



## Genetic Persistency of First Lactation Milk Yield Estimated Using Random Regression Model for Indian Murrah Buffaloes

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**ABSTRACT :** A random regression model was applied for the first time for the analysis of test day records and to study the genetic persistency of first lactation milk yield of Indian Murrah buffaloes. Wilmink's Function was chosen to describe the shape of lactation curves. Heritabilities of test day milk yield varied from 0.33 to 0.58 in different test days. The highest heritability was found in the initial test day (5<sup>th</sup> day) milk yield. Genetic correlations among test day milk yields were higher in the initial test day milk yield and decreased when the test day interval was increased. The magnitude of genetic correlations between test day and 305 day milk yield varied from 0.25 to 0.99. The genetic persistencies of first lactation milk yield were estimated based on daily breeding values using two methods.  $P_1$  is the genetic persistency estimated as a summation of the deviation of estimated daily breeding value on days to attain peak yield from each day after days to attain peak yield to different lactation days.  $P_2$  is the genetic persistency estimated as the additional genetic yield (gained or lost) from days to attain peak yield to estimated breeding value on different lactation days relative to an average buffalo having the same yield on days to attain peak yield. The mean genetic persistency on 90, 120, 180, 240, 278 and 305 days in milk was estimated as -4.23, -21.67, -101.67, -229.57, -330.06 and -388.64, respectively by  $P_1$ , whereas by  $P_2$  on same days in milk were estimated as -3.96 (-0.32 kg), -23.94 (-0.87 kg), -112.81 (-1.96 kg), -245.83 (-2.81 kg), -350.04 (-3.28 kg) and -407.58 (-3.40 kg) respectively. Higher magnitude of rank correlations indicated that the ranking of buffaloes based on their genetic persistency in both methods were similar for evaluation of genetic persistency of buffaloes. Based on the estimated range of genetic persistency three types of genetic persistency were identified. Genetic correlations among genetic persistency in different days in milk and between genetic persistencies on the same day in milk were very high. The genetic correlations between genetic persistency for different days in milk and estimated breeding value for 305 DIM was increased from 90 DIM to 180 DIM, and highest around 240 DIM which indicates a minimum of 240 days as an optimum first lactation length might be required for genetic evaluation of Indian Murrah buffaloes. (**Key Words :** Indian Murrah Buffaloes, Wilmink Function, Daily Breeding Values, Genetic, Persistency)

### INTRODUCTION

Persistency of milk production is the ability of animal to maintain milk production at a high level after peak production, or usually refers to the rate of decline in daily yield after the peak of lactation (Togashi and Lin, 2004), is an economically important trait. More persistent animal has better utilization of feed and fodders thus tends to incur less feed, suffers less to stress, more resistant to diseases (Zimmermann and Sommer, 1973; Solkner and Fuchs, 1987) and makes more profit (Dekkers et al., 1998) by reducing feed cost and reproduction failures and also ensures better performance for longer lactations. With the

introduction of random regression model (RRM) for the analysis of test-day records and the resultant estimation of daily breeding values (DBV's) in most of the developed countries the focus has been shifted to evaluate the animals on the basis of their genetic persistency (Jakobsen, 2000) rather than lactation persistency. The lactation curve is modified by manipulating genetic changes in different lactation stages (Togashi and Lin, 2003) and considering daily estimated breeding values (EBV) as a separate trait on a daily basis (Lin and Togashi, 2005) for improving lactation milk and persistency in cows. Togashi and Lin (2004) also compared five selection criteria in terms of genetic changes in persistency and lactation milk yield. RRM's for test-day yields allow estimating the shape of the genetic lactation curve or genetic persistency for every animal by fitting the curve using daily breeding values individually for each lactation, with simultaneous correction

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for other fixed and random effects on phenotypic performances.

In India, Murrah is one of the best milch breed of buffaloes with tremendous potential for further genetic improvement. Out of total milk produced (88.08 million tonnes) in India, cows account for 39.70 per cent whereas buffaloes contribute about 54.47 percent of total milk even though buffalo population is very low (96.62 million) than indigenous and crossbred cattle (187.38 million) population in the country. 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.

