

Estimation of Genetic Variance and Covariance Components for Litter Size and Litter Weight in *Danish Landrace* Swine Using a Multivariate Mixed Model*

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ABSTRACT : Single trait mixed models have been dominantly utilized for genetic evaluation of the reproductive traits in swine. However, employing multiple trait approach may lead to more accurate genetic evaluations. For 5 litter size and litter weight traits of *Danish Landrace*, genetic parameters were estimated with a multiple trait mixed model. The heritability estimates were 0.02, 0.03, 0.03, 0.05, and 0.07, respectively for litter size at birth, litter size born alive, litter weight at birth, litter size at weaning, and litter weight at weaning. Negative genetic correlation estimates were obtained between litter size at weaning and the other four traits while environmental correlations were all positive. The litter weight at birth showed genetic antagonism with litter size born alive (-0.65) and litter size at weaning (-0.31), but positive with litter size at birth (0.47) and litter weight at weaning (0.31). The estimates of environmental correlations were larger than their corresponding genetic correlation estimates except for those between litter weight at birth and the other four traits. This study recommends simultaneous selection for two or more traits with multivariate mixed models in order to improve overall economic response. (*Asian-Aus. J. Anim. Sci.* 1999, Vol. 12, No. 7 : 1015-1018)

Key Words : Genetic Correlation, Litter Size, Litter Weight, Variance Component

INTRODUCTION

As the genetic level of swine lean rate has reached its optimum, genetic improvement of reproductive performance becomes increasingly important to efficient pig production. Accurate genetic parameters for the reproductive traits were called for to get accurate breeding values, to predict genetic response, and to optimize breeding schemes.

Single trait mixed models have been predominantly used for genetic evaluation of the reproductive traits (Babot et al., 1994; Estany and Sorenson, 1994; Boesch et al., 1998). However, employing multiple trait models may lead to more accurate genetic evaluations (Li and Kennedy, 1998). There are three benefits from joint consideration of several traits in genetic evaluations (Ducrocq, 1994). First, the information provided by correlated traits is sometimes not directly available on the selection candidate. Secondly, regardless of the availability of direct information, the use of additional knowledge can increase the accuracy of the genetic evaluations. Also, systematic biases in the evaluation can be reduced when a multiple trait approach is used. Therefore, accurate genetic parameters can be estimated by employing multiple trait models, and that renders

information on accurate genetic merits of individual animals.

The purpose of this study was to estimate genetic parameters for five litter size and litter weight traits in *Danish Landrace* by employing a multiple trait mixed model.

MATERIALS AND METHODS

Data

Data were collected from a single *Danish Landrace* population under a nucleus breeding scheme in confinement condition. Reproductive traits of the 993 litters of 559 sows farrowed between 1992 and 1997 at Tianjin Ninghe pig breeding farm in China. The total number of animals in the pedigree file was 923. The traits included in this simultaneous analysis were litter size at birth (LSB), litter size born alive (LSBA), litter weight at birth (LWB), litter size at weaning (LSW), and litter weight at weaning (LWW). The length of suckling period was 45 days.

Analytical model

A multiple trait model was employed to simultaneously analyze the 5 traits as follows:

$$\begin{pmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \\ y_5 \end{pmatrix} = (I_5 \otimes X) \begin{pmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \\ \beta_5 \end{pmatrix} + (I_5 \otimes Z) \begin{pmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \\ e_5 \end{pmatrix}$$

where y_i is the observation vector for LSB ($i=1$),

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LSBA (i=2), LWB (i=3), LSW (i=4), or LWW (i=5). The β_i is the unknown vector of fixed effects, which includes farrowing year (1992 to 1997), farrowing season (spring and fall), and parity (1, 2, 3, 4, and ≥ 5). The u_i is the unknown vector of random genetic effects and has the distribution as follows:

$$\begin{pmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \end{pmatrix} \sim N \left(\begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_{a1}^2 & \sigma_{a12} & \sigma_{a13} & \sigma_{a14} & \sigma_{a15} \\ & \sigma_{a2}^2 & \sigma_{a23} & \sigma_{a24} & \sigma_{a25} \\ & & \sigma_{a3}^2 & \sigma_{a34} & \sigma_{a35} \\ & & & \sigma_{a4}^2 & \sigma_{a45} \\ & \text{sym.} & & & \sigma_{a5}^2 \end{pmatrix} \otimes A \right)$$

