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K Sakunthala Devi
Professor & Head, Department
of Animal Genetics and
Breeding, C.V.Sc, Proddatur,
Kadapa, Andhra Pradesh, India

V Anjali
PG scholar, Department of
Animal Genetics and Breeding,
C.VSc, Proddatur, Andhra
Pradesh,
India

K Sudhakar
Associate Professor, Department
of Animal Genetics and
Breeding, C.VSc, Gannavaram,
Andhra Pradesh, India

Ch. Venkatseshaiah
Professor, Department of LFC,
NTR C.VSc, Gannavaram,
Andhra Pradesh, India

Analysing the growth curve in cross-bred cattle using random regression models

K Sakunthala Devi, V Anjali, K Sudhakar and Ch. Venkatseshaiah

Abstract
The data was recorded on around 30,000 number of body weight records at repeated intervals pertaining to 7300 Jersey x Sahiwal crossbred cattle, belonging to 108 sires and 7363 dams from birth to 54 months of age *i.e.* BW0, BW6, BW12, BW18, BW24, BW30, BW36, BW42, BW48 and BW54 and were subjected to random regression analysis for additive genetic, individual permanent environmental, maternal genetic and maternal permanent environmental effects, by using different Legendre polynomials like quadratic, cubic and quartic *etc*. Preliminary analysis revealed that all fixed effects included in the study were having significant ($p \leq 0.01$) influence on the body weight at repeated intervals and were included in the estimation of random regression coefficients. Models using heterogeneous error variance were found to be significantly ($p \leq 0.01$) superior over homogenous error variance. Comparison among 24 models revealed that smaller values of AIC & BIC observed at model 4 (3333B) with minimum number of (33) parameters. The trajectories for 1st and 2nd Eigen functions accounting for >98% and 1.26% of total genetic variation, whereas 3rd Eigen function was found to be zero. In general there were strong positive correlations between intercept (L_0), linear (L_1) and quadratic (L_2) coefficients among all random effects, indicating linear relationship between body weight and age. The correlations between the intercept (L_0) and linear (L_1) coefficients of G and P were higher (0.98) than those of M and C (0.96).

Keywords: RRM, legendre polynomial, eigen function, growth rate, crossbred cattle

1. Introduction
Random regression models (RRM) are extension of repeatability models in which the random animal genetic effect can vary for each time period, without greatly increasing model complexity as occurs in the multiple trait models (Lidauer *et al*., 2003) [1]. When compared with other statistical approaches random regression models enable fitting random genetic and environmental effects over time, which results in higher accuracy of estimated breeding values. It is a popular choice for modeling production traits that change gradually and continually with time and is measured repeatedly on individuals (longitudinal data). Kirkpatrick *et al*. (1990) [2] showed that phenotypic changes with age could be represented by a function of time. Growth is a typical example of such traits. One advantage of RRM is the possibility of calculating variances for every age and covariances between any pair of ages. Random regression models allow the researcher to study changes in genetic variability with time and allow selection of individuals to alter the general pattern of response over time.

In livestock, growth is a crucial characteristic from an economic standpoint. In cow breeding programmes, body weight and weight gain at a certain age or throughout a given period are frequently used as selection criteria. It is vital to accurately predict genetic and environmental factors influencing the growth rate during the test period in order to enhance the growth performance of cattle. Legendre polynomials are generally used to fit the changes in fixed and random effects in models.

Taking this into consideration, the current study was presented with the goals of estimating the coefficient of (co) variance components for body weight at different periods, analysing the growth curve trajectories (Eigen values) at various intervals, and predicting the breeding values for body weight at various ages in Jersey crossbred cattle using random regression models.

