



Lactation and test day random regression models for genetic evaluation of Murrah buffaloes

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ABSTRACT

In this study the variance components, genetic parameters and breeding values for 305 day or less milk yield were estimated using lactation model and random regression models for the first three lactations in Murrah buffaloes. Random regression model were taken both as random regression model with homogeneous residual variance (RRM-HOM) and heterogeneous residual variance (RRM-HET). The estimates of additive genetic variance using RRM were higher than lactation model in all the three lactations. RRM-HET gave higher estimates of additive genetic variance than RRM-HOM in first lactation while RRM-HOM gave higher estimates in second and third lactation. From RRM, it was possible to account for permanent environmental variance arising due to individual milk yield variations during lactation. The heritability estimates were comparable in all the three models. However, in first lactation, the heritability estimates from lactation model RRM-HOM and RRM-HET were 0.319, 0.296 and 0.305, respectively. Likewise in second and third lactations these estimates were 0.004, 0.137, 0.135 and 0.520, 0.315, 0.264, respectively. The breeding value rank correlation was high in all the lactations. More sires were common for each model among the top 10 ranked sires in all three lactations. In conclusion, RRM can be an alternative to lactation model owing to high accuracy, early evaluation, high additive genetic variance, comparable heritability and high rank correlation for breeding values.

Key words: 305 day or less milk yield, Lactation model, Murrah Buffalo, Random regression model, Test day milk yield

Murrah is one of the best buffalo breed in the world found throughout India with predominance in Haryana and Punjab states. This breed is well known for its productive and reproductive performance with scope for more genetic improvement. For genetic improvement, suitable breeding plan needs to be developed and genetic parameters need to be known. The sires in India are traditionally evaluated on the basis of daughter's 305-DMY (Lactation model). In this model, normal length of lactation is fixed to an arbitrary value of 305-days, terminated lactations and records in progress are extended to 305 days to allow early evaluations. It assumes a fixed shape of lactation curves for dams and tend to underestimate 305-day yields from early test-days for more persistent dams and overestimate yields for the less persistent dams (Jamrozik *et al.* 1997). But genetic evaluation of animals based on test day models (TDM) have gained considerable interest in recent time as it considers

all genetic and environmental effects directly on a test-day basis (Swalve, 1995), has higher accuracy due to more records per daughter than one lactation record in 305-day milk yield model. Test day model permits evaluation of lactation curves for each cow by modelling the genetic component of the lactation curve by fitting random regression (RR) coefficients for each animal (Schaeffer and Dekkers, 1994). The orthogonal polynomials function like Legendre polynomials (LP) and reduce correlation among estimated regression coefficients (Schaeffer 2004). The residual variance changes over time and this heterogeneity of residual variance across the lactations have been modelled by dividing the lactation length into different intervals, with an assumption of homogeneity within intervals and heterogeneity between intervals (Prakash *et al.* 2016).

The study on the use of random regression model for the evaluation of longitudinal data in Murrah buffalo is very scanty and there is no report on the comparison between lactation model and various random regression models in Murrah buffaloes. Thus, the present analysis was done to study the random regression model and compare it with the 305-DMY lactation model for the genetic evaluation of Murrah buffaloes.

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MATERIALS AND METHODS

Source of data: Data were collected from the history cum pedigree sheets and daily milk record registers of Murrah buffaloes maintained at Livestock Production and Management Section at ICAR-Indian Veterinary Research Institute (IVRI), Izatnagar, UP, India. The records on first to third lactation traits of Murrah buffaloes, spread over a period of 30 years (1988 to 2017), were collected for the present study. Detail of data structure and basic statistics of the data are given in Table 1. The data was classified into 3 seasons, 5 periods and the age at calving as a co-variable. The farm’s climate is sub-tropical and standard feeding, breeding and management practices are followed. The test-day milk yield records were also collected from

Table 1. Summary of data structure and basic statistics for different lactations in Murrah Buffalo

Particulars of data	First Lactation	Second Lactation	Third Lactation
Number of animals	504	398	313
Number of animals with records	302	235	191
Number of sire with progeny in data	55	29	22
Number of dams	131	99	65
Number of test day records	2945	2253	1810
Mean±SE of 305–day milk yield (kg)	1753.4±27.72	1989.43±33.76	2047.58±38.81
CV% of 305–day milk yield	27.47	26.01	26.19

the daily milk yield recording registers. Daily milk yield was calculated by adding morning and evening milk yield records on the particular day. A total of eleven individual monthly test day milk yields were collected at an interval of 30 days from sixth day to 305th day of lactation. Actual 305 day milk yield was calculated by adding the daily milk yield from sixth day of lactation to 305 day or fewer days in milk. In the study, animals with only normal lactation records were considered.

