RESEARCH ARTICLE

Genetic Evaluation of Growth Traits in Large White Yorkshire Crossbred Pigs using Random Regression Models

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Abstract

The objective of the present study was to determine the heritability estimates and breeding values of body weights in Large White Yorkshire crossbred pigs using random regression models. Data obtained from 51,302 records of 4653 animals, progeny of 155 sires and 291 dams was subjected to random regression analysis using Legendre polynomials of order of fit 3, 4 and 5. Based on AIC values, random regression model with homogenous error variance and order of fit 3 for direct genetic, maternal genetic, maternal permanent environmental, and individual permanent environmental effects was found to be the best model. The first Eigen value accounted for more than 95% of the total genetic variation. The direct genetic heritability estimates tended to increase over time ranging from 0.02±0.00 at 1st week to 0.88±0.08 at 24 weeks of age. The average estimated breeding value for birth weight was 1.15 kg which increased to 39.38 kg at 24 weeks of age.

Keywords: AIC, BIC, Breeding value, Eigen functions, Heritability, Random Regression Model

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Introduction

Pigs have the best feed conversion efficiency and can produce greater weight gain from a given feed weight, making pig farms the most useful source of meat production. Body weight has been a concern for the swine industry as it is related to economic loss or profit for producers. Variation existing in body weight of pigs is inherent and usually high in early stages, it is very likely to be maintained throughout the rest of the growth stages. Kirkpatrick *et al.* (1990) showed that phenotypic changes with age could be represented by a function of time. A typical example of such traits is growth. Random regression models are used to evaluate longitudinal traits or growth traits that are recorded repeatedly during the animal's life, to yield more accurate breeding values and for selection of young animals based on the complete pattern of the growth curve (Oliveria *et al.,* 2019). In addition, random regression models can predict the breeding values at an early age and let decide selection of animals in time. Hence present study was planned to evaluate heritability estimates and breeding values in Large White Yorkshire crossbred pigs which are under long term selection programme for improvement of body weights.

Materials and Methods

Data was collected from the performance records of 75% Large White Yorkshire crossbred pigs (SVVU-T17) during the period from 2005 to 2022 (18 years), maintained at All India Coordinated Research Project on Pig (ICAR-AICRP), SVVU, Tirupati, Chittoor district, Andhra Pradesh. A total of 51,302 records of body weight of 4653 animals, belonging to 155 sires and 291 dams with known history and pedigree, having minimum 3 records per animal were considered. The data was recorded on body weight at weekly interval from birth to 8 weeks and thereafter with 4-week interval up to 24 weeks of age, *i.e.* BW0, BW1, BW2, BW3, BW4, BW5, BW6, BW7, BW8, BW12, BW16, BW20, and BW24. Piglets were identified after birth by ear notching as per their pedigree. Pigs were reared in a uniform manner under same management conditions with *ad libitum* feeding and piglets were weaned at 42 days of age.

Statistical Analysis

The fixed effects included were sex, season (March to June as summer; July to October as rainy and November to February as winter), period and parity. Age at the time of recording body weight was fitted as the control variable to model

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for the mean body weight using Legendre polynomials. Additive genetic, animal permanent environmental, maternal genetic and maternal permanent environmental effects were included as random effects which were modelled using different combinations of quadratic, cubic and quartic Legendre polynomials. The heritability estimates were obtained through Derivative Free Restricted Maximum Likelihood (DFREML) method using Wombat software (Meyer, 2006).

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 i^{th} animal at j^{th} week of age; Xb is fixed effects of sex, season, period, crop 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 environmental effects, with order of fit k_a, k_m, k_w, k_p respectively.

The elements of the different Z matrices are Zi-Fi-Ai(tij), for which Ai are the coefficients of Legendre polynomial and tij are the ages standardised between -1 and +1, as derived by,

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

Where, Tmin is the earliest date (youngest age) and Tmax is the latest date (oldest age) represented in the data. T is the age in original scale for which tij is calculated; e are the random residual heterodastic error variances. Homogeneous residual variance was assumed to be constant for body weight records within, but different between the 12 growth phases (heterogeneous). The best model was decided based on Akaike's Information Criterion value. Breeding values and heritability estimates were calculated using the best model.

The formula for calculation of Akaike's Information Criterion (AIC):

AIC = -2(log-likelihood) + 2K, where, K is the number of model parameters (number of variables in model plus intercept).

