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Random regression models for genetic analysis of body weight in crossbred pigs

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ABSTRACT

Body weight of an animal is represented by a continuous function of time (longitudinal trait) and can be characterized by a trajectory with number of measurements. The present study was carried out to determine heritability estimates of body weight in crossbred pigs (75% Landrace + 25% Bareilly local) using random regression model with Legendre polynomials of quadratic power. Data of 9044 records of 1,292 crossbred piglets, progeny of 86 boars and 98 sows; born in 184 parities between 5 years from 2013–17 was used for the study. Records on weight at birth and at 1 week interval up to 6 week were used. Model included sex, year of birth, season of birth and parity as fixed effect, age of dam at farrowing as co-variable and direct additive genetic effect and maternal permanent environmental effect as random regression. There was a steady increase in body weight over the age from birth (0.96 kg) to 6th week (9.0 kg). Direct additive genetic (0.006 to 7.37 kg^2), maternal permanent environment (0.053 to 70.07 kg^2) and total phenotypic (0.18 to 77.56 kg^2) variance increased continuously from birth to 6 week of age. In general, heritability estimates of body weight at different ages of pre-weaning stage were low ranging from 0.031 to 0.12. The estimate increased up to 1st week (0.119±0.025) with very low value at birth (0.031±0.015) and decreased thereafter to 0.095±0.022 at 6 week. Relative importance of each order of Legendre polynomials showed that quadratic Legendre polynomials with three regression coefficients were enough to capture almost all variability in the model to explain all additive genetic and maternal permanent environment variability. Hence, use of random regression model with quadratic Legendre polynomials was suggested for genetic analysis of pig data for growth.

Key words: Body weight, Crossbred pigs, Heritability estimates, Random regression model

Many phenotypes of an animal like body composition, weight and feed intake change with age. It is evident that changes in performance with age are also affected by genetic factors. The major interest of livestock breeding lies in genetic parameters for description of change in performance traits over time. Body weight of an animal is represented by a continuous function of time (longitudinal trait). Therefore, this trait can be characterized by a trajectory with number of measurements. Repeatability and multiple trait models are generally applied to analyze traits that are measured more than once in lifetime of an animal. Repeatability model assumes unit genetic correlation between subsequent observations and constant variance along trajectory. Observations at subsequent stages are supposed as different traits in multiple trait analyses. Fitting a set of random regression coefficients, describing production over time for each animal (Meyer 1998) is however an appropriate way to deal with longitudinal traits. Main advantages of the random regression models in comparison to multiple-trait models are requirement of fewer parameters to describe longitudinal data, smoother and less biased (co)variance estimates, accounting for genotype×environment interaction, reducing deviation in sire rankings and possibility to predict covariance structure and breeding value of animal at any point along trajectory. Random regression models in pigs are mainly being used for growth, feed intake and litter size (Lukovic *et al.* 2003, Lukovic *et al.* 2004, Martina *et al.* 2015, Ouko *et al.* 2017). The aim of this investigation was to determine heritability estimates of body weight in crossbred pigs using random regression model with Legendre (LP) polynomials of quadratic power.

MATERIALS AND METHODS

The data utilized for this study originated from Swine Production Farm, ICAR-Indian Veterinary Research Institute (IVRI), Izatnagar, Uttar Pradesh, India; a unit of ICAR-All India Coordinated Research Project on Pigs (AICRP on Pigs). AICRP on Pigs was started in 1970 during Fourth Five Year Plan to study the performance of exotic breeds of pigs under different agro-climatic conditions. The IVRI centre came into existence during the year 1971 as

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one of the centres of the project. The research work was only conducted on Landrace breed of pigs up to the Fifth Five Year Plan. Subsequently, the technical program of the project was modified in 1980. One of the main objectives of the revised program was to conduct the research work on indigenous (Bareilly local) pigs under optimum management conditions and to produce crossbred pigs by crossing indigenous gilts with exotic boars. Production and maintenance of 75% Landrace crossbreds was thereafter decided in technical program in 2010. Crossbred pigs with 75% exotic and 25% Bareilly local blood have now been undergone interbreeding for 5 generations.

The Izatnagar centre is located at an altitude of 564 amsl and at latitude of 28°N and longitude of 79°E. The climate of this place touches both the extremes of cold and hot weather experienced in the county and the relative humidity ranges between 15% and 85%. The piglets were housed in *Pakka* system. However, it was ensured that piglets remain in soil for two hours daily. Sufficient space was provided to each individual according to age. Piglets were injected 1 ml iron dextran on 4th and 14th day of birth. Creep ration rich in protein (Protein 21%, Lysine 0.89% and ME 3.36 Mcal/kg) was started from 2nd week onward and was continued up to weaning age (6 weeks of age). Piglets were vaccinated for foot and mouth disease and swine fever, both.

