

Genetic evaluation of Murrah buffalo by fitting random regression models using B-spline function

ASHISH RANJAN^{1✉}, ANAND JAIN², ARCHANA VERMA³, RANJANA SINHA⁴,
POOJA JOSHI⁵ and G R GOWANE⁶

ICAR-National Dairy Research Institute Karnal Haryana 132 001 India

Received: 03 July 2025; Accepted: 08 July 2026

ABSTRACT

In the present study, random regression models with both random and fixed effect regressions fitted by B-spline functions were used to estimate genetic parameters with 5 knots. The common effects for all models were month of recording, year of recording as fixed regressions on daily milk yield records and random regressions for additive genetic and permanent environmental effects. Among different model studied with B-spline functions considering homogeneity and heterogeneity of residual variances, the model that best fit the data was BSQ5H1 (quadratic B-spline model of polynomial order 6 with homogenous residual variance) having knot at 5th, 80th, 155th, 230th and 305th DIM for the first lactation daily milk yield records of Murrah buffaloes. For BSQ5H1, the R² value with estimated arithmetic mean of daily milk yield for first lactation was 93.7%. The highest values of additive genetic (1.22 kg²) and permanent environment variance (5.27 kg²) were observed in the initial (5th) and last (305th) DIM of lactation. Heritability estimates ranged from 0.07±0.05 to 0.21±0.07. It was observed that the heritability estimates were higher in early and late lactation while lower in mid of lactation (DIM 110 to 154). The estimated value of genetic correlation ranged from -0.50 (DIM 5 with DIM 174 to DIM 187) to 1.00. The DIM 5 had negative genetic correlations with peak yield DIM 65 to DIM 243. The rank correlation between sires with 6th order of Legendre polynomial function (RLP6) with BSQ5H1 was more than 0.99 and highly significant (P<0.001). The high rank correlation between two models, indicated that both are equally efficient for genetic evaluation of Murrah buffaloes.

Keywords: Eigenvalue, Lactation curve, Random regression model, Spline function

Animal breeders have worked towards methods or techniques for genetic evaluation of animals with the introduction of organized milk recording and AI (Brotherstone and Goddard, 2005). The major difficulty in the use of 305-day milk yield records for selection is to differentiate the genetic value from non-genetic factors viz the permanent environmental and others environmental factors along the lactation. Alternatively, test-day models are widely in use for genetic evaluations from which the permanent environmental and other environmental factor can be removed along the lactation. One of the best methods that uses test day records is random regression method, with Legendre polynomial as basis function, but have undesirable properties like poor fitting at the extremes

of trajectory (Misztal *et al.* 2000, Meyer 2005a).

As an alternative to Legendre polynomial, the smoothing polynomials and B-splines (Torres and Quaas, 2001, Silvestre *et al.* 2005) were suggested. Bohmanova *et al.* (2008) studied linear spline function using TDMY, in Canadian Holstein Cows, for estimation of genetic parameters and find that RRM with splines functions gave lower estimates of variances at extremes of lactations than Legendre polynomials. Several studies for growth trait in beef cattle with linear spline function were done (Robbins *et al.* 2005, Baldi *et al.* 2010) but still scanty information is available using TD milk yield records with spline functions in Murrah buffaloes. Therefore, the present study on Murrah buffaloes was undertaken for estimation of genetic parameters for days in milk yield records using random regression models with B-spline functions.