The A is the numerator relationship matrix, σ_{ai}^2 is the genetic variance for the i^{th} trait, and σ_{aij} is the genetic covariance between the i^{th} and the j^{th} traits. The e_i is the vector of residuals and has the distribution as follows:

$$\begin{pmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \\ e_5 \end{pmatrix} \sim N \left(\begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_{e1}^2 & \sigma_{e12} & \sigma_{e13} & \sigma_{e14} & \sigma_{e15} \\ & \sigma_{e2}^2 & \sigma_{e23} & \sigma_{e24} & \sigma_{e25} \\ & & \sigma_{e3}^2 & \sigma_{e34} & \sigma_{e35} \\ & & & \sigma_{e4}^2 & \sigma_{e45} \\ & \text{sym.} & & & \sigma_{e5}^2 \end{pmatrix} \otimes I \right)$$

where σ_{ei}^2 is the environmental variance for the i^{th} trait, and σ_{eij} is the environmental covariance between the i^{th} and the j^{th} traits. The X and Z are the known design matrices which relate the observations to their corresponding fixed (β_i) and random (u_i) effects, respectively. The \otimes is a partitioned matrix operation called Kronecker product (Searle, 1982).

Genetic evaluations of reproductive traits in swine have been performed by using animal models which

included additive direct and maternal genetic and permanent environmental effects as random effects (e.g., Babot et al., 1994; Estany and Sorenson, 1994; Noguera et al., 1994). However, maternal genetic and permanent environmental effects were excluded in this study since significance was not found by likelihood ratio tests.

Parameter estimation

Derivative-free REML estimation of variance and covariance components was performed using MTDFREML (Boldman et al., 1995). The method uses the downhill simplex method described by Nelder and Mead (1965) and incorporates FSPAK routines to get the inverse of sparse matrix (Miszta, 1990). The convergence criterion for this method is usually the variance of the likelihood values in the simplex, not the differences in parameter estimates between rounds (Nelder and Mead, 1965). The stopping criterion in this study was less than 10^{-9} of simplex variance. Cold restarts were applied for the analysis.

RESULTS AND DISCUSSION

The parities and farrowing seasons were of great importance to swine reproduction traits (Alfonso et al., 1994; Shostak et al., 1994; Duc et al., 1998). The effects were taken into account for in the analytical model of the current study. The means of the reproductive traits by these effects are presented in table 1. The parity effects were statistically significant ($p < 0.001$) for all the 5 traits (table 1). They had the smallest values at the first litter and had a tendency of increasing up to the fourth parity, thereafter decreasing above the fifth parity. Such pattern was consistently found in previous studies. For example, Duc et al. (1998) reported that litter size increased

Table 1. Least squared means^a ± standard errors of reproductive traits by farrowing season and parity

	n	LSB ^c	LSBA	LWB(kg)	LSW	LWW (kg)
Season	F	0.06	0.02	0.08	0.80	0.80
Spring	558	10.43 ± 0.22	9.50 ± 0.21	12.83 ± 0.29	8.91 ± 0.25	90.79 ± 2.43
Fall	341	10.37 ± 0.19	9.47 ± 0.18	12.93 ± 0.24	8.64 ± 0.23	88.48 ± 2.08
Parity	F	8.96** ^b	9.27**	12.81**	5.51**	12.45**
1	398	9.36 ± 0.19 ^a	8.51 ± 0.18 ^a	11.18 ± 0.25 ^a	7.95 ± 0.22 ^a	77.21 ± 2.16 ^a
2	175	10.67 ± 0.27 ^b	9.88 ± 0.26 ^b	13.47 ± 0.34 ^b	9.44 ± 0.32 ^b	96.06 ± 2.80 ^b
3	171	10.45 ± 0.26 ^b	9.63 ± 0.24 ^b	12.85 ± 0.37 ^b	8.57 ± 0.29 ^c	87.07 ± 2.90 ^c
4	95	11.13 ± 0.36 ^b	9.94 ± 0.34 ^b	13.55 ± 0.45 ^b	8.70 ± 0.40 ^{bc}	94.10 ± 3.60 ^{bc}
≥5	90	10.40 ± 0.35 ^b	9.47 ± 0.33 ^b	13.34 ± 0.46 ^b	9.19 ± 0.36 ^{bc}	93.74 ± 3.63 ^{bc}

^a The means in the same column without the same suffix differ significantly ($p < 0.05$).

^b *: $p < 0.05$, **: $p < 0.001$.

^c litter size at birth (LSB); litter size born alive (LSBA); litter weight at birth (LWB); litter size at weaning (LSW); litter weight at weaning (LWW).

gradually by parity to the maximum at parity 5, and slowly decreased through to parity 10. On the other hand, farrowing season effects were not significant ($p>0.05$) on all the five traits.