2. Materials and Methods
The present research work was under taken through analysis of data on body weights recorded at different time intervals, collected from the performance records of Jersey crossbred cattle maintained by selected field farmers in 28 mandals of Chittoor district, covering a period of

Corresponding Author:
K Sakunthala Devi
Professor & Head, Department
of Animal Genetics and
Breeding, C.V.Sc, Proddatur,
Kadapa, Andhra Pradesh, India

six years *i.e.* from 2013 to 2019, under the field progeny testing program (PTP) of Andhra Pradesh livestock development agency (APLDA). A total of around 30,000 number of body weight records of 7363 animals, belonging to 108 sires and 7363 dams with known pedigree and with minimum three number of records per each animal were considered. The data was recorded on body weight at repeated intervals of six months from birth to 54 months of age *i.e.* BW0, BW6, BW12, BW18, BW24, BW30, BW36, BW42, BW48 and BW54. Data were subjected to random regression analysis for additive genetic, individual permanent environmental, maternal genetic and maternal permanent environmental effects by using different Legendre polynomials like quadratic, cubic and quartic (Meyer, 2005) [3].

The fixed effects included were sex, contemporary group (year of birth), tahasil name and season (March to June as summer; July to October as rainy and November to February as winter). Age at the time of recording body weight was fitted as control variable. Additive genetic, animal permanent environmental, maternal genetic and maternal permanent environmental effects modeled by polynomials of different orders were included as random effects. The random effects were modeled using different Legendre polynomials like quadratic LP_2 (x)=2, cubic LP_3 (x)=3 and quartic LP_4 (x)=4 with their polynomial functions to describe body weight during the different test day records with k_a= 3,4 and 5 random regression coefficients respectively. Preliminary analysis was carried out using univariate analysis to identify the fixed effects having significant influence on body weight and those were included in the random regression models for subsequent genetic analysis. Heterogeneous residual variance was assumed as different across ages between nine growth phases and homogeneous as constant within one age. In this study residual variances for body weight at different ages were modeled using a step up function with one or nine classes respectively.

Different random regression models used with details of order of fit for various random effects along with number of model parameters are presented in Table 2. The order of polynomials were chosen based on the recommendations from previous studies using RRM on growth. In this study a total of 24 models with orders of 3 to 5, including one and nine measurement error classes were compared. All models have the same fixed effects but different number of random effects and so goodness of fit was tested using AIC & BIC values. All investigated models included a direct genetic effect, but different combinations of maternal genetic, maternal permanent environmental and individual permanent environmental effects.

The first model in analyses fitted was model 1, a simple animal model with additive genetic effect as the only random effect (3000). Model 2 considered permanent environmental effect fitting this as an additional random effect (3003). Model 3 attributed maternal effects fitting both maternal genetic and maternal permanent environmental effects as additional effects (3330), whereas in model 4 all random effects (3333) were considered, covariance and correlations were considered between ages. Similarly other models were incorporated with change of order of fit 4 and 5 with different

combinations and analyzed.

The models fitted for the direct, individual permanent environmental and maternal effects were as follows.

$$y = Xb + Z_a a + e \quad \text{model 1}$$
$$y = Xb + Z_a a + Z_{pe} pe + e \quad \text{model 2}$$
$$y = Xb + Z_a a + Z_m m + e \quad \text{model 3}$$
$$y = Xb + Z_a a + Z_m m + Z_{pe} pe + e \quad \text{model 4}$$

where 'y' is the vector of records; b, a, m, p_e and e are the vectors of fixed, direct additive genetic effects, maternal genetic, maternal permanent environmental and the residual effects respectively, with association matrices X, Z_a, Z_m and Z_{pe}. Assumptions for variance (V) involving random effects were $V(a) = A \sigma^2_a$, $V(m) = A \sigma^2_m$, $V(pe) = I \sigma^2_{pe}$, $V(\mathcal{E}) = I\sigma^2_e$, where 'I' represent identity matrix; σ^2_a the direct additive genetic variance, σ^2_m the maternal genetic variance, σ^2_{pe} the variance of the maternal permanent environmental effect and $\sigma^2 e$ is variance of the residuals respectively.

