Estimates Of Genetic Parameters For The Number Of Born Alive At Different Parities In Large White And Landrace Pigs

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Introduction

Number of born alive (NBA) is one of the most important traits in pig breeding. Rothschild and Bidanel (1998) have reported that the heritability for NBA is about 0.1. In many studies, the heritability for NBA was estimated as repeated records from different parities (*e.g.*, Southwood and Kennedy, 1990; Crump et al., 1997). Increasing the total NBA during the reproductive life of a sow has recently become an important objective in pig breeding. Heritability for NBA has been traditionally estimated using a repeatability model. However, the repeatability model cannot clarify the efficiency of improvement in total NBA during the reproductive life of a sow. It is possible to evaluate NBA in different parities as different traits in order to improve NBA during reproductive life of the sow. Roehe and Kennedy (1995), Hanenberg et al. (2001), and Noguera et al. (2002) reported different heritabilities for NBA over the first to the sixth parities. The objective of the present study is to estimate the genetic parameters for NBA by using two models, namely, repeatability and multitrait models.

Material and methods

Animals and traits. The NBA data were obtained from purebred Large White and Landrace sows that had farrowed between 1991 and 2007 in breeding farms participating in National Swine Genetic Evaluation Scheme in Japan. Small farms with less than 20 recorded litters were excluded from the dataset. The edited dataset included 103,413 NBA records from 31,692 Large White sows and 60,860 NBA records from 18,622 Landrace sows. The pedigree file included 43,198 and 28,799 Large White and Landrace individuals, respectively. The basic statistical analyses of NBA at different parities are presented in Table 1.

Repeatability model. To estimate the genetic parameters for NBA, we performed univariate analyses for the (1) 1st parity (NBA1), (2) 2nd to 9th parities (NBA2–9), and (3) 1st to 9th parities (NBA1–9). Random effects were estimated using the following animal model:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wpe} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of observation of NBA; $\mathbf{b}$ is a vector of fixed effects; $\mathbf{a}$, $\mathbf{pe}$, and $\mathbf{e}$ are random vectors of additive genetic, permanent environment, and residual effects, respectively. $\mathbf{X}$, $\mathbf{Z}$, and $\mathbf{W}$ are the incidence matrices that relate elements of $\mathbf{b}$, $\mathbf{a}$, and $\mathbf{pe}$ to $\mathbf{y}$, respectively. The random effects were assumed to be 0 and var($\mathbf{y}$) = $\mathbf{ZAZ}\sigma_a^2$ + $\mathbf{WW}\sigma_{pe}^2$ +

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$\mathbf{I}\sigma_e^2$, where **A** and **I** are the additive genetic relationship and identity matrices, respectively and σ_a^2, σ_{pe}^2, and σ_e^2 represent additive genetic, permanent environment, and residual variance, respectively. The fixed effects included herd, year of farrowing, purebred/crossbred status, parity number, and area and season of farrowing. Parity number was included only in the NBA2–9 and NBA1–9 groups. The area and season of farrowing (6 seasons and 3 areas) were combined to obtain 18 classes.

Bivariate model. We estimated the genetic parameters for NBA at different parities by using a bivariate animal model (Mayer, 1994). The heritabilities are defined as the average of 8 bivariate analyses. We used the following bivariate animal model:

$$\begin{bmatrix}\mathbf{y_1}\\\mathbf{y_2}\end{bmatrix} = \begin{bmatrix}\mathbf{X_1} & \mathbf{0}\\\mathbf{0} & \mathbf{X_2}\end{bmatrix}\begin{bmatrix}\mathbf{b_1}\\\mathbf{b_2}\end{bmatrix} + \begin{bmatrix}\mathbf{Z_1} & \mathbf{0}\\\mathbf{0} & \mathbf{Z_2}\end{bmatrix}\begin{bmatrix}\mathbf{a_1}\\\mathbf{a_2}\end{bmatrix} + \begin{bmatrix}\mathbf{e_1}\\\mathbf{e_2}\end{bmatrix},$$