Estimation of Breeding Value

The estimated breeding value for ith animal at j^{th} age from birth to 24 weeks of age was calculated from ki random solutions with Legendre polynomials corresponding to the j^{th} age group by using the formula: EBV = $\Phi_j a \Phi i$, where, Φ_j is the Legendre polynomial for the j^{th} age group and a'J is the transpose of the vector of random solutions for the i^{th} animal.

Eigen values are useful for analysing and visualising the pattern of variation of functional traits like growth curve (Meyer and Kirkpatrick, 2005). Using random regression method, the Eigen values and Eigen functions were calculated from the covariance matrix of additive genetic effects. Eigen function (ψ) as a component of analysis derived trait wise mathematically as $L\psi(x) = \lambda\Psi(x)$; calculated based on Eigen value (λ), by considering age as variable φ(x), L is a covariance matrix of additive genetic component derived for the best model (Kirkpatrick *et al.* 1990).

RESULTS AND DISCUSSION

The mean body weight along with standard deviation and coefficient of variation from birth to 24 weeks of age in males and females are presented in Table 1. In general, males were found to be heavier than females at all ages, except at 16, 20 and 24 weeks of age. This could be as a consequence of differences in managemental practices implemented in the farm like segregation of animals by gender and body weight and also by providing individual feeding to female piglets during that age. Random regression models were fitted with Legendre polynomial orders of 3, 4 and 5 (quadratic, cubic and quartic) for additive genetic, individual permanent environmental, maternal genetic and maternal permanent environmental effects. Comparison between Legendre polynomials revealed that model fitted with order of fit 3 for all random effects (3333A) considering homogenous residual variance with 25 number of model parameters as the best fit based on AIC values as shown in Table 2. Our results corroborated with findings of Kohn *et al.* (2007), Fernandez *et al.* (2008), Cai *et al.* (2011), Lee and Do (2012), Gaur *et al.* (2019) and Devi *et al.* (2022).

Eigen value indicates the amount of variance explained by its associated Eigen function (Kingsolver *et al.*, 2001). In general, large Eigen value was recorded for the intercept (L_0) followed by linear (L_1) coefficient for all random effects, whereas Eigen value for quadratic (L_2) coefficient was zero. These results were in accordance with findings of Fernandez *et al.* (2008), Gaur *et al.* (2019) and Devi *et al.* (2022).

The intercept (L_0) accounted for >95% of the total variance for additive genetic, maternal genetic and maternal environmental effects, whereas for animal permanent environmental effect the value was 87.5% (Table 3). A large Eigen value represents considerable genetic variation for pattern of growth and changes in the growth curve that can be modified by selection (Bermejo *et al.* 2003). Kohn *et al.* (2007), Fernandez *et al.* (2008), Gaur *et al.* (2019) and Chaudhary *et al.* (2019) reported 89, 84, 97 and >98% contribution of the total additive genetic variation by intercept (L_0).

The Eigen functions of the genetic covariance matrix are especially of interest, as they represent possible deformations of the mean trajectory which can be affected by selection, while the corresponding Eigen function (ef) describes the amount of genetic variation in that direction (Meyer and Kirkpatrick, 2005). The trajectories for first Eigen function accounting >95% of total genetic variation showed uniform trend with positive values and increase at 2nd and 6th week of age, then remained constant after post-weaning age, indicating that selection based on this function will improve body weight at all ages with more response at weaning age as shown in Figure 1.

Second Eigen function (ef2) which accounted for less genetic variation was low at birth, increased at 2 weeks followed by slight decrease at 3 weeks and later showed a straight-line function parallel to age axis, indicating that selection at any age results in an equal response (Chaudhary *et al.* 2019). The third Eigen function (ef3) which contributed less genetic variation oscillated with a negative trend across ages. Opposite directional changes observed in the third Eigen function (ef3) may be due to factors having contrasting effects on body weights at different ages (Akbas *et al.* 2004). Kirkpatrick *et al.* (1990) stated that the Eigen function (ef) with small or zero Eigen value (λ) represents deformations for which there is little or no additive genetic variation. This study revealed that response to selection based on 2nd and 3rd Eigen functions would be both small and slow as each account for little of the additive genetic variation than the 1st Eigen function.

