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# The Pharma Innovation



ISSN (E): 2277-7695 ISSN (P): 2349-8242 NAAS Rating: 5.23 TPI 2022; SP-11(7): 2021-2025 © 2022 TPI

www.thepharmajournal.com Received: 01-04-2022 Accepted: 04-05-2022

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## Application of random regression models for assessment of direct and maternal genetic parameters of growth characters in large white Yorkshire crossbred pigs

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#### Abstract

Body weight is one of the significant profitable traits in swine production. Data on body weight was recorded at monthly intervals from Large White Yorkshire crossbred pigs (75 % LWY & 25% Local desi) kept up at All India Coordinated Research Project on Pig, Sri Venkateswara Veterinary University, Tirupati, Andhra Pradesh. In this study body weight data from 655 animals belonging to 22 sires and 45 dams was subjected to random regression analysis using Legendre polynomials of various orders of fit. Wombat software was used to estimate the covariance components and genetic parameters using the derivative free restricted maximum likelihood method. Best order of fit was identified based on information criterion. The Legendre polynomial with orders of fit 3 for direct genetic and maternal genetic effects and homogeneous residual error variance (11 classes) was considered to be the best fit based on Log 1, Akaikes information and Bayesian information criterion. The quadratic Legendre polynomial revealed the highest Log 1 and the lowest Akaikes information and Bayesian information values (3,3,0,0). The variance for intercept (L<sub>0</sub>) was found to be large (0.51) for direct additive effects and low (0.04) for maternal genetic effects. The trajectories for 1<sup>st</sup> and 2<sup>nd</sup> Eigen functions together accounting for > 99% of genetic variation.

Keywords: Growth characters, genetic parameters, pig, random regression models

#### 1. Introduction

Pig farming profitability is mostly determined by litter size and body weight gain. Pig breeders generally strive for high birth and weaning weights since they are linked to improved performance throughout future rearing periods. The changes in growth performance of pigs overtime are under the influence of genetic and environmental factors. Body weight in pigs is typically assessed multiple times throughout their lives and might be considered as a longitudinal trait. Fitting collection of random regression coefficients representing production across time resulting in a random regression model, is a more appropriate method for evaluation of longitudinal traits (Meyer, 1998)<sup>[1]</sup>.

"Piglet body weight is usually influenced by direct additive genetic, maternal genetic and maternal permanent environmental effects;" (Kaufmann *et al.*, 2000, Alves *et al.*, 2018 and Hermesch *et al.*, 2001) <sup>[2-4]</sup>. According to Kaufmann *et al.*, (2000) phenotypic expression of offspring on growth is contributed by the mother, eliminating the direct additive gene influence. Maternal influence can be determined by genetics and the environment which includes the intrauterine environment as well as the mother's milk supply and care. Several studies have suggested the inclusion of maternal effects in animal models to improve body weight in various pig breeds.

The purpose of this study was application of random regression models to estimate coefficient of (co)variance components and genetic parameters for body weight at different ages, to analyse the trajectory of the growth curve (Eigen values) at different intervals and to find out variance components by estimating Eigen functions along the growth trajectory in Large White Yorkshire crossbred pigs.

#### 2. Materials and Methods

#### 2.1 Data source

In this study data were collected on body weight at monthly intervals from birth to 9 months of age during the period of 4 years *i.e* from 2012 to 2016 from Large White Yorkshire (75%)

crossbred pigs maintained at AICRP on Pig, Sri Venkateswra Veterinary University, Tirupati, A.P. The data was recorded on 655 number of animals belonging to 22 sires and 45 number of dams, were analysed using random regression analysis by including Legendre polynomials with different orders of fit. Piglets were identified after birth by ear notching as per their pedigree. Pigs were reared in a uniform manner under same management settings with adlibidum feeding and piglets were weaned at 42 days of age. Animals having minimum 3 number of body weight records were considered for analysis. Number and percentage of animals along with body weight records are shown in Table 1.