MATERIALS AND METHODS

In present study, random regression models with both random and fixed effect regressions fitted by B-spline functions were studied with 3, 4 or 5 knots. The common effects for all models were month of recording, year of recording as fixed regressions on test days milk yield and random regressions for additive genetic and permanent

Present address: ¹Dairy, Fisheries and Animal Resources Department Patna, Govt of Bihar. ²Division of Animal Genetic Resources, ICAR- NBAGR, Karnal, Haryana, 132001, India. ³Animal Genetics and Breeding Division, ICAR-NDRI, Karnal, Haryana-132001, India. ⁴Livestock Farm Complex, Bihar Veterinary College, BASU, Patna-800014, ⁵Animal Genetics and Breeding Division, ICAR-NDRI, Karnal, Haryana, 132001, India. ⁶Animal Genetics and Breeding Division, ICAR-NDRI, Karnal, Haryana, 132001, India. ✉Corresponding author email: ranjanashish05@gmail.com

environmental effects. Data of 10615 DIM records from year 1975 to 2018 for the first lactation of 965 Murrah buffaloes of National Dairy Research Institute, Karnal herd was used to estimate variance components.

The RRM employing linear and quadratic spline functions were fitted by considering the same polynomial order for additive genetic and permanent environmental effects. The general form of the equation as presented by Meyer (2005b) is as follows:

For Quadratic spline regression model:

$$y(t) = \beta_0 + \beta_1 t + \dots + \beta_p t^2 + \sum_{k=1}^p \beta_{pk} (t - t_k)^2 + e_{(t)}$$

Where: $y(t)$ represents the daily milk yield recorded on day t ; β_0 , β_1 , and β_p are the parameters to be estimated; p order of regression function and; t_k is position of knot;

The matrix form of the random regression model with spline function was as follows:

$$y = Xb + Z_s a + W_s p_e + e$$

Where,

y is the vector of observations;

b is the vector of fixed effects and coefficients of fixed regression;

a is matrix containing the estimates for additive genetic spline effects;

p_e is a matrix containing the estimates for permanent environment spline effects;

e is the vector of random residual effect;

X , Z_s and W_s are the incidence matrices of fixed, animal effects, and permanent environmental effects, respectively.

Day in milk yield records were evaluated by the B-spline functions for considering the homogeneity and heterogeneity of residual variances among classes of days in milk. Residual variance classes selected for heterogeneous variances were 5-34, 35-64, 65-94, 95-154, 155-305 according to changes in lactation curve.

The (co)variance components, models comparison, and

genetic parameters were estimated via average information restricted maximum likelihood (AI-REML) approach, using WOMBAT software (Meyer, 2007). The breeding values for animals were predicted from the solutions of the random regression coefficients based on Mrode (2005). Pearson and Spearman rank correlation were used to compare the ranking obtained by using quadratic spline function with 6th order of Legendre polynomials RRM (LP6 and RLP6) using the homogeneous residual variance structure. In LP6 and RLP6 models, fixed monthly test day and random day in milk yields records were modeled using Legendre polynomial to predict breeding values of Murrah buffaloes.

The goodness of the fit of the models was assessed on the basis of Log likelihood value, Akaike information criterion (AIC) (Akaike, 1974), the Schwarz' Bayesian information criterion (BIC) (Schwarz, 1978). RRM models having lower values for AIC and BIC and higher values for Log L and R^2 indicated better fit.

The B-spline RRM were coded as follows: "BSXkHy", where $X = L, Q$ or C are the degree of the linear, quadratic or cubic polynomial segments, respectively; k is the number of knots of the additive genetic and permanent environmental effects; and y is the number of classes of residual variances.

RESULTS AND DISCUSSION

B-splines, the models that were tested considering homogeneity and heterogeneity of residual variances are shown in Table 1 and 2. Regardless of the B-spline functions used (linear, quadratic and cubic) when we increased the number of knots, AIC and BIC showed higher absolute values indicating better fit. Considering only the same number of knots, the values of AIC and BIC were always lower in models for cubic order of polynomial with three, four and five knots. It was observed that values of Log L, AIC, and BIC improved with higher polynomial orders (Table 1).