where $\mathbf{y_1}$ and $\mathbf{y_2}$ are the vectors of observation of NBA at different parities. The vectors of fixed effects for observation1 ($\mathbf{b_1}$) and observation 2 ($\mathbf{b_2}$) are the same as those described in the repeatability model. The vectors of $\mathbf{a_1}$ and $\mathbf{a_2}$ are random additive genetic effects, and $\mathbf{e_1}$ and $\mathbf{e_2}$ are residual effects for trait 1 and trait 2, respectively. The incidence matrices $\mathbf{X_1}$ and $\mathbf{X_2}$ ($\mathbf{Z_1}$ and $\mathbf{Z_2}$) associate elements of $\mathbf{b_1}$ and $\mathbf{b_2}$ ($\mathbf{a_1}$ and $\mathbf{a_2}$) with the records $\mathbf{y_1}$ and $\mathbf{y_2}$. The expectation of $\mathbf{y_1}$ ($\mathbf{y_2}$) is $\mathbf{X_1b_1}$ ($\mathbf{X_2b_2}$), and the variance-covariance matrix of random effects of the bivariate animal model is as follows:

$$\mathbf{Var}\begin{bmatrix}\mathbf{a_1}\\\mathbf{a_2}\\\mathbf{e_1}\\\mathbf{e_2}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma_{a_1}^2 & \mathbf{A}\sigma_{a_{12}} & \mathbf{0} & \mathbf{0}\\\mathbf{A}\sigma_{a_{21}} & \mathbf{A}\sigma_{a_2}^2 & \mathbf{0} & \mathbf{0}\\\mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_{e_1}^2 & \mathbf{I}\sigma_{e_{12}}\\\mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_{e_{21}} & \mathrm{I}\sigma_{e_2}^2\end{bmatrix},$$

where σ_{a1}^2 and σ_{a2}^2 represent the additive genetic variances, and σ_{e1}^2 and σ_{e2}^2 represent the residual variances for trait 1 and trait 2, respectively; σ_{a12} represents the additive genetic covariance between trait 1 and trait 2, and σ_{e12} represents their residual covariance. The fixed effects are the same as those described in the repeatability model.

Genetic parameters were estimated by performing restricted maximum likelihood analyses in an animal model by using MTDFREML program. The convergence criterion (i.e., the variance of the simplex values) for all runs was 10^{-12}.

Table 1. Basic statistical analysis of number of born alive at different parities.

	Large White			Landrace		
Parity	N	Mean	SD	N	Mean	SD
1	18,993	9.83	2.18	11,553	9.83	2.13
2	16,141	10.30	2.27	9,954	10.14	2.24
3	15,142	10.62	2.23	9,191	10.35	2.22
4	13,750	10.62	2.32	8,022	10.38	2.23
5	11,998	10.55	2.35	6,889	10.35	2.22
6	10,081	10.47	2.36	5,695	10.32	2.26
7	7,894	10.31	2.38	4,373	10.23	2.21
8	5,725	10.15	2.35	3,103	10.23	2.20
9	3,749	10.06	2.39	2,080	10.26	2.13

Results and discussion

Repeatability model. The results of the repeatability model analyses are shown in Table 2. The heritabilities for NBA were estimated to be between 0.11 and 0.14 in Large White and between 0.07 and 0.14 in Landrace; these values were equivalent to those reported in the review by Rothschild and Bidanel (1998). The heritability of NBA1 was higher than that of NBA2–9 and NBA1–9. Hanenberg et al. (2001) reported that the heritability of NBA1 is lower than NBA2–9. However, we observed that the heritability of NBA1 was higher than that of NBA2–9 in Large White and Landrace. In Large White, the permanent environmental ratio for NBA1–9 is similar to that for NBA2–9. However, in Landrace pigs, the permanent environmental ratio for NBA1–9 is higher than that for NBA2–9, and the reason for this difference is unclear.

