



## Genetic parameter estimates for growth performance of crossbred piglets

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Received: 30 March 2019; Accepted: 10 May 2019

**Key words:** Animal model, Birth weight, Heritability, Pig, Weaning weight

The growth performance of pigs has a direct and substantial bearing on the profitability of swine farming. Piglets with lower growth rates are costly to produce due to lower feed conversion efficiency, extra facility costs and management complications (Deen *et al.* 1998, Wolter *et al.* 2003, Baxter *et al.* 2013). Birth weight of pigs is an important component of growth performance as it is directly correlated with piglet survival, behavior, and weight gain (Fix *et al.* 2010; Muns *et al.* 2013, Alves *et al.* 2018). For efficient selection at an early stage, information about genetic parameters of piglet growth is crucial. Weekly body weights of male and female piglets from birth to weaning are important for subsequent selection (Banik *et al.* 2013). Unbiased estimation of such parameters is complicated by the presence of maternal genetic and permanent litter effects (Mondal *et al.* 2014). Presumably due to the labour costs involved in recording such traits and insufficient pedigree information, there is a paucity of studies about the weekly growth performance of individual piglets accounting for the influence of direct additive, maternal genetic and litter environmental effects simultaneously. This study accounted for these factors through 6 different animal models to derive genetic parameter estimates with an aim to optimize piglet growth performance through future selective breeding programs.

The data were collected from the records of Landrace × Desi (Indigenous) pigs (62.5 to 75% Landrace inheritance) maintained at Swine Production Farm, Livestock Production and Management Section, Indian Veterinary Research Institute (ICAR-IVRI), Izatnagar. Records of 5739 Landrace × Desi (indigenous) crossbred pigs born over a period of 18 years (1995–2013) were analyzed to estimate variance components and genetic parameters for growth performance recorded at weekly individual. Traits

considered in pre-weaning stage were weekly body weights from birth (BW) to weaning (W8). Post-weaning weights at weeks 12 (W12) and 32 (W32) were also analyzed during investigation. The breeding and management policy and the climatic conditions at the farm have been described in detail by Mondal *et al.* (2014).

Initially, the influence of different non-genetic factors (periods, seasons, litter size groups) on the traits was determined through least squares analysis. The significant factors affecting the traits were included in six different animal models to derive genetic parameter estimates using restricted maximum likelihood methods. The significant effects were included in the animal models for the estimation of genetic variance and covariance using WOMBAT software package (Meyer 2007), employing a Derivate Free (DF) Restricted Maximum Likelihood (REML) approach (Meyer 1989).

Six different single trait linear models as described by Meyer (1992) were used as follow;

$$Y = X\beta + Z_a\alpha + \epsilon \quad (\text{Model-1})$$

$$Y = X\beta + Z_a\alpha + Z_m m + \epsilon, \text{ with } \text{Cov}(a, m) = 0 \quad (\text{Model-2})$$

$$Y = X\beta + Z_a\alpha + Z_m m + \epsilon, \text{ with } \text{Cov}(a, m) = A\sigma_{am} \quad (\text{Model-3})$$

$$Y = X\beta + Z_a\alpha + Z_c c + \epsilon \quad (\text{Model-4})$$

$$Y = X\beta + Z_a\alpha + Z_m m + Z_c c + \epsilon, \text{ with } \text{Cov}(a, m) = 0 \quad (\text{Model-5})$$

$$Y = X\beta + Z_a\alpha + Z_m m + Z_c c + \epsilon, \text{ with } \text{Cov}(a, m) = A\sigma_{am} \quad (\text{Model-6})$$

where, Y is the vector of observations.  $\beta$ , a, m, c, and  $\epsilon$  are vectors of fixed, direct additive, maternal additive, permanent environmental and residual effects, respectively. X,  $Z_a$ ,  $Z_m$  and  $Z_c$  are incidence matrices that relate these effects to observations. The most appropriate model was determined on the basis of Bayesian Information Criterion (BIC), wherein the best model had the lowest BIC value.