 Table 1: Number and percentage of animals with body Weight records

Data particulars	No. of Animals	Percentage (%)
Animals with 3 records	1965	37.01
Animals with 4 records	651	12.26
Animals with 5 records	627	11.81
Animals with 6 records	596	11.22
Animals with 7 records	423	7.96
Animals with 8 records	377	7.10
Animals with 9 records	361	6.79
Animals with 10 records	305	5.74
Animals with 11 records	3	0.05
Total number of animals	5308	100

#### 2.2 Statistical analysis

The study included fixed effects such as animal sex (male and female), season (summer from March to June; rainy from July to October; winter from November to February) and year of birth. Direct additive, maternal genetic, maternal permanent environmental and individual permanent environmental effects were all taken into consideration as random effects. The age of the animal at the time of recording body weight

[ x′x	$x'z_a$		$x'z_m$		x'z <sub>p</sub>
z <sub>a</sub> x	$Z_a Z_a$	$+ \operatorname{A}^{-1} \operatorname{U} \otimes \operatorname{K}_{\operatorname{a}^{-1}}$	$z_a z_m$	$+ A^{-1}U \otimes K^{-1}{}_{am}$	$z_a z_p$
z <sub>m</sub> x	$Z_m Z_a$	$+ \operatorname{A}^{-1} \operatorname{U} \otimes \operatorname{K}_{\operatorname{ma}^{-1}}$	$\mathbf{z}_{\mathbf{m}}\mathbf{z}_{\mathbf{m}}$	$+ A^{-1}U \otimes K^{-1}{}_m$	$z_m z_p$
z <sub>p</sub> x	$Z_p Z_m$		$z_p \mathbf{z}_m$		$z_p z_p$
z <sub>w</sub> x	$z_w z_a$		$z_w z_m$		$z_w z_p$

Where A represents the numerator relationship matrix, X represents the Kronecker's product and  $K_i$  represents the (co)variance matrix of the random regression coefficients of the effects given in subscript.

"Genetic covariance functions whose Eigen values and Eigen functions provide insight into the impacts of selection over the growth trajectory and are generated from the covariance matrix of the random animal effects, can be estimated using the random regression approach" (Kirkpatrick *et al.*, 1990) <sup>[6]</sup>. The amount of genetic variation in the population corresponding to that Eigen function is proportional to the Eigen value. The Eigen function of the random regression coefficient matrix for the j<sup>th</sup> age and i<sup>th</sup> Eigen value was derived as  $\Phi_{je_i}$ , where e<sub>i</sub> is the Eigen vector for the i<sup>th</sup> Eigen value.

The random regression models used were based on recommendations from prior studies. A total of 12 models with orders of fit 3 to 6 were fitted to the data, comprising one and eleven measurement error classes and a description of each as well as Log l, AIC and BIC is presented in Table 2. The fixed effects are same in all models but the random effects are different. The models fitted for the direct additive,

was used as a control variable. The data recorded on body weight at different periods was subjected for random regression analysis using WOMBAT software (Meyer<sup>5</sup>, 2007) by using restricted maximum likelihood method. The basic general model for random regression analysis were as follows Eq. (1).

#### 2.3 Equations

$$Y_{ij} = Xb + \sum_{k=0}^{k_a - 1} Z_a a_k + \sum_{k=0}^{k_m - 1} Z_m m_k + \sum_{k=0}^{k_p - 1} Z_p p_k + \sum_{k=0}^{k_w - 1} Z_w w_k + e$$
(1)

Where  $Y_{ij}$  is the body weight of the i<sup>th</sup> animal at the j<sup>th</sup> month of age; Xb is the fixed effects of sex, season, and year of birth; and k is the regression of the age of order associated with  $Y_{ij}$ , 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, maternal genetic, maternal permanent environmental and individual permanent environmental effects respectively, with order of fit  $k_a$ ,  $k_m$ , and  $k_w$ . The different Z matrice elements are  $Z_i$ -  $\Phi_i$ - $A_i$  ( $t_{ij}$ ), where  $A_i$  are the Legendre polynomial coefficients and  $t_{ij}$  are the ages standardized between -1 and +1, obtained as Eq. (2),

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

Where  $T_{min}$  is the data's earliest date (youngest age) and  $T_{max}$  is the data's latest date (oldest age).The random residual heterodastic error variances are e; T is the age in original scale for which  $t_{ij}$  is determined. Heterogeneous residual variance (RRM-HET) was considered to be constant for body weight data within the 11 growth period classes, but varied (heterogeneous) across them Eq. (3).

$$\begin{array}{c} x' z_{w} \\ z_{a} z_{w} \\ z_{m} z_{w} \\ + I_{p} U \otimes K_{p^{-1}} z_{p} z_{w} \\ z_{w} z_{w} \\ z_{w} z_{w} + I_{w} U \otimes K_{w^{-1}} \end{array} \right] \begin{array}{c} b \\ a \\ [m] = \\ p \\ w \\ z_{m}' y \\ z_{m}' y \\ z_{p}' y \\ z_{w}' y \\ z_{w}' y \end{array}$$
(3)

maternal and individual permanent environmental effects were as shown below Eq. (4).