Table 1. Spline models with homogenous residual variance

Models	Knot	Order	No of parameters	Log L	AIC	BIC
1. BSL3H1	5,155,305	3	13	-9790.32	9803.32	9850.54
2. BSQ3H1	5,155,305	4	21	-9193.07	9214.07	9290.35
3. BSQ4H1	5,105,205,305	5	31	-9011.33	9042.33	9154.93
4. BSC3H1	5,155,305	5	31	-8964.98	8995.98	9108.58
5. BSQ5H1	5,80,155,230,305	6	43	-8896.94	8939.94	9096.12

Table 2. Spline models with 5 class of heterogeneous residual variance

Models	Knot	Order	No of parameters	Log L	AIC	BIC
1. BSQ3H5	5,155,305	4	25	-9151.44	9176.44	9267.25
2. BSQ4H5	5,105,205,305	5	35	-8995.14	9030.14	9157.27
3. BSC3H5	5,155,305	5	35	-8954.85	8989.85	9116.97
4. BSQ5H5	5,80,155,230,305	6	47	-8886.42	8933.42	9104.13

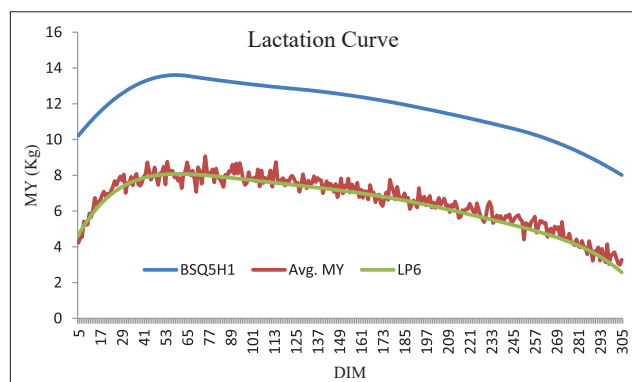


Fig. 1. Estimated DIM yield curve with BSQ5H1 and RLP6 models

For models with five classes for the residual variances of B-spline, the models with the same number of parameters, but with different degrees of the B-spline function, those using a cubic B-spline fitted better in accordance with the adopted comparison criteria (Table 2). Among B-spline functions considering homogeneity and heterogeneity of residual variances, the model that best fit the data was BSQ5H1 (quadratic B-spline model of polynomial order 6 with homogenous residual variance) having knot at 5th, 80th, 155th, 230th and 305th DIM for the first lactation daily milk yield records of Murrah buffaloes.

Similar results were reported by Meyer (2005b) and Baldi *et al.* (2010) using B-splines (linear, quadratic and cubic) to model the growth trajectory of Angus cattle and with Canchim females, find better fit with quadratic polynomial, respectively.

Variance components and genetic parameter estimates:

The random regression models with quadratic spline function estimate a typical mean lactation curve for daily milk yield records of Murrah buffaloes. All models with splines predicted higher milk yield during the lactation and therefore did not create the typical shape of lactation curve like the model using Legendre polynomial function, but curves were smoother for the models using B-splines (Fig. 1). For BSQ5H1 and RLP6 model, the R^2 value with estimated arithmetic mean of daily milk yield for first lactation was 93.7% and 94.1% respectively.

After choosing the best model using B-spline, the (co)variance components and heritability and genetic correlations among milk yield on days 5, 35, 65, 95, 125, 155, 185, 215, 245, 275 and 305 were obtained. The highest values of additive genetic (1.22 kg^2) and permanent environment variance (5.27 kg^2) were observed in the initial (5th) and last (305th) DIM of lactation. The additive genetic variance ranged from $0.19\pm 0.14\text{ kg}^2$ to $1.22\pm 0.45\text{ kg}^2$ for first lactation daily milk yields with homogenous residual variances with 6th orders of polynomial using quadratic spline function (Fig-2). Maximum additive genetic variances were for initial DIM 5 ($1.22\pm 0.45\text{ kg}^2$) and end of lactation stage ($1.12\pm 0.52\text{ kg}^2$) while minimum (0.19 kg^2) for mid of lactation (DIM 125 to DIM 151). Standard errors of DIM 5 (± 0.45) and DIM 305 (± 0.55) were highest which may be due to high variation in additive

genetic effects among animals. Mid of lactation (DIM 125 to DIM 151) had the lowest additive genetic variance and also lower standard errors. The concave shaped curve for additive variance for DIM yields shows a sharp decline during 1st month of lactation which ranged from $1.22\pm 0.45\text{ kg}^2$ (DIM5) to 0.37 ± 0.20 (DIM35). Additive genetic variance decreases up to TD 7 then increased to the end of lactation (TD 11) (Fig. 2).