The least-squares means and genetic parameter estimates for weights at different ages are presented in Tables 1 and 2, respectively. Based on the BIC values, the phenotypic variance partitioning of body weight traits up to 5 weeks of age (BW-W5) was best explained by model 4, containing direct additive and permanent litter effects. For W6, W7 and W8, model 2 containing direct and maternal additive genetic effects was found to be most suitable. For post-weaning weights recorded at week 12 and 32, model 4 was the best. For BW the direct heritability estimate ( $h^2$ ) was

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highest through model 1 (0.46) but even after suitable partitioning of variance in subsequent models, the direct additive variance remained. Model 4 estimated  $h^2$  as 0.33 which suggested ample scope for improvement through

mass selection of piglets for birth weight. Direct heritability for pre-weaning traits in pigs is a manifestation of the genetic potential of the embryo and piglets for growth during gestation and lactation, respectively (Kaufmann *et al.* 2000). Our findings agree with the estimate of 0.32 reported by and Canario *et al.* (2010) in Norwegian Landrace. However, generally low  $h^2$  estimates for birth weight have been reported in the literature, ranging from 0.10–0.13. The variation in heritability estimates reported in literature may be due to differences in breeds, management and the models used in analysis. For litter environmental effects ( $c^2$ ) at birth, the literature estimates ranged from 0.02–0.34 (Kaufmann *et al.* 2000, Solanes *et al.* 2004, Chimonyo *et al.* 2006, Mondal *et al.* 2014). Our estimate of 0.16 was in close agreement with Canario *et al.* (2010) who reported  $c^2$  as 0.15. For W1-W5, the  $h^2$  estimates declined and ranged from 0.18–0.24. This may be due to the increased influence of litter environment which had estimates ranging from 0.21–0.23. Solanes *et al.* (2004) and Ilatsia *et al.* (2008) have reported a similar trend of decreased  $h^2$  and increased  $c^2$

Table 1. Least-squares means ( $\pm$ S.E.) for piglet body weights at different ages.

Trait	N	Mean $\pm$ S.D. (kg)
BW	5739	1.00 $\pm$ 0.01
W1	3618	2.02 $\pm$ 0.02
W2	3468	3.25 $\pm$ 0.03
W3	3392	4.54 $\pm$ 0.05
W4	3338	5.83 $\pm$ 0.06
W5	3302	7.01 $\pm$ 0.07
W6	3219	8.20 $\pm$ 0.09
W7	3000	9.48 $\pm$ 0.10
W8	2803	11.00 $\pm$ 0.15
W12	1788	18.49 $\pm$ 0.25
W32	998	64.52 $\pm$ 0.90

Table 2. Genetic parameter estimates of piglet weights at different ages using REML procedures