The following basic random regression model was applied for genetic analysis of data.

$$Y_{ij} = Xb + \sum_{k=0}^{k_{a-1}} Z_a a_k + \sum_{k=0}^{k_{m-1}} Z_m m_k + \sum_{k=0}^{k_{p-1}} Z_p p_k + \sum_{k=0}^{k_{w-1}} Z_w w_k + e$$

where, Y_{ij} is body weight of ith animal at j^{th} month of age; Xb is fixed effects of year of birth, sex, season, tahasil and k is regression of age of order associated with the Y_{ij}, independent of the time scale (age); a_k, m_k, p_k and w_k are sets of n values (n=number of animals) of k random regression coefficients corresponding to direct genetic, maternal genetic, maternal permanent environmental and individual permanent environment effects, with order of fit k_a, k_m, k_w and k_p respectively. Z_a, Z_m, Z_w and Z_p are incidence matrices with dimensions n x k_a for Za, n x k_m for Z_m, n x kw for Z_w and n x k_p for Z_p.

$$Z_i = \Phi_i = A_i (t_{ij})$$

The elements of the different Z matrices are Z_i-$\square_i$–A_i (t_{ij}), for which A_i are the coefficients of Legendre polynomial, and t_{ij} are the ages standardized between –1 and +1, derived as,

$$t_{ij} = \left(2 \times \frac{T - T_{min}}{T_{max} - T_{min}}\right) - 1$$

Where, T_{min} is the earliest date (youngest age) and T_{max} is the latest date (oldest age) represented in the data. T is the age in original scale for which t_{ij} is calculated; e are the random residual heterodastic error variances. Homogeneous error variance and error variances were independently distributed with heterogeneous values varying with age were considered. Homogeneous residual variance was assumed to be constant for body weight records within, but different between the 9 growth phases (heterogeneous).

Mixed model equations for the effects included in these models were:

$$\begin{bmatrix} X'X & X'Z_a & X'Z_m & X'Z_p & X'Z_w \\ Z_a'X & Z_a'Z_a + A^{-1}U \otimes K_a^{-1} & Z_a'Z_m + A^{-1}U \otimes K_{am}^{-1} & Z_a'Z_p & Z_a'Z_w \\ Z_m'X & Z_m'Z_a & Z_m'Z_m + A^{-1}U \otimes K_m^{-1} & Z_m'Z_p & Z_m'Z_w \\ Z_p'X & Z_p'Z_a & Z_p'Z_m & Z_p'Z_p + I_p U \otimes K_p^{-1} & Z_p'Z_w \\ Z_w'X & Z_w'Z_a & Z_w'Z_m & Z_w'Z_p & Z_w'Z_w + I_w U \otimes K^{-1}_w \end{bmatrix} \begin{bmatrix} b \\ a \\ m \\ p \\ w \end{bmatrix} = \begin{bmatrix} X'y \\ Z_1'y \\ Z_m'y \\ Z_p'y \\ Z_w'y \end{bmatrix}$$

where, A is the numerator relationship matrix, $\otimes$ is the Kronecker's product, and Ki is the (co)variance matrix of the random regression coefficients of the effects indicated in subscript. In general models were compared based on Akaikes information criterion (AIC), Bayesian information criterion (BIC) values. The best model was used in the fixed part of models for random regression analysis.

AIC provides a means for model selection. The Bayesian information criterion (BIC) is a criterion for model selection among a finite set of models. It is based on the likelihood function, and is closely related to Akaike information criterion.

The formula for calculation of AIC and BIC was as follows.

AIC =-2(log-likelihood) + 2K

Where, K is the number of model parameters (number of variables in model plus intercept).

BIC =-2logL + plog(S_z-r(X))

Where 'p' denotes the number of parameters estimated, 'S_z' is the sample size, '$r(X)$' is the rank of the coefficient matrix of fixed effects in the analysis model. Though these two measures (AIC & BIC) are derived from a different perspective, they are closely related. Apparently, the only difference is BIC considers the number of observations in the formula, which AIC does not. Though BIC is always higher than AIC, lower the value of these two measures, better the model.

The Eigen value is proportional to the amount of genetic variation existing in the population corresponding to that Eigen function. Eigen functions are analogous to the Eigen vectors (principal components) from the analysis of coefficient matrices. Using random regression method, the Eigen values and Eigen functions were calculated from the coefficient matrix for all random effects. Eigen function, for j^{th} age and i^{th} Eigen value of random regression coefficient matrix were calculated as Φjei, where ei is the Eigen vector for i^{th} Eigen value (Kirkpatrick *et al.* 1990) [2].