The permanent environmental variances were higher in initial and end of lactation stage and ranged from $1.30\pm 0.15\text{ kg}^2$ (DIM 244 to 253) to $5.27\pm 0.55\text{ kg}^2$ (DIM 305). The phenotypic variance ranged from $2.50\pm 0.10\text{ kg}^2$ (DIM 234 to DIM 238) to $7.31\pm 0.37\text{ kg}^2$ (DIM 305). The disproportionate body condition after parturition, pregnancy stress during last few months of lactation might be few of possible causes for higher permanent environmental and phenotypic variances in the Murrah buffaloes. The value of permanent environment variances decreased along the length of lactation but proportionally contributed more than additive genetic variance for daily milk yield. Its contribution was more important in mid of lactation stage for maximum production and for achieving peak yield. The present findings were in agreement with Silvestre *et al.* (2005), white *et al.* (1999) and Ranjan *et al.* (2023), where high variances were obtained at both end of lactation with concave pattern but oscillation was more in mid of lactation. The present findings differed from estimate obtained for permanent environment and phenotypic variances obtained for Egyptian buffaloes by Amin *et al.* (2015) and the variances estimated showed the same trend as the additive genetic variances for milk yields.

Heritability estimates ranged from 0.07 ± 0.05 to 0.21 ± 0.07 throughout the lactation (Fig. 2). The curve for variances was compatible with obtained estimates of heritability. It was observed that the heritability estimates were higher in early and late lactation while lower in mid of lactation (DIM 110 to 154). Lower heritability (0.07 ± 0.05 from DIM 110 to DIM154) in mid of lactation indicated lower strength of additive genetic variance during this stage. Along the lactation, heritability values were similar indicating that common genotypes may be responsible for milk yield during that period. Similar trend was also reported by Aspilcueta-Borquis *et al.* (2010) in Murrah

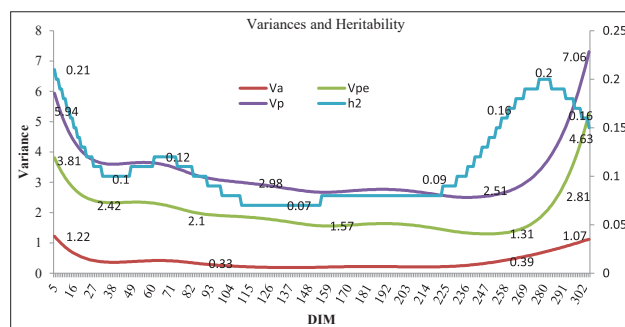


Fig. 2. Variances and heritability for DIM yields records with model BSQ5H1

Table 3. Estimates of additive genetic (lower diagonal) and permanent environment (above diagonal) correlations for test-day milk yield (TDMY) obtained for the model BSQ5H1

