

Estimation of Additive and Dominance Genetic Variances in Line Breeding Swine

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ABSTRACT : Additive and dominance genetic variances were estimated for purebred Landrace selected with line breeding from 1989 to 1995 at Miyazaki Livestock Experiment Station, Kawaminami Branch. Ten body measurements, two reproductive traits and fifteen carcass traits were analyzed with single-trait mixed model analysis. The estimates of narrow-sense heritabilities by additive model were in the range of 0.07 to 0.46 for body measurements, 0.05 to 0.14 for reproductive traits, and 0.05 to 0.68 for carcass traits. The additive model tended to slightly overestimate the narrow-sense heritabilities as compared to the additive and dominance model. The proportion of the dominance variance to total genetic variance ranged from 0.11 to 0.91 for body measurements, 0.00 to 0.65 for reproductive traits, and 0.00 to 0.86 for carcass traits. Large differences among traits were found in the ratio of dominance to total genetic variance. These results suggested that dominance effect would affect the expression of all ten body measurements, one reproductive trait, and nine carcass traits. It is justified to consider the dominance effects in genetic evaluation of the selected lines for those traits. (*Asian-Aust. J. Anim. Sci.* 2001. Vol. 14, No. 1 : 1-6)

Key Words : Dominance Variance, Animal Model, Swine, Body Measurement, Reproductive Trait, Carcass Trait

INTRODUCTION

Recently, mixed model methodologies using animal models have been used widely in animal breeding. In most applications, an additive genetic model was used. It is, however, necessary to consider dominance effect if it exists, because of increased accuracy of predicted breeding values (Uimari and Mäki-Tanila, 1992), or selection of mates based on their specific combining ability (Allaire and Henderson, 1965; DeStefano and Hoeschele, 1992).

Selection based on BLUP under an animal model certainly increases inbreeding coefficients (Belonsky and Kennedy, 1988). The complicated genetic relationships, especially dominance relationships in the population would increase over time. Under such situations, it is necessary to consider dominance effect in addition to additive effect to evaluate genetic effects more accurately (Uimari and Mäki-Tanila, 1992; Ishida and Mukai, 1994). Swine is a prolific species so that a large percentage of dominance relationships may accumulate rapidly in a selected line, suggesting that an animal model with dominance effect would fit well in the genetic evaluation.

The objective of this study is to estimate both additive and dominance genetic variances for some body measurements, and reproductive and carcass traits of line breeding swine using single-trait REML procedure under animal models.

MATERIALS AND METHODS

Data

The data were on purebred Landrace, which were selected with line breeding test for seven generations from 1989 to 1995 at Miyazaki Livestock Experiment Station, Kawaminami Branch in Japan. The selection in this line breeding system was carried using average daily gain, ultrasonically scanned *M. longissimus thoracis* area and back fat thickness. The details of selection procedure were described by Duran et al. (1995). Three categories of performance records were analyzed in this study. First, ten body measurements taken at the finish of test when the body weight was approximately 90 kg were body length (BL), heart girth (HG), cannon circumference (CC), withers height (WH), chest depth (CD), shoulder width (SW), chest width (CW), hip width (HW), hip height (HH) and average daily gain (DG) approximately 30 to 90 kg. Secondly, two reproductive traits were the number of piglet born in total (NP) and the number weaned (NW). The NP was the sum of the number of piglet born alive and dead. Thirdly, fifteen carcass traits at the end of testing were: body weight before slaughter (BWS), cold carcass weight (CWT), carcass length (CL), carcass width (CWD), back loin length I, the length from the front end of the first *Vertebrae thoracicae* to the front end of *Os pubis* (BLI), back loin length II, from the front end of the first *Vertebrae thoracicae* to the back end of the last *Vertebrae lumbales* (BLII), percentage of shoulder weight (PS), percentage of ham weight (PH), *M. longissimus thoracis* area (MLA), *M. longissimus thoracis* length (MLL), *M. longissimus thoracis* weight

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(MLW), average back fat thickness (ABF), average *M. gluteus medius* fat thickness (AGF), kidney fat weight (KFW) and the number of *Vertebrae thoracicae* (NVT). Body measurements and carcass traits were obtained according to the methods of Yazama and Tomoda (1986). Seven generations of body measurements and carcass traits and six generations of reproductive traits are available for analysis. The number of pigs with body measurements, and reproductive and carcass traits were 1528, 285 and 567, respectively. The basic statistics were shown in table 1. In order to improve the connectedness among these pigs, a total of 1595, 376 and 977 was used in the final analysis.