So there is a need to estimate the genetic persistency based on daily breeding values estimated using random regression test-day model. RRM not only improves the accuracy of genetic evaluations, but also provides a potential for evaluating genetic persistency (Jamrozik et al., 1997). Jamrozik et al. (1998) defined the genetic persistency as the slope of the animal's lactation curve between days in milk (DIM) 60 and 280 in cattle and measured as the difference between estimated daily breeding values on day 280 and 60 in lactation (Jamrozik et al., 1998; Strabel, 1999). The genetic persistency was also measured as a summation of deviation of estimated breeding value on days to attain peak yield from each days after days to attain peak yield to lactation length (Jamrozik et al., 1997) in dairy cattle.

Togashi and Lin (2004) developed five selection criteria for genetic improvement in persistency of cows and concluded simultaneous improvement of both lactation milk and persistency by selection of cows based on  $P_{280/65}$  (ratio of partial lactation EBV) or  $r_{280/65}$  (ratio of daily estimated breeding value).

The aim of this study is to estimate the genetic persistency based on daily breeding values estimated using random regression model for first lactation milk yield of Indian Murrah buffaloes. The genetic correlation between genetic persistency for different DIM and estimated breeding value for 305 DIM is also discussed.

## MATERIALS AND METHODS

### Data

The data set comprised of 791 TD records from 80 Indian Murrah buffaloes that were calved from 1995 through 2003 using 11 bulls at NDRI herd. Data were restricted to first lactations DIM with TD between 5 and

305 d. Test days and test dates were taken with an equal interval of 30 days, resulting in 11 TD records (5, 35, 65.....305 days) and 12 test dates. A range of 4 to 11 TD records was used for the estimation of nine parameters. It includes three fixed regression coefficients per subclass, three additive genetic and three permanent environment coefficients for each buffalo were estimated by solving 516 number of equations through single trait random regression (RR) mixed model analysis. Buffaloes were assigned to one of six subclasses for age at first calving (<36, 36-40, 41-45, 46-50, 51-55 and >55) and to one of two seasons of calving i.e. least calving (January to June) and most calving (July-December) seasons, which combined into twelve age-season subclasses. The records of buffaloes with pedigree were included and no phantom parent groups were found for unknown parents in this study.

### Choice of function

Several different functions have been applied to fixed regression models as well as random regression models (Ali and Schaeffer, 1987; Wilmink, 1987; Guo and Swalve, 1997; Van der Werf et al., 1998; Olori et al., 1999). For developing suitable random regression models where the function is linear and have as few parameters as possible, Wilmink's Function in third order of fit (Wilmink, 1987) was chosen to describe the shape of the lactation curves. The function is

$$y_t = w_0 z_0 + w_1 z_1 + w_2 z_2$$

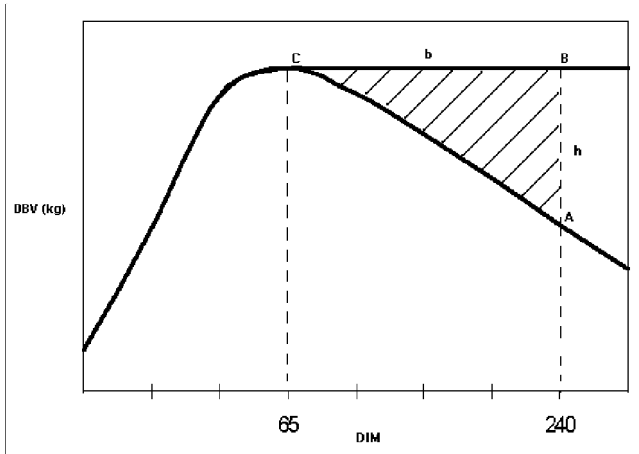
where  $z_0 = 1$ ,  $z_1 = d$  and  $z_2 = e^{-0.05d}$ ,  $d$  is days in milk,  $y_t$  is milk yield in kg,  $t$  is day in milk,  $w_0$ ,  $w_1$  and  $w_2$  is associated with the level of production, production decrease after peak yield and production increase towards peak yield, respectively.

