



Original Article

Estimation of additive and dominance variance for reproductive traits from different models in Duroc purebred

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Abstract

The additive and dominance genetic variances of 5,801 Duroc reproductive and growth records were estimated using BULPF90 PC-PACK. Estimates were obtained for number born alive (NBA), birth weight (BW), number weaned (NW), and weaning weight (WW). Data were analyzed using two mixed model equations. The first model included fixed effects and random effects identifying inbreeding depression, additive gene effect and permanent environments effects. The second model was similar to the first model, but included the dominance genotypic effect. Heritability estimates of NBA, BW, NW and WW from the two models were 0.1558/0.1716, 0.1616/0.1737, 0.0372/0.0874 and 0.1584/0.1516 respectively. Proportions of dominance effect to total phenotypic variance from the dominance model were 0.1024, 0.1625, 0.0470, and 0.1536 for NBA, BW, NW and WW respectively. Dominance effects were found to have sizable influence on the litter size traits analyzed. Therefore, genetic evaluation with the dominance model (Model 2) is found more appropriate than the animal model (Model 1).

Keywords: pigs, inbreeding, dominance, genetic parameters

1. Introduction

Mixed model methodologies for genetic evaluations in swine currently use an additive genetic model. Production and reproduction traits in swine may have a substantially higher heritability in the broad sense relative to the narrow sense. Under these conditions the selection accuracy is reduced under an additive model (Falconer and Mackay, 1996). The prediction of additive and dominance genetic effects concurrently should allow for a more precise prediction of total genetic merit and breeding value, and may prove beneficial in the estimation of the dominance effects for a mate selection program (Henderson, 1989). These conditions are particularly valid in full sib populations with a large number of dominance relationships that use specialized sire and dam lines (DeStefano and Hoeschele, 1992). Then, because swine are a litter bearing species with a large expres-

sion of dominance relationships and possibly useful magnitude of dominance effects in reproductive traits, swine genetic evaluation seems well suited for dominance models. However, before an implementation, the relative importance of the dominance genetic effects must be characterized. Consequently, the objective of this study was to estimate the dominance variance for reproductive and growth traits in swine.

2. Materials and Methods

Data were obtained from a commercial farm and included 5,801 reproductive and growth records from purebred Duroc swine. The litter records were adjusted for parity, age of dam, age of litter at weaning, and number after transfer (Culbertson *et al.*, 1997). Phenotypic means and standard deviations are presented in Table 1. The dominance relationship matrix was formed using the method of Hoeschele and VanRaden (1991). In this method, dominance effects are defined and predicted as a specific mating pair or parental

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Table 1. Number of observations, means, and standard deviations for number born alive (NBA), birth weight (BW), number weaned (NW), and weaning weight (WW).

Item	NBA	BW	NW	WW
Number of observations	1,481	1,477	1,422	1,421
Mean	8.05	1.62	6.95	4.90
SD	2.72	0.28	1.84	0.94

dominance class. Number born alive (NBA), birth weight (BW), number weaned (NW), and weaning weight (WW) were analyzed separately using two mixed models.

$$y = X\beta + Zb\Delta + Za + Zp + e \quad \text{Model 1}$$

$$y = X\beta + Zb\Delta + Za + Wf + Zp + e \quad \text{Model 2}$$

where y is the vector of records, β is the vector of fixed effects, D is the regression of y on inbreeding coefficient, b is the vector of inbreeding coefficients, a is the vector of additive animal effects, f is the vector of parental dominance effects, p is the vector of animal permanent environmental effects, e is the vector of residuals, and X , Z and W are known matrices that relate records to respective effects. The variances of the two mixed models are

$$\text{var} \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_p^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix} \quad \text{Model 1}$$

$$\text{var} \begin{bmatrix} a \\ d \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 & 0 \\ 0 & F\sigma_f^2 & 0 & 0 \\ 0 & 0 & I\sigma_p^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix} \quad \text{Model 2}$$

where σ_a^2 is the additive variance, σ_f^2 is the parental dominance variance and thus 1/4 of the total dominance variance, σ_p^2 is the animal permanent environmental variance, σ_e^2 is the residual variance, A is the additive relationship matrix, and F is the parental dominance relationship matrix. The estimations were done using BULPF90 PC-PACK (Duangjinda and Misztal, 2001).

3. Results and Discussion

Estimates of inbreeding depression and variances for NBA, BW, NW and WW are presented in Table 2. All variances are expressed as a percentage of the phenotypic variance. Estimates of inbreeding depression for the four traits show small percentages, which are in general agreement with a previous work on reproductive traits (Culbertson *et al.*, 1998). Estimates of additive and permanent environmental variances are in general agreement with previous studies for four traits (Mabry *et al.*, 1988; Kaplon *et al.*, 1991; Ferraz and Johnson, 1993). Estimates of dominance variance were 0.1024, 0.1625, 0.0470 and 0.1536 for NBA, BW, NW and WW respectively, and that is agreement with previous studies (Ishida *et al.*, 2001). Dominance variance for NBA, BW, NW and WW traits were found to be 59.67, 93.55, 12.63, and 101.32 % of the additive variance; these figures are considerably higher than those reported by Culbertson *et al.* (1998). The results indicate that dominance effects may be important

Table 2. Estimation of inbreeding depression and variance components for number weaned and weaning weight from additive model (1) and dominance model (2).

Traits	Models	Inbreeding depression	Variance (%phenotypic)		-2logL
			Additive	Dominance	
Born alive	1	0.00025	0.1558		3308
	2	0.00026	0.1716	0.1024	3298
Birth weight	1	-0.0003	0.1616		2932
	2	-0.0003	0.1737	0.1625	2913
Number weaned	1	0.0000	0.0874		2265
	2	0.0002	0.3720	0.0470	2242
Weaning weight	1	0.0000	0.1584		5052
	2	0.0000	0.1516	0.1536	5035

for reproductive and growth traits in swine. Therefore, specific mating systems may allow for selection of dominance effects for these traits and subsequently increase the phenotypic performance. Additional studies are needed to analyze the relative improvements in prediction of additive effects by accounting for dominance and inbreeding effects in both purebred and crossbred swine.

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