Table 2. Estimates of phenotypic variance (σ_P^2), heritability (h^2), and permanent environmental ratios (pe^2) for NBA

Breed	Trait[1)]	σ_P^2	h^2	pe^2
Large White	NBA1	4.218	0.14	-
	NBA2–9	4.943	0.13	0.07
	NBA1–9	4.812	0.11	0.06
Landrace	NBA1	3.928	0.14	-
	NBA2–9	3.977	0.07	0.07
	NBA1–9	3.996	0.08	0.23

[1)] See the text.

Bivariate model. Table 3 and Table 4 show the results of bivariate analyses for NBA at different parities in Large White and Landrace, respectively. In general, the NBA heritabilities obtained by using a bivariate model were lower than those determined in the repeatability analyses. Hanenberg et al. (2001) and Noguera et al. (2002) used records for parities 1 to 6 and reported that the heritability for NBA increased with parity number. Similarly, in this study, the heritability for NBA in Large White also showed the tendency to increase with parity between parities 1 and 6, with exception of the first parity. However, the estimated heritability of NBA in the 6th parity was higher than that in the subsequent parities. In contrast, the heritability for NBA decreased with parity in Landrace. These results suggest that the NBA at different parities may be affected by different environmental effects and/or different genes. The genetic correlations between adjacent parities were generally high except the genetic correlation between the first and second parities in Large White. The genetic correlations between different parities in Large White were higher than those in Landrace. In Large White, genetic correlations between the first and later parities were lower than those between the other parities. Similar results were obtained for Landrace pigs. Noguera et al. (2002) and Hanenberg et al. (2001) also reported. NBA at the first parity is genetically different from NBA at later parities. These results suggest NBA in the first parity and later parities should be evaluated as different traits. Environmental correlations for NBA were low between all parities.

To improve the total NBA during the reproductive life of the sow, various models, such as the repeatability model or multi-trait model can be considered. Selection for total NBA using the long-term data obtained during the reproductive life of the sow, decreases selection intensity per year. We will consider the optimal model and selection design to improve the total NBA during the reproductive life of sows.

Table 3. Estimates of heritabilities (on the diagonal), genetic correlations (below the diagonal), and environment correlations (above the diagonal) for number of born alive over parities in Large White

parity	1	2	3	4	5	6	7	8	9
1	**0.14**	0.09	0.07	0.03	0.06	0.06	0.07	0.02	0.02
2	0.67	**0.12**	0.04	0.07	0.07	0.03	0.05	-0.01	-0.01
3	0.58	0.98	**0.13**	0.11	0.12	0.09	0.10	0.11	0.11
4	0.73	0.92	0.93	**0.13**	0.12	0.08	0.15	0.08	0.08
5	0.52	0.82	0.87	0.85	**0.14**	0.12	0.13	0.07	0.07
6	0.53	0.76	0.89	0.87	1.00	**0.16**	0.07	0.09	0.10
7	0.33	0.68	0.66	0.67	0.96	1.00	**0.10**	0.17	0.15
8	0.46	0.87	0.83	0.76	0.94	1.00	1.00	**0.12**	0.10
9	0.46	0.87	0.83	0.76	0.94	0.66	0.83	1.00	**0.14**

Table 4. Estimates of heritabilities (on the diagonal), genetic correlations (below the diagonal), and environment correlations (above the diagonal) for number of born alive over parities in Landrace

Parity	1	2	3	4	5	6	7	8	9
1	**0.15**	0.06	0.08	0.06	0.05	0.02	0.03	0.07	0.07
2	0.79	**0.12**	0.08	0.05	0.09	0.02	0.05	0.04	0.04
3	0.53	0.79	**0.11**	0.07	0.10	0.07	0.08	0.03	-0.06
4	0.60	0.82	0.90	**0.08**	0.13	0.09	0.09	0.06	0.06
5	0.50	0.64	0.87	0.83	**0.05**	0.13	0.17	0.12	0.01
6	0.73	0.62	0.75	0.89	0.82	**0.08**	0.14	0.08	0.01
7	0.53	0.23	0.44	0.53	0.66	0.79	**0.07**	0.14	0.09
8	0.33	0.27	0.50	0.47	0.75	0.76	0.96	**0.05**	0.11
9	0.33	0.27	0.48	0.47	0.55	0.75	0.59	0.50	**0.09**

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