cattle and the average days to attain peak yield in first lactation for Murrah buffaloes was found 65 days at NDRI herd, India. Moreover, under the existing buffalo improvement programme, 305-day milk yield is the basis to estimate breeding value for milk production without taking into account of variation in lactation days though the variation on lactation length of animals is reflected in persistency. 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 length.

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

In the present study, information were collected from 7 sets of progeny testing under Network Project on Murrah buffalo Improvement. In 7 sets of progeny testing 95 (11, 12, 15, 14, 15, 16, and 12) Murrah bulls were evaluated. Lactation records of 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).

Sires were evaluated on the basis of first lactation 305-days or less milk yield (FL305DMY) and first lactation monthly test-day 6 milk yield i.e. 155th day milk yield (FLMTD6MY) in the present study. The records of the buffaloes with normal lactation were considered for this 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. The buffaloes showing abortion, dystocia and other reproductive disorders were not included in the study. To ensure the normal distribution of records, the outliers were removed and data within the range of Mean ± 3 standard deviation was only considered for the study. Hence after 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 was 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 \( i^{th} \) observation in \( K^{th} \) farm, \( j^{th} \) season and \( i^{th} \) year of calving; \( \mu \) 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, \( \sigma^2_e \)).

First lactation monthly test-day6 milk yield (FLMTD6MY) had the highest genetic and phenotypic correlation with FL305DMY as obtained by Kumar et al. (2014). So FLMTD6MY of daughter was used in the present study. After adjusting data for significant fixed effects, EBVs of Murrah buffalo bulls were estimated for FL305DMY and FLMTD6MY. In 7 sets of progeny testing 95 Murrah bulls were evaluated by least-squares model (Harvey, 1979) as follow:

\[ Y_{ij} = \mu + s_i + e_{ij} \]

where, \( Y_{ij} \) is the observation on \( j^{th} \) progeny of \( i^{th} \) sire on the data corrected for significant non-genetic factor for the trait; \( \mu \) is overall mean for the corrected data; \( s_i \) is effect of the \( i^{th} \) sire and \( e_{ij} \) is random error~NID (0, \( \sigma^2_e \)).

For this model, the data adjusted for non-genetic factors were used. The software programme used was LSMLMW of Harvey (1990).
The magnitude of genetic correlation between 215 and 245 DIM Holstein cows and Kettunen et al. (1998) in Finnish Ayrshire cows. Confirmation with the results obtained by Gadini et al. (1998) in TD were found very high throughout the lactation, which was in agreement with the results obtained by Gadini et al., Kettunen et al., Lidauer et al. Increased. Similar findings were obtained by many workers including Kettunen et al. (1998; Rekaya et al., 1999; Lidauer et al., 2003). It was also found that the genetic correlations between consecutive test days were highly statistically significant indicating that both traits of sire evaluation were equally effective to discriminate amongst sires. The Spearman’s rank correlation method was used to judge the effectiveness of test-day and lactation models of sire evaluation. To compare two models, Spearman’s rank correlations were estimated using ranks of bulls based on EBVs for FLMTD6MY and FL305DMY. Two models were compared for the 7 sets separately and significance of rank correlations were tested.

The data were adjusted for significant non-genetic factors. In the present study FLMTDMY and FL305DMY were significantly affected by farm. EBVs of sires based on FL305DMY and FLMTD6MY were estimated by LS methods and then sires were ranked subsequently (Table 1 and Table 2). Comparison of two models of sire evaluation was done by comparing the spearman’s rank correlations between ranks of sires based on EBVs for FL305DMY and FLMTD6MY. The rank correlations between corresponding ranks (Table 3) based on FL305DMY and FLMTD6MY ranged from 0.594 (in set 2) to 0.888 (in set 6). The rank correlations between two traits for sire evaluation were highly statistically significant indicating that both traits of sire evaluation were equally effective to discriminate amongst sires.

Chakraborty et al. 2010 reported genetic correlations among 305 days milk yield and test day records ranged from 0.11 (TD2 × TD7) to 0.89 (305 days milk yield × TD5). The genetic correlations of 305 days milk yield with test day yields were high except with TD1 and TD2, where, moderate genetic correlations were obtained with other test day records. Test day records have moderate to high positive genetic correlations among themselves barring few exceptions. Tonhati et al. (2008) reported higher genetic correlations among test day records.

Geetha et al., 2006 reported genetic correlations were higher in the initial TD yield and decreased when the TD interval were increased. Similar findings were obtained by many workers (Kettunen et al., 1998; Rekaya et al., 1999; Lidauer et al., 2003). It was also found that the genetic correlations between consecutive TD were found very high throughout the lactation, which was in confirmation with the results obtained by Gadini et al. (1998) in Holstein cows and Kettunen et al. (1998) in Finnish Ayrshire cows. The magnitude of genetic correlation between 215 and 245 DIM with 305 days in milk (DIM) was found very high ranging from 0.95 to 0.98, which indicated that for genetic evaluation of Indian Murrah buffaloes a minimum of 215-245 DIM first lactation length is needed as 82.39% of the total buffaloes completed 245 days first lactation length in comparison to only 55.11% of buffaloes that completed total 305 days milk yield in the herd.

Use of test-day record is more advance method than lactation record as in this case only one or two particular day (test-day) record is required instead of taking all day records up to 305 days of lactation. Test-day milk yields offered a better modeling opportunity and more accurate in genetic evaluation. Also, test-day milk yields in farm should be taken into consideration for selection of the buffalo for milk yield. The test-day models have been suggested as the method of choice for the analysis of milk yield traits in order to maximize the use of all available information. This method becomes even more important in smaller herd size and without well-established milk recording schemes. In fact, the test-day model appears to be a better alternate of 305-day lactation model because early selection on the basis of test-days could reduce generation interval. It could economize the genetic evaluation of dairy animals and improve accuracy of evaluation. 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.

Conclusions

The aim of the study was to investigate efficiency of test-day model (TDM) compared to lactation model (LM) for genetic evaluation of Murrah buffalo bulls. Use of TDM instead of LM is of more interest in genetic evaluation because of variability of lactation days in dairy animals. Data pertaining to first lactation monthly test-day milk yield (FLMTDMY) and first lactation 305-days or less milk yield (FL305DMY) of Murrah buffalo during 1993 to 2010 were collected and adjusted against significant environmental influences. It was found that test-day6 milk yield (FLMTDMY) had the highest genetic and phenotypic correlation with FL305DMY. An attempt is being made in the present investigation to compare the estimated breeding values (EBVs) of Murrah bulls through least-squares method for FL305DMY and FLMTD6MY. The rank correlations between two traits were highly statistically significant indicating that FLMTD6MY equally effective to discriminate amongst sires.

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