### Model

A single-trait random regression model as described by Schaeffer and Dekkers (1994) was applied to TD records of Murrah buffaloes. The model equation was

$$y_{ijkl} = \text{HTD}_i + \sum \beta_{km} z_{jlm} + \sum \alpha_{jm} z_{jlm} + \sum p_{jm} w_{jlm} + e_{ijkl}$$

Where  $y_{ijkl}$  is  $i^{\text{th}}$  TD record of first lactation belonging to subclass  $k$  for age-season group for  $j^{\text{th}}$  buffalo in  $i^{\text{th}}$  herd test date subclass;  $\text{HTD}_i$  is fixed effect of  $i^{\text{th}}$  herd-test date;  $\beta_{km}$  are fixed regression coefficients for subclass  $k$  of age-season group;  $\alpha_{jm}$  are random regression coefficients related to additive genetic effects on buffalo  $j$ ;  $z_{jlm}$  are covariates for fixed regressions estimated using Wilmink Function (Wilmink, 1987) having the random regression coefficients as  $z_{j10}$ ,  $z_{j11}$  and  $z_{j12}$ , where  $z_{j10} = 1$ ,  $z_{j11} = d$ ,  $z_{j12} = \exp(-0.05d)$  and  $d = \text{days in milk}$ ;  $p_{jm}$  are random regression coefficients



**Figure 1.** Measure of genetic persistency for a Indian Murrah buffalo completed 240 days lactation milk yield.

related to permanent environment effects on buffalo  $j$ ;  $e_{ijkl}$  is random residual effect;  $z_{jlm}$  and  $w_{jlm}$  are covariates for fixed and random regressions estimated using Wilmlink Function (Wilmlink, 1987) having the random regression coefficients as  $z_{j10}$ ,  $z_{j11}$  and  $z_{j12}$ , where  $z_{j10} = 1$ ,  $z_{j11} = d$ ,  $z_{j12} = \exp(-0.05 d)$  and  $d =$  days in milk.

In matrix notation the model can be written as

$$Y = Xb + Za + Wp + e$$

where  $b$  includes  $HTD_i$  and  $\beta_{km}$ ;  $a$  include  $a_{jm}$ ;  $p$  include  $p_{jm}$ ;  $e$  is vector of residual effects and  $X$ ,  $Z$  and  $W$  are incidence and covariate matrices with the assumption.

$$\begin{pmatrix} a \\ p \\ e \end{pmatrix} \sim N(0, V) \text{ and}$$

$$V = \begin{pmatrix} G \otimes A & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & R \end{pmatrix}$$

where  $G$  and  $P$  are variance-covariance matrix of additive genetic and permanent environment random regression coefficients, respectively;  $A$  is additive genetic relationship matrix among the buffaloes;  $\otimes$  is Kronecker product function;  $I$  is identity matrix and  $R$  is diagonal matrix of temporary environmental variances.

The mixed model equations for this model would be

$$\begin{pmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + G^{-1} \otimes A^{-1} & Z'W \\ W'X & W'Z & W'W + I \otimes P^{-1} \end{pmatrix} \begin{pmatrix} b \\ a \\ p \end{pmatrix} = \begin{pmatrix} X'Y \\ Z'Y \\ W'Y \end{pmatrix}$$

**Estimation of genetic (co) variances and parameters**

The genetic variance for each TD yield is a function of covariates (Wilmlink Function) in the model for day  $i$  of lactation as described by Jamrozik and Schaeffer (1997) as  $z_i' = (z_{i0}, z_{i1}, z_{i2})$  where  $z_{i0} = 1$ ;  $z_{i1} = d$ ,  $z_{i2} = \exp(-0.05 d)$  and  $d$  is days in milk. The estimate of genetic variance of TD yield on day  $i$  is  $\sigma_{a_i}^2 = z_i' \hat{G} z_i$ . The estimate of genetic covariance between TD yields on day  $i$  and  $j$  is  $\sigma_{a_{ij}} = z_i' \hat{G} z_j$  where  $\hat{G}$  is variance-covariance matrix of additive genetic random regression coefficients.

The genetic parameters such as heritability and genetic correlations of TD yields were estimated as described by Jamrozik and Schaeffer (1997) as follows;

$$h_i^2 = \frac{\sigma_{a_i}^2}{\sigma_{a_i}^2 + \sigma_{pe_i}^2 + \sigma_{e_i}^2}$$

where  $h_i^2$  is the heritability for  $i^{th}$  TD yield;  $\sigma_{a_i}^2$  is the additive genetic variance on  $i^{th}$  TD yield;  $\sigma_{pe_i}^2$  is the permanent environment variance on  $i^{th}$  TD yield and  $\sigma_{e_i}^2$  is the residual variance on  $i^{th}$  TD yield.

$$rg_{ij} = \frac{\sigma_{a_{ij}}}{\sqrt{\sigma_{a_i}^2 \sigma_{a_j}^2}}$$

where  $rg_{ij}$  is genetic correlation between milk yields on TD  $i$  and  $j$ ;  $\sigma_{a_{ij}}$  is genetic covariance between milk yields on TD  $i$  and  $j$ ;  $\sigma_{a_i}^2$  is the additive genetic variance on  $i^{th}$  TD yield and  $\sigma_{a_j}^2$  is the additive genetic variance on  $j^{th}$  TD yield.