The estimated breeding value for i^{th} animal at j^{th} age from birth to 54 months of age was calculated from k_i random solutions with Legendre polynomial corresponding to the jth age group by using the following formula.
EBV=$\Phi_j a_i'$

Where, Φ_j is the Legendre polynomial for the jth age group and a_i' is the transpose of vector of random solutions for the ith animal.

All models differed in the order of polynomial fit used to model the additive genetic, maternal genetic, maternal permanent environmental, individual permanent environmental effects (between repeated records on the same animal) and the number of measurement error classes included (homogeneous and heterogeneous).

3. Results and Discussion

The results obtained in the present investigation (Table 1) revealed that body weight in males and females increased from birth to 54 months of age. In cows body weight has shown increased trend from birth upto 42 months of age (323.3±5.92 kg) then decreased at 48 months (317.1±11.84 kg) and again increased at 54 months (368.10±44.98 kg), it may be due to negative energy balance in cows during transition period after calving, differences in managemental systems and climatic conditions over years (Bauman and Currie 1980) [4]. In males almost linear growth was noticed with increased body weights from birth (26.36±0.18 kg) to 48 months of age (452.2 kg). In general males were found to be heavier than females at all ages. The mean body weight estimates in this study are higher than the values reported in literature in Fogera cattle (Kassahun, 2021) [5], at birth and at 6 months in Madura cattle (Harati and Putra 2021) [6], at 12 months in crossbred Jersey cattle (Vijayakumar *et al.,* 2019) [7], at 18 and 24 months of age in Gobra cattle (Diop *et al.,* 1997). Whereas mean values at birth and at 6, 12, 18 and 24 months of age are lesser than the reported estimates in crossbred (Sreedhar, 2015) [8] and Vrindhavani cattle (Sagar *et al*., 2017) [9]. The changes in the value of standard deviation across ages may owe to decrease in population size and due to managemental practices of culling some animals.

Table 1: Statistical description of data for body weights (kg) at different ages in Jersey crossbred cattle

Age (months)		No. of records	Minimum (kg)	Maximum (kg)	Mean ± SE	SD (kg)	C.V (%)
BW0	Male	186	19.20	30.00	26.36±0.18	2.51	9.50
	Female	7177	13.50	26.90	23.17±0.02	2.51	10.83
BW6	Male	186	65.65	98.50	83.30±0.63	8.70	10.40
	Female	7177	60.12	99.73	79.19±0.10	8.70	10.90
BW12	Male	186	120.00	180.60	144.60±1.19	16.30	11.20
	Female	7177	89.99	159.78	122.50±0.20	17.28	14.10
BW18	Male	165	175.22	233.30	205.90±2.17	34.90	16.90
	Female	5309	116.90	382.30	174.90±0.47	34.80	19.80
BW24	Male	128	214.50	371.20	277.30±3.56	40.30	14.50
	Female	3810	150.10	396.80	215.40±0.65	40.15	18.60
BW30	Male	86	258.40	432.80	328.90±4.66	43.26	13.10
	Female	2071	210.10	486.90	275.20±1.05	47.87	17.30
BW36	Male	47	281.80	519.00	377.40±9.40	64.50	17.09
	Female	794	200.00	504.00	300.30±2.27	64.19	21.37
BW42	Male	23	334.15	482.15	414.90±12.8	61.35	14.78
	Female	185	225.50	534.10	323.30±5.92	80.61	24.93
BW48	Male	1	-	452.20	452.20±0.00	-	-
	Female	21	245.40	455.39	317.10±11.8	54.27	17.11
BW54	Female	3	305.40	455.30	368.10±44.9	77.92	21.16

Preliminary analysis revealed that all fixed effects considered have significant ($p \leq 0.01$) influence on body weight at different ages and therefore all effects were included in random regression models. Results revealed that 3rd order *i.e.* quadratic (k=3) with heterogeneous residual variance of 9 classes was more appropriate than other polynomial orders.