$y = Xb + Z_a a + e$	model 1
$y = Xb + Z_a a + Z_{pe} pe + e$	model 2
$y = Xb + Z_a a + Z_m m + e$ with Cov $(a_m, m_o) = A\sigma_{am}$	model 3
$y = Xb + Z_aa + Z_mm + Z_{pe}pe + e$ with $Cov (a_m, m_o) = A$	$\sigma_{am}$ model 4
(4)	

Where 'y' is the vector of records; b, a, m, pe, and e are the vectors of fixed, direct additive genetic effects, maternal genetic, maternal permanent environmental and residual effects respectively and X,  $Z_a$ ,  $Z_m$ , and  $Z_{pe}$  are the association matrices; The direct and maternal genetic effects are represented by  $a_m$  and  $m_0$  respectively. A is the numerator relationship matrix between animals and  $\sigma_{am}$  is the covariance between maternal genetic and direct additive genetic effects.

#### 3. Results and Discussion

In general it was noted that body weight of animals increased steadily from birth to nine months (1.27 to 77.40 kg) of age and males were found to be heavier than females at all ages.

The mean body weight at birth, 30, 42, 60, 90, 120, 150, 180, 210, 240 and 270 days of age were found to be 1.27, 6.22, 7.86, 9.73, 14.82, 23.42, 36.36, 47.77, 60.83, 70.23, 77.40 and 1.23, 6.12, 7.73, 9.58, 14.48, 23.25, 35.72, 46.87, 60.20, 68.84, 76.80 kg in males and females respectively. The mean body weight values at 30, 42, 60, 90 days of age are nearer to the reported values of Rajni Chaudhary et al., (2019)<sup>[7]</sup> in crossbred pigs. Compare to these values Panda et al., (2020) <sup>[8]</sup> reported lower birth weight and higher body weight at 42 days of age in Landly pigs. The coefficient of variation decreased as the age of the animal increases and the highest value (17%) was observed for birth weight. The standard deviation of body weight was low initially but increased progressively upto 210 days and then decreased upto 240 days of age, may be due to culling of some of the animals. Direct additive genetic (4.26 to 177.18 kg<sup>2</sup>), maternal genetic (5.47 to 211.12 kg<sup>2</sup>) and total phenotypic (14.37 to 389.72 kg<sup>2</sup>) variances were high at birth and decreased slightly upto 90 days and again showed increasing trend with minor fluctuations at later ages. Similar kind of changes in variance for body weight over time was observed by Rajni Chaudhary *et al.*, (2019)<sup>[7]</sup> in crossbred pigs.

According to preliminary analysis, all fixed effects have a significant impact on body weight, hence all were included in regression analysis. Table 2 shows the various random regression models that were utilised, as well as the order of fit for various effects and the information criterion. Initially a quadratic polynomial model was fitted with the order of fit 3 for additive and maternal genetic effects as random effects (3,3,0,0) and then maternal permanent environmental and individual permanent environmental effects were added one by one. Then polynomial order was increased for all random effects and models were integrated by changing order of fit to 4, 5 and 6 with different combinations.

 Table 2: Order of polynomial fit of the different models, the number of model parameters (NP), Residual variance (R), log likelihood values, AIC and BIC.

Madal	D	м	C	р	Nm	р	Information criteria		
Model	U	IVI	C	r	мр	к	Log l	AIC	BIC
3300A	3	3	0	0	13	1	-11068.25	-11081.38	-11124.13
3300B	3	3	0	0	13	11	-7387.27	-7400.27	-7443.02
3330A	3	3	3	0	19	1	-6820.25	-6839.25	-6901.72
3333B	3	3	3	3	25	11	-6812.11	-6837.11	-6919.30
3333A	3	3	3	3	25	1	-6811.50	-6836.50	-6918.69
3330B	3	3	3	0	19	11	-6815.65	-6834.65	-6897.12
4444A	4	4	4	4	41	1	-5720.97	-5761.97	-5896.77
4440B	4	4	4	0	31	11	-5720.18	-5751.18	-5853.10
4440A	4	4	4	0	31	1	-5719.94	-5750.94	-5852.87
4400B	4	4	0	0	21	11	-5719.82	-5740.82	-5809.86
4400A	4	4	0	0	21	1	-5719.24	-5740.24	-5809.28
5550B	5	5	5	0	46	11	-5317.49	-5363.49	-5514.72
4444B	4	4	4	4	61	11	-5302.19	-5363.19	-5563.74
5555B	5	5	5	5	61	11	-5302.19	-5363.19	-5563.74
5555A	5	5	5	5	61	1	-5301.95	-5362.95	-5563.51
5550A	5	5	5	0	46	1	-5315.51	-5361.51	-5512.75
5500B	5	5	0	0	31	11	-5318.86	-5349.86	-5451.78
5500A	5	5	0	0	31	1	-5315.78	-5346.78	-5448.70
6660A	6	6	6	0	64	1	-4902.22	-4966.22	-5176.63
6666A	6	6	6	6	85	1	-4867.91	-4952.91	-5232.36
6666B	6	6	6	6	85	11	-4867.12	-4952.12	-5231.57
6660B	6	6	6	0	64	11	-4880.93	-4944.93	-5155.34
6600B	6	6	0	0	43	11	4887.10	-4930.10	-5071.47
6600A	6	6	0	0	43	1	-4882.09	-4925.09	-5066.45