The estimates of genetic and environmental (co)variances for the 5 traits are presented in table 2, and their corresponding heritabilities and correlations in table 3. Heritability estimates were small for all the traits, ranging from 0.02 to 0.07. In general, reproductive traits have had low heritabilities. The heritability estimates for LSB and LSBA obtained in this study accorded with those in the studies of Alfonso et al. (1994) and Babot et al. (1994). However, they were smaller than those reported by Estany and Sorenson (1994, 0.11–0.14 for LSB) and by Boesch et al. (1998, 0.07–0.08 for LSBA), where single trait models were used.

Table 2. Genetic and environmental (co)variance estimates for reproductive traits; diagonal elements are genetic (environmental) variances, upper off-diagonal elements are genetic covariances, and lower off-diagonal elements are environmental covariances

	LSB ^a	LSBA	LWB	LSW	LWW
LSB	0.225 (9.898)	0.020	0.115	-0.002	-1.050
LSBA	6.257	0.165 (5.771)	-0.136	-0.006	-0.175
LWB	-0.027	2.290	0.270 (9.326)	-0.079	1.005
LSW	4.520	4.217	1.766	0.244 (4.982)	-0.433
LWW	35.716	33.144	12.943	44.859	39.339 (564.897)

^a litter size at birth (LSB); litter size born alive (LSBA); litter weight at birth (LWB); litter size at weaning (LSW); litter weight at weaning (LWW).

Roehe and Kennedy (1995) also reported larger estimates with univariate model than those obtained in the current study. Their heritability estimates ranged from 0.10 to 0.15, from 0.09 to 0.14, and from 0.06 to 0.08 respectively for LSB, LSBA, and LSW. Beniwal et al. (1994) and Alfonso et al. (1994) also investigated that heritability estimated with a multiple trait model was smaller than that with a single trait model. This suggests that potential bias might have been produced by employing a univariate model. The heritability estimate for LWB (0.03) was larger than that (0.00) obtained by Silio et al. (1994) where maternal genetic and common environmental effects were included in the analytical model. The estimate of heritability for LSW (0.05) was larger than that (0.02) for LSB, which did not agree with Roehe and

Kennedy (1995) and Johansson and Kennedy (1985). The heritabilities for LSW might have been underestimated due to crossfostering (Roehe and Kennedy, 1995).

The LWB showed the negative genetic relationship with LSBA (-0.65) and LSW (-0.31), but positive with LSB (0.47) and LWW (0.31) (table 3). Because the difference between LSB and LSBA is the number of dead pigs, the genetic correlation (-0.01) between LSW and LSB is likely to be smaller than that (-0.03) between LSW and LSBA. All the environmental correlation estimates were positive while some negative genetic correlations were observed. Especially, negative genetic correlation estimates were obtained between litter size at weaning and the other four traits. On the other hand, their environmental correlations were all positive. The estimates of environmental correlations were larger than their corresponding genetic correlation estimates except for those between LWB and the other four traits.

Table 3. Heritability (diagonal) and genetic (above diagonal) and environmental (below diagonal) correlation estimates for reproductive traits

	LSB ^a	LSBA	LWB	LSW	LWW
LSB	0.02	0.10	0.47	-0.01	-0.35
LSBA	0.83	0.03	-0.65	-0.03	-0.07
LWB	0.00	0.31	0.03	-0.31	0.31
LSW	0.64	0.79	0.26	0.05	-0.14
LWW	0.48	0.58	0.18	0.85	0.07

^a litter size at birth (LSB); litter size born alive (LSBA); litter weight at birth (LWB); litter size at weaning (LSW); litter weight at weaning (LWW).

When estimating such genetic parameters, the decision as to which analytical models to use becomes critical. The importance of maternal genetic effects excluded in this study has been controversial. Mercer and Crump (1990) and Perez-Enciso and Gianola (1992) found no maternal genetic effects while Southwood and Kennedy (1990) and Irgang et al. (1994) showed significance of the effects. Ferraz and Johnson (1995) reported that maternal genetic and permanent environmental effects were significant in LSBA, but not for direct and maternal genetic correlation. For LWB, they found no significance even in maternal genetic effects. In the study of Roehe and Kennedy (1995), maternal genetic variance was smaller with more pedigree information, which showed lack of maternal genetic effects. Probably this could have been partially influenced from crossfostering. Roehe and Kennedy (1995) mentioned about confounding between direct and maternal genetic effects.

As previously addressed, another concern on the

analytical model was about employing multiple trait models. Often simultaneous selection for two or more traits is recommended to improve overall economic response. For example, in swine breeding, improvement of litter size results in reduction of piglet birth weight which in turn increases pre- and postnatal mortality and decreases early postnatal growth (Roehe, 1998). In such case, multivariate models utilized in this study are recommended. Employing the models also decrease prediction error variance (Schaeffer, 1984).

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