Data consisted of 9044 records of 1292 crossbred (75% Landrace + 25% Bareilly local) piglets, which were progeny of 86 boars (Table 1). The piglets were born in 184 parities of 98 sows between 5 years from 2013–17. Records on weight at birth and at 1 week interval up to 6 week were used in this investigation. Each year of birth was divided into 4 seasons based on agro-climatic conditions of the locality, i.e. December to February, March to May, June to August and September to November. Data were analysed with random regression model (RRM). The direct additive genetic effect and maternal permanent environmental effect were fitted as random regression on age at weighing using Legendre polynomials (LP). The age at weight recording was rescaled to a standardized age (t*) for the orthogonal functions using following formula:

$$t^* = \left[\frac{2(t - t_{min})}{(t_{max} - t_{min})}\right] - 1$$

where, t_{min}, youngest age; t_{max}, oldest age.

The random regression animal model was:

$$y_{ijklm}(t) = \mu + S_i + Y_j + SE_k + P_l + \beta(A_{ijklm} - A_{ijklm}) + \sum_{s=1}^{s} \alpha_{ijklm}\varphi_s(t^*) + \sum_{s=1}^{s} \gamma_{ijklm}\varphi_s(t^*) + \varepsilon_{ijklm}$$

where y_{ijklm} (t), weight of animal m at age t; S_i, fixed effect of sex i; Y_j, fixed effect of year of birth j; SE_k, fixed effect of season of birth k; P_l, fixed effect of parity l; β, fixed regression coefficient of age of dam at farrowing (A_{ijklm}) on weight of piglet at weighing; t, age in week; t*, age standardized to the range –1 to 1; φ_s, value of the sth LP at standardized age t*; α_{ijklm}, random regression coefficient for animal additive genetic effect; γ_{sijklm}, random regression coefficient for maternal permanent environmental effect; ε_{ijklm}, random measurement error.

The random regression coefficients for additive genetic effect and maternal permanent environmental effect were fitted with quadratic LP having 3 terms. Covariance components for the random regression coefficients were estimated through Restricted Maximum Likelihood Method (REML) using VCE6 (Groeneveld *et al.* 2010). Additionally, SAS 9.3 was used for computation of covariance components at different stages and eigen values for covariance matrices of regression coefficients to quantify contribution of higher orders of LP.

RESULTS AND DISCUSSION

Average body weight at different ages has been shown in Table 2. Birth weight averaged 0.96 kg. There was a steady increase in weight over the age. The weight at 6th week (weaning) averaged 9 kg. Standard error of all the weights was within the acceptable limit ranging from 0.01 to 0.06 kg. Coefficient of variation was the lowest for body weight at birth (24.37%) and the highest for body weight at 1st week (29.32%). The performance of crossbreds in present study was better than those in other investigations, especially at later ages (Kaushik *et al.* 2013, Mondal and Kumar 2015, Kumar *et al.* 2018).

Variance of random animal effect and maternal permanent environment effect are shown in Table 3. The variance of random animal effect increased continuously up to 6 week of age. It ranged from 0.006 to 7.37 kg^2. The lowest value was noticed for body weight at birth. The variance for maternal permanent environment effect also

Table 1. Data and pedigree structure

Parameter	Observation
Records	9044
Animals	1292
Dams	98
Average progeny per dam	13.18
Sires	86
Average progeny per sire	15.02
Base animals	465
Pedigree records	1950

Table 2. Average, standard error and coefficient of variation of pre–weaning weight at different ages

Age (week)	Observation	Average (kg)	Standard error (kg)	Coefficient of variation (%)
0	1292	0.96	0.01	24.37
1	1292	2.13	0.02	29.32
2	1292	3.45	0.03	27.09
3	1292	4.88	0.04	26.92
4	1292	6.25	0.05	26.88
5	1292	7.65	0.06	26.44
6	1292	9.00	0.06	25.63

Table 3. Variance components and proportion of phenotypic variance for live weight with quadratic polynomial model