DIM	5	35	65	95	125	155	185	215	245	275	305
5	1	0.74±0.04	0.47±0.07	0.48±0.07	0.48±0.07	0.49±0.07	0.45±0.07	0.40±0.07	0.34±0.08	0.18±0.08	0.01±0.08
35	0.57±0.22	1	0.93±0.01	0.80±0.03	0.67±0.05	0.63±0.05	0.57±0.05	0.51±0.05	0.42±0.07	0.25±0.07	0.06±0.07
65	-0.03±0.32	0.80±0.12	1	0.91±0.02	0.77±0.04	0.69±0.04	0.58±0.05	0.50±0.06	0.43±0.07	0.27±0.07	0.08±0.07
95	-0.10±0.36	0.73±0.20	0.98±0.07	1	0.96±0.01	0.84±0.02	0.64±0.05	0.53±0.05	0.48±0.06	0.31±0.07	0.09±0.07
125	-0.19±0.44	0.60±0.32	0.91±0.21	0.97±0.05	1	0.93±0.01	0.73±0.04	0.62±0.05	0.56±0.06	0.37±0.07	0.12±0.07
155	-0.40±0.42	0.41±0.34	0.82±0.21	0.91±0.12	0.97±0.07	1	0.92±0.01	0.84±0.02	0.72±0.05	0.48±0.06	0.20±0.07
185	-0.50±0.42	0.27±0.38	0.73±0.26	0.84±0.27	0.93±0.26	0.99±0.07	1	0.97±0.01	0.82±0.04	0.57±0.06	0.28±0.07
215	-0.34±0.38	0.21±0.39	0.56±0.30	0.72±0.32	0.86±0.33	0.91±0.14	0.94±0.05	1	0.92±0.02	0.67±0.04	0.33±0.06
245	0.05±0.29	0.15±0.34	0.23±0.32	0.41±0.31	0.57±0.32	0.57±0.26	0.60±0.24	0.84±0.11	1	0.84±0.02	0.44±0.07
275	0.20±0.23	0.09±0.29	0.04±0.29	0.21±0.30	0.37±0.32	0.35±0.28	0.37±0.27	0.68±0.19	0.97±0.05	1	0.84±0.03
305	0.20±0.29	0.05±0.36	-0.02±0.35	0.15±0.37	0.31±0.42	0.29±0.36	0.32±0.35	0.63±0.31	0.94±0.24	1.00±0.08	1

buffalo of Brazil. These results differed from Amin *et al.* (2015) in Egyptian buffalo and find lower heritability at the beginning of the test day (0.049) then gradually increased.

Genetic and phenotypic correlation: In present study, the estimates of genetic, permanent environment and phenotypic correlations were obtained from RRM models using quadratic order of spline function for each test day milk yield. But it was difficult to present each and every correlation between day in milk yield, so correlations at monthly interval were tabulated (Table 3).

For the model studied, the obtained correlations between successive days in milk were higher without any exception. The estimated value of genetic correlation ranged from -0.50±0.42 (DIM 5 with DIM 174 to DIM 187) to 1.00. The DIM 5 had negative genetic correlations with peak yield DIM 65 to DIM 243. The estimate of permanent environment correlation ranged from 0.01±0.08 (DIM 5 with DIM 305) to 0.97±0.01 (DIM 185 and 215). The genetic and permanent environment correlations decreased as the distance between the test day increased.

Genetic correlations for milk yield were higher between adjacent days of milk yield. The permanent environmental correlations were also higher, close to unity, between adjacent DIM, decreased as the distance between the two DIM increased.

The values of correlations obtained in present study were in agreement with estimates obtained for WTDY records of Khuzestan buffalo by Madad *et al.* (2016). They found that estimates for genetic and permanent environmental correlations ranged from -0.03 to 1.0 and from -0.94 to 1.0 for weekly test day milk yields. Sesana *et al.* (2010) had also reported negative genetic correlation estimates between TDMY records for the first weeks with the middle to the end of lactation records with random regression models using Legendre polynomials (LPs) for Brazilian Murrah buffaloes.