**Estimation of genetic persistency**

The genetic persistencies ( $P_1$  and  $P_2$ ) for first lactation milk yields (FLMY) of Indian Murrah buffaloes are estimated based on daily breeding values estimated through RRM.  $P_1$  is the genetic persistency estimated as a summation of the deviation of estimated breeding value (EBV) on days to attain peak yield (65 days) from each day after days to attain peak yield (66 days) to different lactation days (90, 120, 180, 240, 278 and 305 days) as suggested by Jamrozik et al. (1997) as follows:

$$P_1 = \sum_{k=66}^{LD} (EBV_k - EBV_p)$$

where  $LD$  is the different lactation days (90, 120, 180...305 days),  $EBV_k$  is estimated breeding values after average days to attain peak yield to different lactation days,  $EBV_p$  is estimated breeding value on average days to attain peak yield (65 days).

**Table 1.** Estimates of heritabilities and Genetic correlations in different first lactation test day milk yield of Indian Murrah buffaloes

DIM	5	35	65	95	125	155	185	215	245	275	305
5	0.58	0.51	0.36	0.34	0.33	0.33	0.32	0.31	0.29	0.27	0.25
35		0.39	0.98	0.96	0.93	0.89	0.83	0.75	0.68	0.60	0.52
65			0.41	0.99	0.97	0.93	0.88	0.81	0.74	0.66	0.59
95				0.42	0.99	0.97	0.93	0.87	0.81	0.74	0.67
125					0.39	0.99	0.97	0.93	0.87	0.82	0.76
155						0.37	0.99	0.97	0.93	0.88	0.83
185							0.43	0.99	0.97	0.94	0.90
215								0.39	0.99	0.97	0.95
245									0.37	0.99	0.98
275										0.33	0.99
305											0.41

DIM = Days in milk, diagonal values are the estimates of heritabilities, values in upper triangle indicate the genetic correlations between different test day milk yields.

$P_2$  is the genetic persistency estimated as the additional genetic yield (gained or lost) from day 65 to estimated breeding value on 90, 120, 180... 305 day relative to an average buffalo having the same yield on day 65 as described by Jamrozik et al. (1997) between days in milk 60 and 280 in cattle. For example, the shaded area of Figure 1 is approximated as the area of triangle (ABC) with a base (b) is equal to 175 d and a height of  $(EBV_{240} - EBV_{65})$ . Thus,

$$P_2 = (EBV_{240} - EBV_{65}) \times 87.5$$

## RESULTS AND DISCUSSION

The heritabilities of TD yield varied from 0.33 on 275 DIM to 0.58 on 5 DIM (Table 1). The highest heritability on the initial days of lactation also reported by Jamrozik and Schaeffer (1997) in Holstein cows. The reason for the highest heritability estimates might be due to the fact that milk yield during the first 5-10 days is critical to calf survival in terms of both volume and content and, as such, could have a large genetic component. The heritability estimates of rest of the TD yield although varied from medium to high but that variation was not found wide. On the other hand, low to medium heritability for TD yield was obtained in cattle by many workers (Machado et al., 1998; Lidauer et al., 2003). However, no literature is available on heritability estimates of TD yield estimated through RRM in Murrah buffaloes.

The genetic correlations were higher in the initial TD yield and decreased when the TD interval were increased (Table 1). 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. No literature is available on genetic correlations among TD yield estimated through RRM in buffaloes.

The mean genetic persistency was variable in different DIM in first lactation. About 65.91% of Indian Murrah buffaloes completed the average first lactation length (278 days) in the population and only 55.11% of the total buffaloes were able to complete the 305 days in the first lactation. Jamrozik et al. (1998) and Jakobsen (2000) estimated the genetic persistency by using the above methods in cattle.

Based on the mean and standard deviation (SD) of genetic persistency  $P_1$  and  $P_2$ , the range of genetic persistency were estimated and three types of genetic persistency were categorized for 90, 120, 180, 240, 278 and 305 DIM and also the number of buffaloes in different categories of genetic persistency in different DIM were identified (Tables 2 and 3).