The most acceptable model for predicting (co)variance components for each trait was determined using Log l, Akaikes information criterion (AIC), and Bayesian information criterion (BIC). Usually amodel with a lower information criterion based on AIC and BIC values is superior to a model with a higher value, however a model with a higher value based on Log l has greater goodness of fit.

Results of this study revealed that the highest Log l, lowest AIC and BIC values were found with quadratic Legendre polynomial. Hence according to the model comparison criterion, the model (3300) with order of fit 3 for direct additive and maternal genetic effects and homogeneous residual variance (11 classes) was found to be the best fit and most appropriate to describe the covariance structure of body weight over the test period. It suggesting that both direct and maternal genetic effects influence pig body weight.

These results are similar to the reports of Kohn *et al.*, (2007) <sup>[9]</sup> stating that the model with 3<sup>rd</sup> order was the best fit for

estimating genetic parameters of body weight using RRM in Mini pigs. Rajni Chowdhary *et al.*, (2019)<sup>[7]</sup> originate that the BIC value with 4<sup>th</sup> order of fit (4,4,3,4) including direct genetic, maternal genetic and maternal permanent environmental effects and 3<sup>rd</sup> order of fit with individual permanent environmental effect was best fitting when modelling growth records of crossbred pigs using random regression models.

Panda *et al.*, (2020) <sup>[8]</sup> observed the smallest AIC value for birth weight in model 4 with direct additive and maternal genetic effects and for body weight at 3, 6 and 8 weeks in model 6 with direct additive, maternal genetic and maternal permanent environmental effects, while evaluating animal models for genetic analysis of growth performance in Landly pigs. Table 3 shows the estimated covariance function, coefficient matrices (kr) and related Eigen values with percent contribution to total variance, as well as the correlation between regression coefficients for additive (G) and maternal genetic (M) effects. The variance (diagonal) for intercept ( $L_0$ ) was found to be high (0.51) for direct additive and low (0.04)

for maternal genetic effects.

<b>Fable 3:</b> Estimated coefficient matrices $(k_r)$ of the covariance function and the corresponding Eigen values with percentage contribution to the
total variance and the correlation between them for additive (G), and maternal genetic (M) effects

Effect		Lo	$L_1$	$L_2$	λ	%Contribution of Eigenvalue
	L <sub>0</sub>	0.51	0.99	-0.59	48.97	85.52
Direct Additive (G)	L <sub>1</sub>	2.84	15.82	-0.62	8.29	14.47
	$L_2$	-2.72	-15.98	40.91	0.00	0.00
Maternal Genetic (M)	L <sub>0</sub>	0.04	-0.96	-0.47	54.94	82.61
	L <sub>1</sub>	-1.25	39.16	-0.63	11.57	17.39
	$L_2$	0.51	-20.85	27.30	0.00	0.00

The amount of genetic variation in the population corresponding to that Eigen function is proportional to the Eigen value. For direct additive and maternal genetic effects, the first and second Eigen value of coefficient matrices jointly explained a large fraction of the total variation (99.99 and 100%, respectively), demonstrating that additive and maternal genetic effects account for a significant portion of variance. It suggests that a rapid change corresponding to that Eigen function will occur and that selection based on these functions will enhance body weight at all ages, but finding of the 3<sup>rd</sup>

Eigen value was zero which means that the change will be sluggish.

In Figure 1, the influence of factors corresponding to each Eigen value was displayed using Eigen functions. The trajectories of the first and second Eigen functions together accounted for more than 99 percent of genetic variation. These findings are consistent with Rajni Chowdhary *et al.*, (2019)<sup>[7]</sup>, who found >98 percent genetic variation in crossbred pigs, with a minor rise with age until weaning and then a rapid increase in post-weaning age.