Eigenvalues: The intercept among (co)variances for both additive genetic and permanent environmental matrix were positive and have largest value among all values (5.97;13.61) (Table 4). The element of additive genetic

Table 4. Estimates of (co)variances and correlations matrix with eigenvalues (λ) with relative percent proportion for each additive genetic and permanent environmental effect for model with BSQ5H1 model

Additive genetic (co)variance matrix							Permanent environment (co)variance matrix						
	a0	a1	a2	a3	a4	a5		p0	p1	p2	p3	p4	p5
a0	5.97	-0.90	-0.33	-1.04	0.50	0.697	p0	13.61	-0.958	1.424	1.097	0.676	-1.071
a1	-0.438	0.706	0.282	0.311	-0.068	-0.186	p1	-0.137	3.568	1.130	1.162	0.531	0.115
a2	-0.331	0.815	0.169	0.173	0.139	0.234	p2	0.251	0.388	2.376	0.846	0.734	-0.241
a3	-0.803	0.698	0.794	0.282	0.063	0.106	p3	0.201	0.416	0.371	2.185	0.882	0.966
a4	0.282	-0.111	0.464	0.162	0.530	0.993	p4	0.147	0.226	0.383	0.480	1.546	0.459
a5	0.203	-0.157	0.404	0.143	0.970	1.977	p5	-0.067	0.014	-0.036	0.151	0.086	18.632
λ	6.51	2.4	0.69	0.04	0	0	λ	18.91	13.82	5.26	1.68	1.42	0.83
(%)	67.54	24.88	7.16	0.41	0.01	0	(%)	45.12	32.96	12.55	4	3.38	1.99

Diagonal, above and below diagonal value are variances, (co)variances and correlation matrix for respective effects (λ = eigenvalue)

Sire evaluation: A total 62 sires having ≥ 5 progeny were evaluated. Ranking of sires were done by above three models i.e. LP6, RLP6 and BSQ5H1 to find out rank correlation.

Table 5. Rank correlation and number of common sire (sire ≥ 5 progeny) with different models; total no of sire= 61

Models	Rank correlation	Number of common sires	
		Top 10	Top 15
BSQ5H1	1	10	15
RLP6	0.99	9	14
LP6	0.91	7	11

correlation matrix ranged from -0.803 (for a0 and a3) to 0.970 (between a4 and a5) while the element of permanent environment correlation matrix ranged from -0.137 (p0 and p1) to 0.480 (p4 and p5). The first eigenvalues obtained for additive genetic (co)variances matrix accounted for 67.54% of additive genetic variances, while first three were able to account for more than 99% variation. The first eigenvalue obtained for permanent environment (co)variances was able to explain 45.12% of variation, while, the first five eigenvalues were able to account more than 95% variation, for the RRM with quadratic spline function having homogenous residual variance structure.

The average 305-day milk yield breeding value of Murrah sires was evaluated on the basis of quadratic spline function. The highest and lowest breeding value for predicted first lactation 305-day milk yield was 154.9 kg and -172.9 kg. The predicted breeding values of 32 sires (52.5%) were above the average breeding value, while the remaining 29 sires (47.5%) had lower breeding value than the average breeding value. It was observed that 9 sires out of top 10 sires, having ≥ 5 progeny, were common for BSQ5H1 and RLP6 models, while number of common sires were 7 for models LP6 and BSQ4H1 for predicted 305-day MY traits. For top 15 sire) of total sires (61 sire), the number of common sires were 11 and 14 for models LP6 and RLP6 model with BSQ5H1 (Table 5).

The rank correlation between sires with model RLP6 model was 0.99 with BSQ5H1 while with monthly TDMY record (LP6), the rank correlation obtained was 0.91 and were highly significant ($P < 0.001$) (Table 5). The high rank correlation obtained with two models using random regression analysis, with 6th order of Legendre polynomial function and quadratic B-spline function with five knots, indicate that both would be equally efficient. From both models, genetic evaluation and selecting bulls can be used in breeding programs.

The present study revealed that quadratic B-spline with five knots at 5th, 80th, 155th, 230th, 305th DIM (BSQ5H1) fit the lactation curve efficiently and can be used for modeling daily milk yield variations for Murrah buffaloes. It was able to account 93.7% of variation along the trajectory. On the basis of relative efficiency, the BSQ5H1 model may be used for sire evaluation and it would be as accurate as evaluation RRM with Legendre polynomial function.