Similar results were reported by Meyer (1999) [10] with k=3 while analyzing monthly body weights in Herefords and Wokalup cattle.
Order of polynomial fit of the different models along with the number of model parameters, AIC and BIC values are shown in Table 2.

Table 2: Order of polynomial fit of the different models along with the number of model parameters (Np), AIC and BIC.

Model no.	Model	Order of fit				R	Np	Information criteria	
		D	M	MPE	IPE			AIC	BIC
1	3000B	3	0	0	0	9	15	-129468.08	-129700.98
	3000A	3	0	0	0	1	7	-124045.19	-129641.39
2	3003B	3	0	0	3	9	21	-1492454.50	-1492501.00
	3003A	3	0	0	3	1	13	-129470.80	-1071184.12
3	3330B	3	3	3	0	9	27	-1825102.41	-1825157.36
	3330A	3	3	3	0	1	19	-1809509.68	-1809537.20
4	3333B	3	3	3	3	9	33	-1978329.27	-1978326.44
	3333A	3	3	3	3	1	25	-1893918.86	-1893948.60
5	4000B	4	0	0	0	9	19	-122165.45	-122335.93
	4000A	4	0	0	0	1	11	-122146.45	-122334.33
6	4004B	4	0	0	4	1	21	-112039.30	-122228.55
	4004A	4	0	0	4	9	29	-111817.46	-122228.55
7	4440B	4	4	4	0	9	39	-107078.33	-107369.99
	4440A	4	4	4	0	1	31	-107075.62	-107331.66
8	4444B	4	4	4	4	9	49	-107065.29	-107310.83
	4444A	4	4	4	4	1	41	-107061.97	-107306.83
9	5000B	5	0	0	0	9	24	-107056.39	-107248.93
	5000A	5	0	0	0	1	15	-107047.74	-107248.27
10	5005B	5	0	0	5	9	39	-107045.90	-107238.60
	5005A	5	0	0	5	1	24	-107043.68	-107237.95
11	5550B	5	5	5	0	1	54	-107019.12	-107106.21
	5550A	5	5	5	0	9	36	-106980.12	-107161.70
12	5555B	5	5	5	5	9	59	-122139.78	-107080.56
	5555A	5	5	5	5	1	58	-122139.78	-104765.00
13	3344B	3	3	4	4	9	41	-122200.04	-124184.69
	3344A	3	3	4	4	1	33	-122194.00	-122383.60
14	3434B	3	4	3	4	9	41	-122189.34	-122351.84
	3434A	3	4	3	4	1	33	-122185.34	-122344.88
15	3443B	3	4	4	3	9	41	-122184.58	-122340.22
	3443A	3	4	4	3	1	31	-122168.36	-122336.82
16	4333B	4	3	3	3	9	37	-110883.78	-112188.97
	4333A	4	3	3	3	1	29	-107270.15	-112178.79
17	4343B	4	3	4	3	9	41	-107264.41	-111956.95
	4343A	4	3	4	3	1	33	-107260.19	-111023.27
18	4443B	4	4	4	3	9	45	-107074.96	-107322.71
	4443A	4	4	4	3	1	37	-107072.09	-107321.48
20	4545B	4	5	4	5	9	59	-107057.43	-107304.23
	4545A	4	5	4	5	1	51	-107056.85	-107294.31
21	4554B	4	5	5	4	9	59	-107056.44	-107263.56
	4554A	4	5	5	4	1	51	-107056.43	-107263.05
22	5554B	5	5	5	4	9	64	-106979.02	-107106.21
	5554A	5	5	5	4	1	56	-104765.00	-107081.57
23	5444B	5	4	4	4	9	54	-107043.25	-107226.83
	5444A	5	4	4	4	1	46	-107039.11	-107226.38
24	5454B	5	4	5	4	9	59	-107039.00	-107216.99
	5454A	5	4	5	4	1	51	-107025.89	-107202.30

D-Direct genetic; M-Maternal genetic; MPE-Maternal permanent environmental
IPE-Individual permanent environmental; R-Residual variance