In  $P_1$  and  $P_2$ , the maximum percent of medium and high genetic persistent buffaloes were observed as 98.86 and 96.02, respectively when the objective of breeding programme is to retained 100% buffaloes based on 90 DIM, which however may not be the selection criteria since most of the elite buffaloes remains in the ascending phase of lactation. On the other hand, if the objective is to take 305 DIM, then only 50% ( $P_1$ ) and 46.59% ( $P_2$ ) of medium and high genetic persistent elite buffaloes can be retained in the herd. However, since the objectives of the buffalo breeding programme is to retain a minimum of two third buffaloes as elite animals (medium and high genetic persistent buffaloes) in the population then a minimum of 240 DIM to be considered for the genetic evaluation of Indian Murrah buffaloes for genetic persistency of first lactation milk yield in the herd.

**Table 2.** Parameters and types of genetic persistency ( $P_1$ ) of first lactation milk yield in Indian Murrah buffaloes

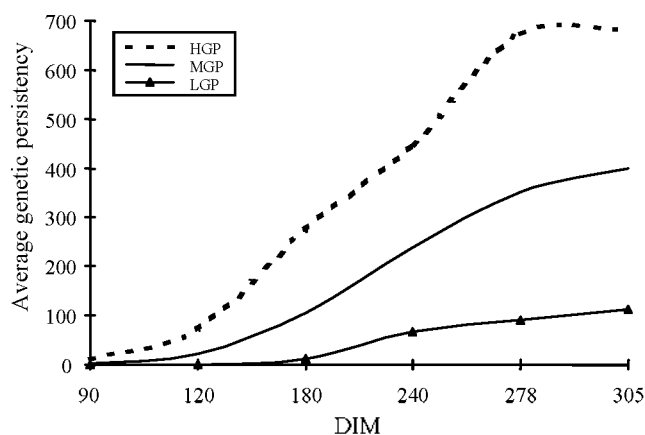
Genetic persistency (GP)	Days in milk (DIM)					
	90	120	180	240	278	305
Mean	-4.23	-21.67	-101.67	-229.57	-330.06	-388.64
Standard deviation	5.90	17.84	58.23	118.59	183.94	191.27
No. of observations	176	174	170	145	116	97
% of buffaloes completed DIM	100	98.86	96.59	82.39	65.91	55.11
Range of GP						
HGP (>MGP)	>-10.13	>-39.51	>-159.90	>-348.16	>-504.00	>-529.91
MGP (Mean $\pm$ 1 SD)	1.67 to -10.13	-3.83 to -39.51	-43.44 to -159.90	-110.98 to -348.16	-156.12 to -504.00	-147.37 to -529.91

HGP and MGP = High and medium genetic persistency

**Table 3.** Parameters and types of genetic persistency ( $P_2$ ) of first lactation milk yield in Indian Murrah buffaloes

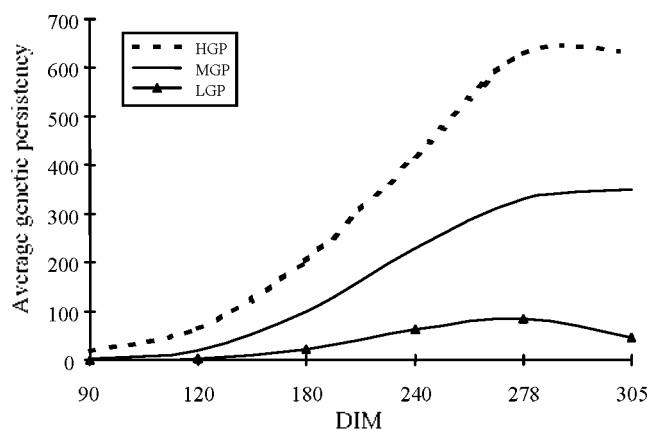
Genetic persistency (GP)	Days in milk (DIM)					
	90	120	180	240	278	305
Mean	-3.96 (-0.32)	-23.94 (-0.87)	-112.81 (-1.96)	-245.83 (-2.81)	-350.04 (-3.28)	-407.58 (-3.40)
Standard deviation	3.43	19.58	73.78	126.13	183.04	194.83
No. of observations	176	174	170	145	116	97
% of buffaloes completed DIM	100	98.86	96.59	82.39	65.91	55.11
Range of GP						
HGP (>MGP)	>-7.39 (>0.59)	>-43.52 (>1.58)	>-186.59 (>3.25)	>-371.96 (>4.25)	>-533.08 (>5.01)	>-602.41 (>5.02)
MGP (Mean $\pm$ 1 SD)	-0.53 to -7.39 (0.04-0.59)	-4.36 to -43.52 (0.16-1.58)	-39.03 to -186.59 (0.68-3.25)	-119.70 to -371.96 (1.37-4.25)	-167.00 to -533.08 (1.57-5.01)	-212.75 to -602.41 (1.77-5.02)