Age (week)	Variance component (kg^2)				Proportion of phenotypic variance	
	Additive genetic	Maternal permanent environment	Error	Total	Maternal permanent environment (p^2)	Additive genetic (h^2)
0	0.006	0.053	0.12	0.179	0.298	0.031±0.015
1	0.368	2.597	0.12	3.085	0.842	0.119±0.025
2	1.153	8.958	0.12	10.231	0.876	0.113±0.024
3	2.228	18.987	0.12	21.335	0.890	0.104±0.023
4	3.562	32.566	0.12	36.248	0.898	0.098±0.023
5	5.221	49.610	0.12	54.951	0.903	0.095±0.022
6	7.371	70.068	0.12	77.559	0.903	0.095±0.022

increased steadily over the examined time period ranging from 0.053 to 70.07 kg^2. Total variance also had trend similar to random animal and maternal permanent environmental effect and increased from birth (0.18 kg^2) to 6th week (77.56 kg^2). Huisman *et al*. (2002) in pigs and Begli *et al*. (2016) in poultry also noticed steady increase in additive genetic and maternal permanent environmental variance over time for live-weight using random regression models. Increase in phenotypic variance with age has also been observed in previous investigations in Large White pigs in Kenya (Ouko *et al.* 2017).

The heritability estimates for body weight were within the acceptable range in the present study. The heritability estimate increased up to 1st week with very low value at birth and decreased afterwards (Table 3). Values ranged from 0.031 at birth to 0.12 at 1st week. In general, heritability estimates at different ages of pre-weaning stage were low. The proportion of variance for maternal permanent environment effect increased steadily over age. There was a remarkable increase in the proportion from birth (0.30) to 1st week (0.84) and little increase thereafter up to 6th week (0.90). Body weight at 5th and 6th week had equal proportion of variance for maternal permanent environment effect. The results showed that maternal permanent environment became more powerful with the advancement of age for introducing random variation.

Sevon-Aimonen *et al*. (1997) and Huisman *et al*. (2002) used third-degree polynomials to estimate genetic parameters of body weight in pigs. Their heritability estimates were also low ranging between 0.13 and 0.20 and were comparable to the heritability estimates of our investigation. Ouko *et al*. (2017) also estimated variance components of growth in Large White pigs in Kenya using random regression models by fitting different orders of Legendre polynomials. They observed direct heritability estimates ranging between 0.20±0.04 and 0.52±0.08 and permanent environmental heritability between 0±0.01 and 0.15±0.10.

Relative importance of each order of Legendre polynomials was determined by the eigen values of the additive genetic and maternal permanent environment covariance matrices of random regression coefficients. Eigen values for Legendre polynomials from linear to quartic power are given in Table 4 for additive genetic and maternal permanent environment effect. The eigen values of additive genetic covariance functions showed that the constant (zero) term accounted between 95 and 99% of the additive genetic variability for body weight. This reflected that approximately 1 to 5% of the variability was explained by individual genetic curve of the piglet, which could be utilized through selection on the shape of production curve for body weight. This proportion of variability was mainly covered by linear (0.60 to 3.42%) and quadratic (0.71 to 0.99%) coefficients. Maternal permanent environment functions also explained high variability through constant term ranging from 99.92 to 99.98% for body weight, leaving little variability for individual curve, which was mainly covered by linear (0.02 to 0.08%) and quadratic (0.01 to 0.03%) coefficients.

Table 4. Eigen values and proportion (%) for the additive genetic and maternal permanent environment effect with different powers of LG polynomials

Eigen value	LG1	LG2	LG3	LG4
Additive genetic effect				
0th	5.119 (99.40)	5.197 (97.32)	5.292 (96.18)	5.305 (95.40)
1st	0.031 (0.60)	0.143 (2.68)	0.171 (3.11)	0.191 (3.43)
2nd	–	0.000 (0)	0.039 (0.71)	0.055 (0.99)
3rd	–	–	0.000 (0)	0.010 (0.18)
4th	–	–	–	0.000 (0)
Maternal permanent environment effect				
0th	47.933 (99.98)	48.620 (99.92)	52.040 (99.92)	50.905 (99.90)
1st	0.008 (0.02)	0.038 (0.08)	0.036 (0.07)	0.033 (0.07)
2nd	–	0.002 (0)	0.008 (0.01)	0.015 (0.03)
3rd	–	–	0.000 (0)	0.000 (0)
4th	–	–	–	0.000 (0)

The results showed that quadratic Legendre polynomials with 3 regression coefficients were enough to capture almost all variability in the model to explain all additive genetic and maternal permanent environment variability. Hence, use of random regression model with quadratic Legendre polynomials was suggested for genetic analysis of pig data for growth. Lukovic *et al*. (2003), Lukovic *et al*. (2004) and Ouko *et al*. (2017) also observed that the first three eigen values of the coefficient matrix of the additive genetic covariance accounted for >98% of the sum of the eigen values. Meyer (2000) also concluded that random regression models were well suited to the analysis of growth data in Australian beef cattle. Albuquerque and Meyer (2001) explained that RRM is capable of determining covariance of a trait at different ages and hence adjustment of age is not required with this model. As a result, error associated with an adjustment may be avoided.

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