Trait	Model	$h^2$	$m^2$	$c^2$	BIC	Trait	Model	$h^2$	$m^2$	$c^2$	BIC
BW	1	0.46 $\pm$ 0.03	–	–	–32639.8	W6	4	0.24 $\pm$ 0.06	–	0.23 $\pm$ 0.03	21663.2
	2	0.25 $\pm$ 0.05	0.25 $\pm$ 0.03	–	–33132.2		5	0.24 $\pm$ 0.06	0.0002 $\pm$ 0.04	0.23 $\pm$ 0.04	21663.2
	3	0.4 $\pm$ 0.08	0.35 $\pm$ 0.05	–	–33129.6		6	0.34 $\pm$ 0.09	0.19 $\pm$ 0.08	0.15 $\pm$ 0.05	21701.4
	4	0.33 $\pm$ 0.05	–	0.16 $\pm$ 0.02	–33191.4		1	0.49 $\pm$ 0.04	–	–	25230.4
	5	0.31 $\pm$ 0.05	0.03 $\pm$ 0.04	0.14 $\pm$ 0.03	–33160.7		2	0.18 $\pm$ 0.05	0.31 $\pm$ 0.04	–	24742.0
	6	0.41 $\pm$ 0.07	0.10 $\pm$ 0.06	0.13 $\pm$ 0.03	–33139.2		3	0.24 $\pm$ 0.07	0.37 $\pm$ 0.05	–	24764.4
W1	1	0.41 $\pm$ 0.04	–	–	–6695.8	4	0.26 $\pm$ 0.06	–	0.23 $\pm$ 0.03	24770.4	
	2	0.14 $\pm$ 0.05	0.27 $\pm$ 0.03	–	–7146.1	5	0.19 $\pm$ 0.06	0.22 $\pm$ 0.07	0.07 $\pm$ 0.05	24769.2	
	3	0.24 $\pm$ 0.07	0.36 $\pm$ 0.05	–	–7141.7	6	0.26 $\pm$ 0.08	0.28 $\pm$ 0.09	0.06 $\pm$ 0.06	24792.6	
	4	0.18 $\pm$ 0.05	–	0.21 $\pm$ 0.03	–7262.5	W7	1	0.53 $\pm$ 0.04	–	–	26342.4
	5	0.18 $\pm$ 0.05	0.0005 $\pm$ 0.04	0.21 $\pm$ 0.04	–7230.5		2	0.19 $\pm$ 0.06	0.37 $\pm$ 0.04	–	25612.4
	6	0.32 $\pm$ 0.09	0.08 $\pm$ 0.06	0.19 $\pm$ 0.04	–7222.0		3	0.26 $\pm$ 0.08	0.42 $\pm$ 0.05	–	25635.2
W2	1	0.43 $\pm$ 0.04	–	–	5119.5	4	0.30 $\pm$ 0.06	–	0.28 $\pm$ 0.03	25672.6	
	2	0.13 $\pm$ 0.05	0.31 $\pm$ 0.03	–	4631.7	5	0.21 $\pm$ 0.06	0.30 $\pm$ 0.08	0.05 $\pm$ 0.06	25640.8	
	3	0.26 $\pm$ 0.08	0.40 $\pm$ 0.05	–	4638.1	6	0.27 $\pm$ 0.08	0.35 $\pm$ 0.09	0.05 $\pm$ 0.06	25663.4	
	4	0.15 $\pm$ 0.05	–	0.24 $\pm$ 0.03	4492.6	W8	1	0.59 $\pm$ 0.04	–	–	29493.8
	5	0.15 $\pm$ 0.05	0.00 $\pm$ 0.05	0.24 $\pm$ 0.05	4524.5		2	0.20 $\pm$ 0.06	0.30 $\pm$ 0.04	–	29086.6
	6	0.31 $\pm$ 0.09	0.06 $\pm$ 0.06	0.23 $\pm$ 0.04	4536.0		3	0.23 $\pm$ 0.08	0.33 $\pm$ 0.06	–	29115.0
W3	1	0.52 $\pm$ 0.04	–	–	12576.3	4	0.32 $\pm$ 0.06	–	0.21 $\pm$ 0.03	29142.8	
	2	0.19 $\pm$ 0.05	0.28 $\pm$ 0.04	–	12099.0	5	0.21 $\pm$ 0.06	0.25 $\pm$ 0.07	0.04 $\pm$ 0.05	29115.2	
	3	0.27 $\pm$ 0.08	0.39 $\pm$ 0.06	–	12087.0	6	0.25 $\pm$ 0.08	0.28 $\pm$ 0.09	0.04 $\pm$ 0.05	29143.8	
	4	0.21 $\pm$ 0.05	–	0.23 $\pm$ 0.03	12013.8	W12	1	0.53 $\pm$ 0.05	–	–	25720.6
	5	0.20 $\pm$ 0.05	0.02 $\pm$ 0.04	0.22 $\pm$ 0.05	12045.0		2	0.21 $\pm$ 0.09	0.28 $\pm$ 0.05	–	25414.2
	6	0.33 $\pm$ 0.09	0.09 $\pm$ 0.08	0.22 $\pm$ 0.05	12065.6		3	0.31 $\pm$ 0.12	0.34 $\pm$ 0.07	–	25412.0
W4	1	0.52 $\pm$ 0.04	–	–	18011.4	4	0.31 $\pm$ 0.08	–	0.21 $\pm$ 0.04	25408.2	
	2	0.22 $\pm$ 0.06	0.27 $\pm$ 0.04	–	17590.9	5	0.31 $\pm$ 0.09	0.00 $\pm$ 0.08	0.21 $\pm$ 0.07	25429.8	
	3	0.25 $\pm$ 0.08	0.37 $\pm$ 0.06	–	17561.1	6	0.37 $\pm$ 0.13	0.062 $\pm$ 0.11	0.19 $\pm$ 0.08	25434.8	
	4	0.21 $\pm$ 0.06	–	0.23 $\pm$ 0.03	17490.2	W32	1	0.60 $\pm$ 0.06	–	–	18339.1
	5	0.21 $\pm$ 0.06	0.01 $\pm$ 0.04	0.22 $\pm$ 0.04	17521.8		2	0.26 $\pm$ 0.13	0.41 $\pm$ 0.07	–	18059.7
	6	0.30 $\pm$ 0.09	0.09 $\pm$ 0.08	0.45 $\pm$ 0.05	17546.6		3	0.36 $\pm$ 0.18	0.46 $\pm$ 0.10	–	18084.5
W5	1	0.49 $\pm$ 0.04	–	–	22154.4		4	0.33 $\pm$ 0.13	–	0.36 $\pm$ 0.07	18039.4
	2	0.23 $\pm$ 0.06	0.27 $\pm$ 0.04	–	21758.4		5	0.33 $\pm$ 0.14	0.00 $\pm$ 0.18	0.36 $\pm$ 0.16	18066.2
	3	0.31 $\pm$ 0.08	0.39 $\pm$ 0.06	–	21696.8		6	0.35 $\pm$ 0.20	0.0013 $\pm$ 0.23	0.36 $\pm$ 0.17	18093.1