Two strategies were considered for modelling the residual variance. In the first strategy, homogeneity of the residual variance (R=1) within the age was considered for the whole period. In the second strategy, heterogeneity of residual variance across ages was modeled as a step function of the covariable along growth trajectory, by dividing the growth trajectory into 9 growth phases, *i.e.* 1-179, 180-359, 360-539, 540-719, 720-899, 900-1079, 1080-1259, 1260-1439, 1440-

1620 days of age and allocating a residual variance to each phase. Heterogeneous error variance contributed 30% percent of the total variance value at each phase for all body weight records.
In the first quadratic model (3000A,B) the available random effect other than residual effect was direct additive genetic effect. Later addition of individual permanent environmental effect to the additive genetic effect (3003A,B) without

increasing the order of fit has reduced AIC and BIC values compared to model 3000A,B. Then addition of maternal effects (maternal genetic and maternal permanent environmental effect) to the additive genetic effect (3330A,B) has further reduced AIC, BIC values compared to model 1 and 2 (3000A,B & 3003A,B).

In general it was observed that by including random effects one after the other to the first model (3000A, B) *i.e.* inclusion of all four random effects in quadratic model (3333B) with 33 number of parameters and residual variance of 9 classes has shown better improvement in with smaller AIC, BIC values as compared with previous models (3000A, B; 3003A,B; 3330A,B). Similar trend was observed with cubic (k=4) and quartic (k=5) polynomials also.

Based on AIC and BIC values best RRM model was selected for estimation of variance, covariance, genetic parameters and breeding values for body weight at different ages.

When comparison was made among 24 models, based on AIC

and BIC smaller values with heterogeneous error variance, the quadratic model (3333B) with orders of 3, 3, 3 and 3 for direct additive genetic, maternal genetic, maternal permanent environmental and individual permanent environmental effects was found to be as best fit model. So based on AIC and BIC values, Model 4 (3333B) was able to describe the covariance structure adequately and was selected as the parsimonious model. According to this criterion, the model considering functions with the orders of 3333B with 33 number of parameters was superior to the other models in fitting of covariance along the growth curve. It was observed that the values of AIC & BIC did not improve with the increase of order of fit and legendre polynomials *i.e* from quadratic (3) to quartic (5).

Eigen values of various random regression coefficients along with the percentage contribution to the total variation for the best model (3333B) based on AIC and BIC values are presented in Table 3.

Table 3: Estimates of variances (diagonal), covariances (below) and correlations (above) between random regression coefficients of coefficient matrix and the corresponding eigen values (λ) wirh their percentage contribution to the total variation for best model with order of fit 3, 3, 3, 3

Effect		Coefficient of K_r^a (k=3, 3, 3, 3)			Eigen value (λ)	Eigen function Contribution %
		L_0	L_1	L_2		
Additive genetic (G)	L_0	1340.30	0.98	0.86	2375.36	98.74
	L_1	1134.00	987.28	0.94	30.20	1.26
	L_2	281.20	260.92	77.98	0.00	0.00
Maternal genetic (M)	L_0	137.48	0.96	0.76	249.69	97.20
	L_1	118.20	108.65	0.90	7.18	2.80
	L_2	29.37	30.85	10.74	0.00	0.00
Maternal permanent environmental (C)	L_0	136.14	0.96	0.76	248.38	97.20
	L_1	117.63	108.66	0.90	7.16	2.80
	L_2	29.22	30.84	10.74	0.00	0.00
Animal permanent environmental (P)	L_0	1852.60	0.99	0.99	3696.61	99.94
	L_1	1765.50	1685.70	0.99	2.30	0.06
	L_2	543.51	519.82	160.64	0.00	0.00

L_o is intercept; L_1 is linear term; L_2 is quadratic.

In general the large Eigen value was recorded for intercept (L_0) followed by linear (L_1) coefficient for all random effects, whereas the Eigen value for quadratic coefficient was found to be zero. Among all the effects more than 90% of the contribution to the total variation was explained by the intercept (L_0) (97.20 to 99.94%). The linear (L_1) coefficient accounted for 1.26, 2.8,2.8 and 0.06% to the total variation for

additive genetic, maternal genetic, maternal permanent environmental and individual permanent environmental effects respectively, indicating a small fraction of contribution to the total variation.