Statistical Analysis: Using univariate animal model as well as single trait random regression test-day animal model, the variance components for 305-day milk yield were estimated for first to third lactation.

Lactation model: A univariate animal model was used for variance component estimation of 305-day or less milk yield. A mixed model analysis using software WOMBAT (Meyer 2007) was carried out to obtain restricted maximum likelihood estimate of covariance components.

$$Y_{ijkmn} = \mu + S_i + P_j + A_k + a_m + e_{ijkmn}$$

where, Y_{ijkmn} , 305-day or less milk yield, S_i is fixed effect of i th season of calving; P_j , fixed effect of j th year of calving; A_k , effect of age at calving as co-variable; a_m , animal’s random additive genetic effect with assumption NID (0, σ^2a)

and e_{ijkmn} , random residual effect with assumption NID (0, σ^2e).

Random regression test-day model: In this model, single trait mixed random regression test-day model was applied for all the three lactation’s monthly test-day records of Murrah buffalo. The analysis was performed using a single trait random regression model by WOMBAT software (Meyer 2007). The random regression model used in the analysis was:

$$y = Xb + Za + Wp + e$$

where y , vector of test-day milk yields of Murrah buffalo; b , vector of fixed effects (season of test-day recording month, year of calving and age at calving); X , incidence matrix relating test-day milk yields to fixed effects; p , vector of permanent environmental random regression coefficients (RRC); a , vector of additive genetic RRC, Z and W are covariate matrices for ‘ a ’ and ‘ p ’, respectively, and ‘ e ’ is the vector of random residual effects associated with y . The assumption of this model was:

$$\begin{bmatrix} a \\ p \\ e \end{bmatrix} \sim N(0, V) \text{ with } V = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I \otimes p & 0 \\ 0 & 0 & R \end{bmatrix}$$

where G , variance-covariance matrix of additive genetic RRC; A , additive genetic relationship matrix among the animals; “ \otimes ”, Kronecker product function; P , variance-covariance matrix of permanent environmental RRC; I , Identity matrix and R is diagonal matrix of residual variances.

The average lactation curve was modelled using 6th order Legendre polynomial (LP). The test day milk yield data was modelled using a random regression model considering different order of LP. Different combinations of Legendre polynomial order were fitted for additive genetics as well as permanent environment effects. Legendre polynomials of order 2 to 6 were fitted in various combinations for both the effects and in total 30 models were fitted. For Random regression models with homogenous residual variance (RRM-HOM), the residual variances were taken to be independently distributed with a constant variance along lactation days in milk. And for random regression model with heterogeneous residual variance (RRM-HET), residual variance was assumed to be constant for test-day records within, but different between the following eleven lactation period classes (4–33, 34–63, 64–93, 94–123, 124–153, 154–183, 184–213, 214–243, 244–274, 275–303 and 304–310 DIM). The σ^2e of RRM-HET was calculated as,

$$\sigma^2e = 1/n \left(\sum_{i=0}^n \sigma^2e \right)$$

where n is number of residual variance class. Most suitable model was identified on the basis of residual variance and Schwarz’s Bayesian information criteria (BIC) value.

Estimation of 305-day milk yield variance from random regression test-day estimates: The additive genetic, permanent environmental and error variance for

homogenous and heterogeneous models were estimated as follows:

Additive genetic variance of 305-day milk yield,

$$\Sigma^2_{A305MY} = Z_{C305MY}GZ'_{C305MY}$$

Permanent environmental variance of 305-day milk yield,

$$\Sigma^2_{PE305MY} = Z_{C305MY}PZ'_{C305MY}$$

where Z_{C305MY} , vector of the summations of LP corresponding to 6th to 305th day lactation milk production; P, permanent environmental RRC matrix and G is additive genetic RRC matrix.