HGP and MGP = High and medium genetic persistency. figures in parentheses indicates absolute values (kg).

**Figure 2.** Types of genetic persistency ( $P_1$ ) in different DIM (DIM = days in milk, HGP, MGP and LGP = High, medium and low genetic persistency).

There is lot of variability in the genetic persistency of three types of buffaloes categorized using both the methods in different DIM. Critical appraisal of Figures 2 and 3 revealed that the genetic persistency in the population has not been declined true to the shape of typical lactation curve which may be due to the reason of the types of genetic persistency were measured by taking daily breeding values up to 305 DIM for Indian Murrah buffaloes.

The genetic correlations among genetic persistency in

**Figure 3.** Types of genetic persistency ( $P_2$ ) in different DIM (DIM = Days in milk, HGP, MGP and LGP = High, medium and low genetic persistency).

different DIM were found very high between any two DIM, which indicated that the genetic persistency between two successive DIM is highly correlated as estimated using both the methods. Similarly, the genetic correlations between genetic persistency estimated by both the methods on same day in milk was also found very high and varying from 0.73 on 90 DIM to 0.99 on 305 DIM as given in Table 4.

The magnitude of genetic correlation between genetic persistency and estimated breeding value for 305 DIM was

**Table 4.** Genetic correlations among estimated genetic persistency ( $P_1$  and  $P_2$ ) in different DIM and  $EBV_{305}$  DIM

DIM	90	120	180	240	278	305	$EBV_{305}$
90	0.73	0.86	0.63	0.70	0.65	0.51	0.07
120	0.85	0.84	0.97	0.96	0.95	0.94	0.09
180	0.88	0.71	0.91	1.00	0.99	0.99	0.19
240	0.89	0.96	0.89	0.97	0.99	0.99	0.27
278	0.91	0.97	0.92	0.98	0.98	0.99	0.23
305	0.90	0.97	0.99	0.99	0.99	0.99	0.27
$EBV_{305}$	0.07	0.10	0.19	0.27	0.20	0.25	-

DIM = Days in milk;  $EBV_{305}$  = Estimated breeding value for 305 DIM; Values in upper and lower triangle indicate the genetic correlation among estimated genetic persistency ( $P_1$  and  $P_2$ ), respectively; Diagonal values are the genetic correlations between  $P_1$  and  $P_2$ .

found low up to 180 days in milk ranging from 0.07 on 90 DIM to 0.19 on 180 DIM in both the methods. The genetic correlations between genetic persistency for different days in milk and estimated breeding value for 305 day in milk was increased from 90 DIM to 180 DIM and found highest around 240 DIM, indicates a minimum of 240 days as an optimum first lactation length might be required for genetic evaluation of Indian Murrah buffaloes.

### CONCLUSIONS

The TD model can be used in future to analyze the individual TD records of Indian Murrah buffaloes instead of 305-day lactation milk yield, which are currently used in India. It has been observed that lactation length of buffaloes is comparatively shorter than in cattle. A single-trait random regression model (RRM) was thus proposed for the first time for the analysis of TD records of first lactation of Indian Murrah buffaloes. Estimation of genetic persistency based on daily breeding values estimated using RRM not only improves the accuracy of genetic evaluations, but also provides a potential for evaluating genetic persistency and in a dairy animal context, a better understanding of the genetics of lactation. The genetic persistency for different DIM and the genetic correlations among genetic persistency and  $EBV_{305}$  were estimated. The highest genetic correlation around 240 DIM between genetic persistency and  $EBV_{305}$ , indicates a minimum of 240 days as an optimum first lactation length might be required for genetic evaluation of Indian Murrah buffaloes for genetic persistency of first lactation milk yield.

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