Table 1: Body weights at different ages in Large White Yorkshire crossbred pigs

Age (weeks)		No. of Records	Minimum (kg)	Maximum (kg)	Mean ± SE (kg)	SD (kg)	CV (%)
BW0	Male	2354	0.50	1.31	1.18±0.00	0.22	18.64
	Female	2299	0.50	1.30	1.12±0.00	0.21	18.75
BW1	Male	2354	0.75	3.60	1.58±0.00	0.31	19.62
	Female	2299	0.91	3.70	1.55±0.00	0.29	18.71
BW2	Male	2354	1.40	5.30	2.78±0.01	0.55	19.78
	Female	2299	1.30	5.10	2.75±0.01	0.53	19.27
BW3	Male	2354	1.70	6.85	4.10±0.01	0.80	19.51
	Female	2299	1.72	6.35	4.03±0.01	0.78	19.35
BW4	Male	2353	2.12	8.60	5.40±0.02	1.08	20.00
	Female	2295	2.20	8.30	5.31±0.02	1.07	20.15
BW5	Male	2309	3.02	9.20	6.30±0.02	1.03	16.34
	Female	2267	3.10	9.00	6.22±0.02	1.07	17.20
BW6	Male	2302	3.65	10.60	7.25±0.02	1.15	15.86
	Female	2264	3.60	10.90	7.18±0.02	1.20	16.71
BW7	Male	2228	4.15	12.60	8.33±0.02	1.30	15.60
	Female	2165	4.19	12.60	8.21±0.02	1.35	16.44
BW8	Male	2194	4.60	17.30	9.73±0.03	1.78	18.29
	Female	2145	4.60	17.03	9.57±0.03	1.81	18.91
BW12	Male	1811	5.60	23.30	14.23±0.05	2.52	17.71
	Female	1701	5.90	23.25	14.22±0.06	2.57	18.07
BW16	Male	1466	10.50	32.60	20.03±0.09	3.78	18.87
	Female	1522	7.80	32.96	20.08±0.09	3.66	18.23
BW20	Male	959	13.40	45.20	28.10±0.22	6.83	24.31
	Female	982	12.00	43.00	28.17±0.20	6.45	22.90
BW24	Male	840	14.60	57.00	34.16±0.32	9.52	27.87
	Female	887	16.60	55.20	35.03±0.30	9.14	26.09

Table 2: Order of polynomial fit of the different models along with the number of model parameters (N_P), residual variance (R), Akaike's Information Criterion (AIC)

S. No	Model	Order of Fit				R	N_P	AIC
		D	IPE	M	MPE			
1	3333A	3	3	3	3	1	25	-27923.01
	3333B	3	3	3	3	12	36	-11832.17
2	3334A	3	3	3	4	1	29	-24530.91
	3334B	3	3	3	4	12	40	-8280.19
3	3344A	3	3	4	4	1	33	-24537.87
	3344B	3	3	4	4	12	44	-8407.09

4	3444A	3	4	4	4	1	37	-22255.71
	3444B	3	4	4	4	12	48	-6580.40
5	4444A	4	4	4	4	1	41	-21697.47
	4444B	4	4	4	4	12	52	-6451.39
6	4445A	4	4	4	5	1	46	-18105.31
	4445B	4	4	4	5	12	57	-5839.42
7	4455A	4	4	5	5	1	51	-18117.57
	4455B	4	4	5	5	12	62	-5973.18
8	4555A	4	5	5	5	1	56	-16025.04
	4555B	4	5	5	5	12	67	-3141.31
9	5555A	5	5	5	5	1	61	-14461.00
	5555B	5	5	5	5	12	72	-2410.09
10	3335A	3	3	3	5	1	34	-21201.73
	3335B	3	3	3	5	12	45	-7324.66
11	3355A	3	3	5	5	1	43	-21211.67
	3355B	3	3	5	5	12	54	-7264.44
12	3555A	3	5	5	5	1	52	-16280.94
	3555B	3	5	5	5	12	63	-3429.40
13	4443A	4	4	4	3	1	37	-21688.76
	4443B	4	4	4	3	12	48	-6428.91
14	4433A	4	4	3	3	1	33	-21716.53
	4433B	4	4	3	3	12	44	-6456.83
15	4333A	4	3	3	3	1	29	-21737.54
	4333B	4	3	3	3	12	40	-6451.75
16	5553A	5	5	5	3	1	52	-14442.93
	5553B	5	5	5	3	12	63	-2400.63
17	5533A	5	5	3	3	1	43	-14496.19
	5533B	5	5	3	3	12	54	-2461.55
18	5333A	5	3	3	3	1	34	-15735.07
	5333B	5	3	3	3	12	45	-2872.29
19	5554A	5	5	5	4	1	56	-14463.45
	5554B	5	5	5	4	12	67	-2882.59
20	5544A	5	5	4	4	1	51	-14494.99
	5544B	5	5	4	4	12	62	-2424.94
21	5444A	5	4	4	4	1	46	-14460.39
	5444B	5	4	4	4	12	57	-2811.12

Model 3333A means the quadratic model with order of fit 3,3,3,3 for additive genetic (D), permanent environmental (IPE), maternal genetic (M) and maternal environmental (MPE) effects. 'A' means considering homogeneous residual variance. In this study model 3333(A) explained the covariance structure adequately.