REFERENCES

Amin A M S, Khalil M H, Mourad K A, Afifi E A and Ibrahim M K. 2015. Genetic and phenotypic trends for test day

milk, fat and protein yields applying random regression model in Egyptian buffaloes. *Egyptian Journal Animal Production* **52**: 19–29.

- Aspilcueta-Borquis R B, Sesana R C, Mu.oz-Berrocac M, Seno L O, Bignardi, A B, El Faro L, Albuquerque L G, Camargo, G M and Tonhati H. 2010. Genetic parameters for milk, fat and protein yields in Murrah buffaloes (*Bubalus bubalis* Artiodactyla Bovidae). *Genetics and Molecular Biology* **33**: 71–77.
- Baldi F, Alencar M M and Albuquerque L G. 2010. Random regression analyses using B-splines functions to model growth from birth to adult age in Canchim cattle. *Journal of Animal Breeding and Genetics* **127**: 433–441.
- Bohmanova J, Miglior F, Jamrozik J, Misztal I and Sullivan P G. 2008. Comparison of random regression models with Legendre polynomials and linear splines for production traits and somatic cell score of Canadian Holstein cows. *Journal of Dairy Science* **91**: 3627–3638.
- Brotherstone S and Goddard M. 2005. Artificial selection and maintenance of genetic variance in the global dairy cow population. *Philosophical Transactions of the Royal Society of London B* **360**: 1479–1488.
- Madad M, Ghavi HosseinZadeh N and Shadparvar A A. 2016. Estimation of genetic parameters for testday milk yield in Khuzestan buffalo. *Pesq agropec bras Brasilia* **51**: 890–897.
- Meyer K. 2005a. Estimates of genetic covariance functions for growth of Angus cattle. *Journal of Animal Breeding and Genetics* **122**: 73–85.
- Meyer K. 2005b. Random regression analyses using B-splines to model growth of Australian Angus cattle. *Genetics Selection Evolution* **37**: 473–500.
- Meyer K. 2007. WOMBAT – A tool for mixed model analyses in quantitative genetics by REML. *Journal of Zhejiang University- Science* **8**: 815–821.
- Misztal I, Strabel T, Mantysaari E A, Meuwissen, T H E and Jamrozik J. 2000. Strategies for estimating the parameters needed for different test-day models. *Journal of Dairy Science* **83**: 1125–1134.
- Mrode R A. 2005. *Linear models for the prediction of animal breeding values*. 2nd ed. CABI Publishing, Wallingford.
- Ranjan A, Jain A, Verma A, Sinha R, Joshi P, Gowane G R and Alex R. 2023. Optimization of test day for milk yield recording and sire evaluation in Murrah buffaloes. *Journal of Animal Breeding and Genetics* **00**: 1–13.
- Robbins K R, Misztal I and Bertrand J K. 2005. A practical longitudinal model for evaluating growth in Gelbvieh cattle. *Journal of Animal Science* **83**: 29–33.
- Sesana R C, Bignardi A B, Borquis R R A, El Faro L, Baldi F, Albuquerque, L G and Tonhati H. 2010. Random regression models to estimate genetic parameters for testday milk yield in Brazilian Murrah buffaloes. *Journal of Animal Breeding and Genetics* **127**: 369376.
- Silvestre A M, Petim-Batista F and Colaco J. 2005. Genetic parameter estimates of Portuguese dairy cows for milk, fat and protein using a spline test-day model. *Journal of Dairy Science* **88**: 1225–1230.
- Torres R A and Quaas R L. 2001. Determination of covariance functions for lactation traits on dairy cattle using random-coefficient regressions on B-splines. *Journal of Animal Sciences* **79**: 112.
- White I M, Thompson R and Brotherstone S. 1999. Genetic and environmental smoothing of lactation curves with cubic splines. *Journal of Dairy Science* **82**: 632–638.