Eigen functions (ef) of the random regression genetic covariance matrix of growth upto 48 months of age are depicted in Fig 4 to understand the influence of factors corresponding to each Eigen value.
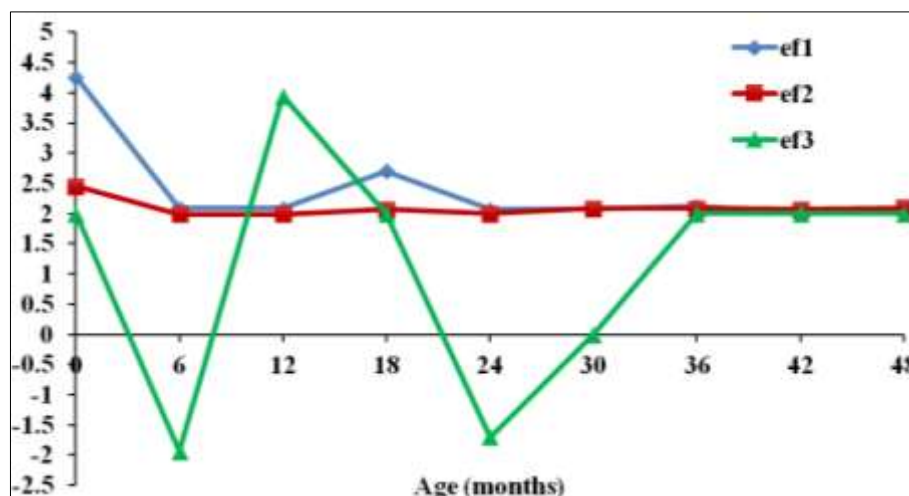
Fig 1: Plot of Eigen functions of the random regression genetic covariance matrix of growth upto 48 months of age.

Eigen functions for 1st and 2nd Eigen value showed positive trend. The trajectories for 1st Eigen function (ef1) accounting for more than 98% of total genetic variation) was high at birth and steep decrease upto 6 months, again increased upto 18 months of age, after this decreased again at 24 months and then remained constant upto 48 months of age (Fig 1). Eigen function 2 (ef2) accounts for 1.26% of total genetic variation showed a straight-line function parallel to age axis, whereas Eigen function 3 (ef3) which accounted for less genetic variation showed interesting patterns, were high at birth and steep decrease during 6 months with rapid increase at 12 months then steep decline upto 24 months of age. After this Eigen function increased upto 36 months and then remained constant at later ages.

The average, minimum, maximum breeding value (kg) for body weight across ages along with number of animals above average breeding value (%) are shown in Table 4. The average breeding value for birth weight was found to be 23.24 kg, which improved to 321.10 kg at 48 months of age. Maximum breeding value (333.49 kg) was recorded at 42 months of age. As age of the animal increased the average breeding value also increased upto 42 months (333.49 kg) and slightly decreased at 48 months (321.10 kg) of age. There was large variation observed in the breeding value and the numbers of animals above average breeding value (% cows) were ranging from 36.36% (BW48) to 57.32% (BW0).

Table 4: Average, minimum, maximum breeding values (kg) for body weight at different ages

Trait	Average Breeding value (Minimum to maximum)	No. of animals above average breeding value (% of cows)
BW0	23.24 (13.21-29.96)	4221 (57.32)
BW6	79.39 (57.90-147.69)	3588 (48.73)
BW12	123.24 (81.10-191.65)	3672 (49.87)
BW18	175.73 (70.81-401.10)	2625 (47.98)
BW24	215.98 (128.56-432.06)	1995 (50.66)
BW30	276.02 (184.98-540.98)	948 (43.94)
BW36	304.64 (181.54-529.37)	357 (42.55)
BW42	333.49 (152.32-683.37)	90 (43.47)
BW48	321.10 (191.56-565.33)	8 (36.36)

4. Conclusion
It was concluded that Quadratic Legendre Polynomial was found to be more suitable to describe the covariance structure of growth traits in jersey crossbred cattle, based on AIC and BIC values.

Large variation observed in breeding values for body weights, gives scope for selection of superior sires for further improvement of body weights.

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