Table 3: Eigen values with their percentage contribution to the total variation for the best model

Effect	Eigen value (λ)	Contribution (%)	R^2 (%)
Direct additive genetic	26.23	95.10	95.13
	1.35	4.90	4.85
	0.00	0.02	0.02
Maternal genetic	1.74	95.60	95.32
	0.08	4.40	0.046
	0.00	0.00	0.002
Maternal permanent environmental	1.74	95.60	95.32
	0.08	4.40	0.046
	0.00	0.00	0.002
Animal permanent environmental	0.07	87.5	87.62
	0.01	12.5	12.36
	0.00	0.00	0.01

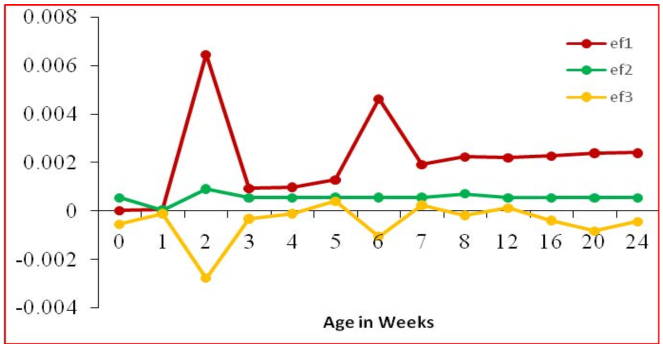

Fig. 1: Plot of Eigen functions of the random regression genetic covariance matrix of growth from birth up to 24 weeks of age, ef1-Eigen function1, ef2- Eigen function2, ef3-Eigen function 3.

Table 4: Heritability estimates for body weights at different ages from the best model

Trait	h^2 (SE)	m^2 (SE)	c^2 (SE)	p^2 (SE)	e^2(SE)
BW0	0.09(0.01)	0.02(0.01)	0.02(0.01)	0.01(0.01)	0.86(0.05)
BW1	0.02(0.00)	0.01(0.00)	0.01(0.00)	0.01(0.00)	0.94(0.02)
BW2	0.09(0.01)	0.01(0.01)	0.01(0.01)	0.01(0.01)	0.88(0.04)
BW3	0.23(0.03)	0.02(0.01)	0.02(0.01)	0.01(0.02)	0.73(0.03)
BW4	0.36(0.04)	0.03(0.02)	0.03(0.02)	0.01(0.01)	0.58(0.01)
BW5	0.47(0.05)	0.04(0.02)	0.04(0.02)	0.01(0.01)	0.46(0.01)
BW6	0.54(0.05)	0.04(0.02)	0.04(0.02)	0.01(0.01)	0.37(0.02)
BW7	0.60(0.06)	0.05(0.03)	0.05(0.03)	0.01(0.02)	0.30(0.03)
BW8	0.65(0.06)	0.05(0.03)	0.05(0.03)	0.01(0.02)	0.24(0.14)
BW12	0.76(0.07)	0.06(0.02)	0.06(0.03)	0.01(0.00)	0.11(0.01)
BW16	0.83(0.07)	0.06(0.03)	0.06(0.03)	0.01(0.00)	0.05(0.01)
BW20	0.87(0.08)	0.06(0.05)	0.06(0.05)	0.01(0.01)	0.02(0.02)
BW24	0.88(0.08)	0.05(0.05)	0.05(0.05)	0.01(0.02)	0.01(0.01)

h^2 -Direct genetic heritability; m^2 -Maternal genetic heritability; c^2 -Maternal permanent environmental variance ratio; p^2 - Individual permanent environmental variance ratio; e^2 - Residual error variance ratio

Table 5: Average, minimum, maximum breeding values for body weights at different ages in Large White Yorkshire crossbred pigs