Error variance (σ^2_e) for homogenous residual variance was estimated as $\sigma^2_e = \sigma^2_e \times (300)^2$ and for heterogeneous residual variance as $\sigma^2_e = 1/n (\sum_{i=0}^n \sigma^2_e) \times (300)^2$ where n is residual variance class.

Estimation of breeding values: The daily breeding value was estimated as

$$EBV_{jt} = C_t \beta_j$$

where EBV_{jt} is estimated breeding value for an animal (j) in any given days in milk (t), β_j is solutions for additive genetic RRC of animal j and C_t is vector of covariates of LP on day t of lactation. While the 305-day milk yield breeding value was estimated from daily breeding value as:

$$EBV_{305} = \sum_{j=6}^{305} EBV_{jt}$$

where, EBV_{jt} , expected breeding value of jth animal in any day in milk t.

Spearman's rank correlation: To judge the effectiveness of different methods Spearman's rank correlations between breeding values of sires and dams derived from various methods was used. The rank correlation was estimated as per Spearman (1904). The significance of rank correlation was tested by t-test with (n-2) degrees of freedom as given:

$$t = r^2) t = r \sqrt{\frac{(n-2)}{(1-r^2)}}$$

RESULTS AND DISCUSSION

Most suitable model was identified on the basis of lower residual variance and lower Schwarz's Bayesian information criteria (BIC) value. The model with a second order LP to model additive genetic effect and fourth order LP to model permanent environmental effect was found best for first and second lactation from RRM-HOM and RRM-HET. However the model with a second order LP to model additive genetic effect and fifth order LP to model permanent environmental effect was found best for third

Table 2. Description of best random regression test-day models fitted for different lactations in Murrah buffalo

Lactation No.	Order of fit (k)		Number of parameters (np)	RRM-HOM		RRM-HET	
	(k _a)	(k _p)		BIC value	σ^2_e	BIC value	σ^2_e
First Lactation	2	4	14	4465.5	0.95	4455.33	0.90
Second Lactation	2	4	14	3803.44	1.15	3794.93	1.07
Third Lactation	2	5	24	3397.85	1.19	3423.97	1.22

σ^2_e , error variance; k_a, order of fit for additive genetic effect; k_p, order of fit for permanent environmental effect; np, number of parameters; BIC, Bayesian information criteria.

Table 3. Comparison of 305 day or less milk yield variance, heritability and rank correlation of breeding values estimated with different models in Murrah buffalo

Component	First lactation 305-day milk yield			Second lactation 305-day milk yield			Third lactation 305-day milk yield		
	Lactation Model	RRM-HOM	RRM-HOT	Lactation Model	RRM-HOM	RRM-HOT	Lactation Model	RRM-HOM	RRM-HOT
Additive genetic variance (kg ²)	52394.1	63360.04	64116.04	892.1	33750.92	32182.67	114665.1	82224.05	69516.04
PE variance (kg ²)	-	65040.75	64971.82	-	108646.65	112857.33	-	71734.2	84177.2
Residual variance (kg ²)	111873.41	85779.90	81396.24	205266.39	103410	96772.5	105763.01	107262	110007.24
Phenotypic variance (kg ²)	164267.21	214180.69	210484.1	206158.01	245807.57	241812.5	220428.1	261220.25	263700.49
Heritability (Va/Vp)	0.319	0.296	0.305	0.004	0.137	0.133	0.52	0.315	0.264
Spearman's rank Correlation Sire breeding value	1	0.81	0.81	1	0.88	0.87	1	0.72	0.70
Spearman's rank Correlation Cow breeding value	1	0.81	0.81	1	0.60	0.59	1	0.78	0.78

lactation from RRM-HOM and RRM-HET (Table 2).

The estimates from different methods, and its comparison are presented in Table 3. In all the three lactations, the estimate of additive genetic variance using RRM were higher than lactation models. Similar result have been reported by Prakash *et al.* (2017) while contrarily reported by Sawalha *et al.* 2005 and Kaygisiz (2013) for higher estimates of additive variance for lactation model. Among the random regression model, RRM-HET gave higher estimates of additive genetic variance in first lactation while RRM-HOM gave higher estimates in second and third lactation. From RRM, it was possible to account for permanent environmental variance arising due to individual milk yield variations during lactation. The estimates of permanent environmental variance were higher for RRM-HET in second and third lactation while in first lactation the estimate of RRM-HOM is slightly higher. While Prakash *et al.* (2017) have reported the higher estimates from RRM-HET in first three lactations. The estimate of residual variance is lower in RRM than in lactation model for first and second lactation.