$h^2$ , direct heritability;  $m^2$ , maternal heritability;  $c^2$ , variance ratio due to permanent environmental component of the litter; BIC, Bayesian Information Criterion.

estimates from birth until 3 weeks of age. Literature estimates for  $h^2$  at W3 were generally lower than ours and ranged from 0.03–0.18 (Solanes *et al.* 2004, Chimonyo *et al.* 2006, Canario *et al.* 2010).

For W6 and weaning weight (W8), the  $h^2$  estimates (0.18–0.20) further diminished. There was a significant role of maternal influence ( $m^2$ ) ranging from 0.30–0.37. Maternal genetic effects are presumably due to genetically controlled components of uterine nutrient supply, uterine capacity, and milk production (Kaufmann 2000). There was no significant role of litter effects as determined by the best model. The trend of decreasing heritability estimates from birth to weaning agreed with the findings of Solanes *et al.* (2004) and Alves *et al.* (2018) although trends to the contrary have also been reported (Kaufmann *et al.* 2000, Mondal *et al.* 2014). The heritability estimates at weaning were within range (0.06–0.47) of literature estimates (Kaufmann *et al.* 2000, Zhang *et al.* 2000, Solanes *et al.* 2004, Ilatsia *et al.* 2008). There was a moderate proportion of direct heritability (0.31–0.33) and permanent litter effects (0.21–0.36) for post-weaning piglet weights recorded at 12 and 32 weeks of age. The maternal effects were non-significant after the piglets had weaned from their mothers. Ilatsia *et al.* (2008) reported similar moderate estimates of post-weaning  $h^2$  (0.26–0.39) and non-significant maternal effects.

#### SUMMARY

The direct heritability estimates for piglet weights in pre and post weaning stages were moderate and improvement through mass selection is plausible. In the pre-weaning stage, the piglets had maximum genetic potential at birth (BW) to be exploited through direct selection. The 3 random effects, namely direct additive, maternal additive and litter permanent environmental effects had significant roles during different phases of pre-weaning growth and all must be included in the model used for formulating a breeding program. For post-weaning traits, the direct additive and permanent litter effects were the predominant factors governing the variability. The non-significance of post-weaning maternal influence was as per expectation because the piglets moved away from maternal care after 8<sup>th</sup> week of age.

#### ACKNOWLEDGEMENTS

The authors are thankful to the Director, ICAR-IVRI, Izatnagar and Incharge, AICRP on Pigs for providing necessary facility to execute the research programme.

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