Age (weeks)	Average breeding value (minimum to maximum)	No. of animals above average breeding value (% of sires)
BW0	1.15 (0.51 - 2.30)	73 (47.10)
BW1	1.61 (1.07 - 2.62)	60 (38.71)
BW2	2.78 (1.37 - 4.50)	83 (53.55)
BW3	4.03 (1.70 - 6.53)	82 (52.90)
BW4	5.28 (2.34 - 8.48)	81 (52.26)
BW5	6.23 (2.90 - 10.24)	76 (49.03)
BW6	7.16 (3.57 - 12.37)	71 (46.10)
BW7	8.33 (4.05 - 17.18)	65 (45.45)
BW8	9.75 (4.65 - 18.12)	66 (46.15)
BW12	15.19 (7.87 - 25.99)	68 (51.90)
BW16	20.57 (10.55 - 37.36)	61 (47.65)
BW20	31.15 (14.75 - 53.12)	52 (47.70)
BW24	39.98 (24.59 - 72.70)	51 (48.57)

Results of the present study revealed that the direct heritability (h^2) estimates at later ages were superior to the estimates obtained at younger ages ranging from 0.02±0.00 (BW1) to 0.88±0.08 (BW24), indicating that direct additive genetic effect was the main random effect influencing post-weaning piglet performance as shown in Table 4. This increasing trend of direct heritability towards later ages was in agreement with reports of Zhang *et al.* (2000), Chimonyo *et al.* (2008), Lee and Do (2012) and Mondal *et al.* (2013). Meyer (2005) stated that high heritability at extremities arises from the sensitivity of Legendre polynomials to data structure and named it as "end effect of polynomials" or "Runge's phenomenon" which tends to be more outstanding at the extremities. Maternal genetic (m^2) and maternal permanent environmental heritability (c^2) estimates were similar with low magnitude, slightly increasing from birth upto 24 weeks of age (0.01±0.00 to 0.06±0.05).

The low maternal heritability values suggest that selection based on maternal components will be less responsive than that of additive genetic effect, indicating that the traits are more under direct genetic control. The increasing trend of maternal heritability accounts for both pre-natal environment (uterine nutrition and capacity) and rearing dam's condition, *i.e.,* milk production (Ouko *et al.* 2016). Low maternal heritability estimates were also observed by Zhang *et al.* (2000), Chimonyo *et al.* (2008), Tomiyama *et al.* (2010) and Jayasree *et al.* (2019). Estimates of maternal heritability higher than this study were obtained by Darfour-Oduro *et al.* (2009) in Ashanti black, Ouko *et al.* (2016) in LWY pigs.

Random regression models allow breeding values to be estimated continuously rather than at fixed points (0, 7, 14, 20….148 days). The average breeding value for birth weight was found to be 1.15 kg which was improved to a value of 39.98 kg at 24 weeks as detailed in Table 5. It was observed that greater number of animals (53.55% sires) above average breeding value was noted for body weight at 2 weeks of age.However, the average breeding values for body weight in the present study were lower than the reported values of Mondal and Kumar (2014) at 8 weeks but higher than the values revealed by Chaudhary *et al.* (2019) at 20 and 24 weeks of age. The number of records in this study pertaining to males and females did not remain the same, since data is non-orthogonal, so breeding values varied from BW0 to BW24.

The breeding value for body weights in this study was not fixed. As a longitudinal trait it varied across growth stages, may be due to several factors like animal's age, growth stage, genetic, environmental factors (GXE interaction) and is influenced by multiple genes at different growth stages, the same genetic potential for body weight may express differently in different environments, causing variations in estimated breeding values. If animals with higher body weight breeding values are consistently selected also, the overall breeding values in the population will increase over generations. As more data become available, the estimated breeding values (EBVs) can be updated and refined, understanding these differences allows breeders to optimise selection strategies.

CONCLUSION

Growth traits in Large White Yorkshire crossbred pigs were analysed using Random regression models and based on AIC values, quadratic Legendre polynomial was found to be most suitable for modelling the growth curve in these pig populations. The trajectories for first Eigen function accounting >95% of total genetic variation, and selection based on this function will improve body weight at all ages with more response at weaning age. The direct heritability estimates of body weight increased as age advanced and demonstrated genetic variability rather than the non-genetic factors in the population and conceivable response to selection. An increase in heritability over time within same population indicates that genetic factors are playing a progressively larger role than the non-genetic factors in the variation of a particular trait. Means data of this study pertaining to long term selection for improvement of body weights, the influence of environmental factors is decreasing overtime relative to the influence of additive effects of genes within that population. Based on this it is suggested that breeder has two ways to increase heritability, concentrating breeding of more genetic variance populations or by reducing non-genetic contributions to phenotypic variance. The values obtained for different parameters provide input to review the ongoing breeding program for the genetic improvement of LWY crossbred pigs (SVVU T-17).

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