In first and third lactation, the heritability estimates were high and in second lactation the estimates were low in all the models, which is similar as reported by Prakash *et al.* (2017). More comparing the heritability between RRM and lactation model, the estimates were always higher for later in first and third lactation while in second lactation the estimate of former were higher than later. Moderate to high heritability value estimates for first lactation 305 day or less have being reported by Geetha *et al.* (2006), Singh *et al.* (2016), Sahoo *et al.* (2014), Kumar *et al.* (2014), Jakhar *et al.* (2016) and Yousuf *et al.* (2017).

Breeding value and rank correlations: The average test-day breeding value of sires ranged from 4.94 kg to 7.10 kg for first lactation, from 5.37 kg to 7.58 kg for second lactation, and from 5.68 kg to 8.25 kg for third lactation by RRM-HOM model. For RRM-HET model the values ranged from 4.50 kg to 6.55 kg for first lactation from 5.40 kg to 7.53 kg for second lactation and from 5.69 kg to 8.16 kg for third lactation. Prakash *et al.* (2017) reported similar increase in average test day breeding value in subsequent lactations.

The rank correlation among the dams as well as sire 305-day or less milk yields breeding values, from RRM and lactation model were high. For all lactations, rank correlation was more than 0.7 except for dam's breeding value in second lactation where the rank correlation were 0.60 and 0.59 for RRM-HOM and RRM-HET, respectively (Table 3). Likewise high rank correlation between test-day model and lactation model were reported by Prakash *et al.* (2017), Zavadilova *et al.* (2005) and Cilek *et al.* (2008). Also when the top ten sires based on breeding value were ranked in each lactation, there were seven sires common for first lactation, eight sires common for second lactation and seven sires common for third lactation. (Table 4).

In conclusion, 305-day or less milk yield estimates from random regression model gave higher additive

Table 4. Top ten sires based on estimated breeding value (EBV) of 305 day or less milk yield (kg) as deviation from population mean.

Rank	First Lactation			Second Lactation			Third Lactation							
	Lactation Model		RRM-HOM	Lactation Model		RRM-HOM	Lactation Model		RRM-HOM					
	Sire I.D	EBV	Sire I.D	EBV	Sire I.D	EBV	Sire I.D	EBV	Sire I.D	EBV				
1	1078*	313.32	1078*	289.59	1043*	295.63	1039*	257.05	1082*	298.49	1078	428.23	1078	402.08
2	1043*	304.11	1043*	286.38	1078*	290.63	1043*	217.20	1043*	252.62	1043*	331.42	1082*	301.92
3	1005*	257.07	1076*	251.54	1076*	250.54	1008*	188.81	1048*	226.29	1048*	281.39	1002*	250.58
4	1031*	231.99	1031*	172.26	1031*	172.29	1019	186.84	1039*	147.18	1036	194.07	1008*	219.01
5	1085	215.90	1039	131.93	1039	129.31	1082*	182.07	1028*	142.92	1007*	180.67	1039*	178.35
6	1082	205.84	1097	127.53	1097	124.83	1048*	166.09	1085*	126.44	1048*	161.78	1003	167.19
7	1076*	198.22	1005*	118.40	1095*	119.91	1014	143.00	1036	119.98	1102*	149.21	1048*	145.28
8	1020	173.33	1095*	118.14	1028*	117.10	1028*	136.00	1102*	117.65	1036	133.52	1040*	141.28
9	1095*	172.91	1028*	116.29	1106	116.72	1102*	133.96	1101	78.59	1101	99.70	1083	115.29
10	1028*	164.08	1106	112.53	1005*	116.10	1085*	98.72	1008*	66.22	1081	61.54	1007*	51.45

*denotes common sire.

genetic variance, and high rank correlation for breeding value. In RRM major part of the residual variance is partitioned into permanent environmental effects. Thus, RRM can be an alternative to lactation model owing to high accuracy, early evaluation, accounting test day environmental effect as well as individual variation in the shape of lactation curve.

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