Fig 1: Plot of Eigen functions along growth curve in Large White Yorkshire crossbred pigs

Eigen function 1 which accounted for higher genetic variation was high at birth, then decreased slowly upto 120 days of age and then increased rapidly upto 270 days (Fig 1), indicating that selection based on this variable may increase body weight at later ages. Whereas Eigen function 2 showed interesting pattern, which was low at birth then drastically increased upto 30 days and again decreased upto 60 days then rapidly increased upto 270 days of age. Eigen function 1 and 2 increased uniformly during post weaning age stating that selected animals would reach mature body weight early based on these factors. Eigen function 3, which accounted for lesser genetic variation, was high at birth and steep decrease during pre-weaning age upto 30 days and again increased upto weaning age of 42 days, then remained almost constant upto 270 days of age, indicating that selection based on this variable will lead to decrease in pre weaning body weight, then lead to equal response at later ages after weaning.

The heritability estimates calculated from best model are presented in Table 4. The direct genetic heritability estimates increased steadily and were found to be 0.45+0.21 at birth and low (0.17+0.09) at BW60 and high (0.63+0.23) at BW120. The high additive genetic heritability for body weight at all ages except 60 days implies that direct genetic variance contributes significantly to phenotypic variance, resulting in a relatively low impact of non-genetic factors on growth performance observed between animals. Low heritability at 60 days may be owing to strict weight selection throughout the first 60 days, indicating low genetic variability. It suggests that selection during the steady period will be more effective for improving body weight. Rajni Chaudhary et al., (2019) [7] reported similar values while estimating genetic parameters for growth traits by using random regression models in Landrace x desi crossbred pigs.

**Table 4:** Estimates of heritability from additive genetic (h<sup>2</sup>) and maternal genetic (m<sup>2</sup>) effects for body weight at different ages in Large White Yorkshire crossbred pigs obtained from the best model.

Age (d)	h <sup>2</sup>	$m^2$
BW0	$0.45\pm0.21$	$0.54\pm0.21$
BW30	$0.37\pm0.18$	$0.61\pm0.19$
BW42	$0.30\pm0.16$	$0.66\pm0.17$
BW60	$0.17\pm0.09$	$0.76\pm0.12$
BW90	$0.51\pm0.18$	$0.38\pm0.21$
BW120	$0.63\pm0.23$	$0.32 \pm 0.24$
BW150	$0.59 \pm 0.23$	$0.38\pm0.24$
BW180	$0.51 \pm 0.21$	$0.45 \pm 0.23$
BW210	$0.37\pm0.16$	$0.58\pm0.18$
BW240	$0.38\pm0.15$	$0.57\pm0.17$
BW270	$0.57\pm0.21$	$0.41\pm0.21$

Estimates of maternal heritability for body weight varied from moderate  $(0.32\pm0.24)$  to high  $(0.76\pm0.12)$  at BW120. It demonstrates that the mother's environment has an impact on the offspring's phenotype. These findings are consistent with Panda *et al.*, (2020) <sup>[8]</sup>, who evaluated animal models for genetic analysis of growth performance in Landly pig.

Whereas Rajni Chaudhary *et al.*, (2019)<sup>[7]</sup> claimed that the maternal impact was crucial in modelling growth traits and that removing the dam effect could lead to overstated findings of heritability. Solanes *et al.*, (2004)<sup>[10]</sup> on the other hand, found that the maternal impact was reduced at weaning compared to early body weight in White piglets.

The direct genetic correlation of body weight between different ages were found to be positive and high (0.25to 0.99) suggesting that these traits are under the control of same set of genes and selection for increasing body weight at early age would have a positive effect at later ages. The maternal genetic correlation between birth weight and body weight at 30, 42, 60 and 90 days of age were found to be substantially positive ranging from 0.89 to 0.99, indicating that the same set of maternal genes functioned to promote growth upto 60 days of age. Whereas maternal genetic correlation for body weight between other ages was negative with a range of -0.03 to -1.0, reason may be due to reduction in maternal effects with advancement of age.

#### 4. Conclusions

The results of the present study showed that based on Log l, AIC and BIC values quadratic polynomial model with homogeneous residual variance was identified as the best model for estimation of genetic parameters in this pig population. It was found that the best fit for predicting genetic parameters for body weight was a model that included additive genetic and maternal genetic effects. The direct and maternal variations increased steadily as the animal's age increased. This suggests existence of sufficient additive genetic diversity among animals, which can be utilized for improvement of body weight in this pig population through selection.

#### 5. Acknowledgement

Authors are immensely thankful to the technical and financial support given from the ICAR to All India Coordinated Research Project on pig.

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