Table 1. Basic statistics for three categories of traits

Traits ¹	No.	Mean	Min.	Max.	SD
Body measurements					
ATF (day)	1528	163.09	108.00	229.00	15.09
IC (%)	1528	1.85	0.00	13.48	2.12
BL (cm)	1528	111.26	100.00	129.00	4.14
HG (cm)	1528	96.93	88.00	105.00	2.11
CC (cm)	1528	16.02	14.00	19.20	0.69
WH (cm)	1528	62.09	51.20	73.00	2.27
CD (cm)	1528	31.32	25.50	37.00	1.22
SW (cm)	1528	28.12	23.40	33.00	1.45
CW (cm)	1528	25.68	22.00	33.50	1.61
HW (cm)	1528	29.87	24.00	34.00	1.46
HH (cm)	1528	66.58	54.80	76.20	2.62
DG (g)	1528	741.65	427.20	1064.30	98.84
Reproductive traits					
AP (month)	285	11.97	10.68	13.58	0.54
IC (%)	285	1.85	0.00	13.48	2.19
NP	285	9.13	2.00	15.00	2.28
NW	285	8.02	2.00	14.00	2.15
Carcass traits					
ATF (day)	567	166.85	122.00	229.00	15.09
IC (%)	567	1.81	0.00	13.48	2.15
BWS (kg)	567	86.13	79.60	93.80	2.70
CWT (kg)	567	62.39	56.20	70.80	2.19
CL (cm)	567	93.50	84.00	100.00	2.50
CWD (cm)	567	31.76	28.50	35.00	1.01
BLI (cm)	567	77.78	69.50	89.00	2.33
BLII (cm)	567	68.63	60.00	76.00	2.22
PS (%)	567	10.12	8.25	13.50	0.65
PH (%)	567	10.35	8.95	12.50	0.49
MLA (cm ²)	567	23.72	14.13	40.60	3.39
MLL (cm)	567	53.19	46.00	64.50	2.43
MLW (kg)	567	3.17	2.19	4.19	0.28
ABF (cm)	567	2.48	1.50	3.67	0.35
AGF (cm)	567	2.04	1.00	3.77	0.43
KFW (g)	567	497.26	189.00	1090.50	143.52
NVT	567	15.77	15.00	17.00	0.45

¹ See text for detailed description of the traits.

The mating structures in three categories of traits were shown in table 2. As for each category of trait, the average number of piglets produced by sire or dam ranged from 4 to 18 or 1 to 5, respectively, and the average number of mates with sire or dam ranged from 3 to 4 or 1 depending upon the traits. The percentage of full-sib progeny varied from 60 to 99%.

Genetic evaluation model

In order to solve the mixed model equations, the inverse of the additive (A^{-1}) and/or the dominance (D^{-1}) relationship matrices are necessary, but setting up the D^{-1} is more complicated than A^{-1} . In non-inbred populations, the dominance relationship matrix can be computed from the additive genetic relationship matrix, and then the inverse of D is applied to mixed model equations (Henderson, 1985). In this study, D^{-1} was obtained by direct inversion of D , which was formed by gametic relationship matrix developed by Schaeffer et al. (1989). The calculation of A^{-1} was based on the rapid method of Quaas (1976).

Additive and dominance genetic variance components were estimated using single-trait REML (Patterson and Thompson, 1971) by expectation maximization (EM) algorithm (Dempster et al., 1977) under two mixed linear models as follows:

[Model A]

$$y_{ijk} = G_i + S_j + t_1(T_{ijk} - \bar{T}) + t_2(T_{ijk} - \bar{T})^2 + b(F_{ijk} - \bar{F}) + a_{ijk} + e_{ijk}$$

[Model D]

$$y_{ijk} = G_i + S_j + t_1(T_{ijk} - \bar{T}) + t_2(T_{ijk} - \bar{T})^2 + b(F_{ijk} - \bar{F}) + a_{ijk} + d_{ijk} + e_{ijk}$$

where y_{ijk} is the ijk^{th} observation; G_i is the fixed effect of the i^{th} generation ($i=1$ to 7 for body measurements and carcass traits; $i=1$ to 6 for reproductive traits); S_j is the fixed effect of the j^{th} sex ($j=1$ or 2) applied for body measurements and carcass traits; T_{ijk} is the age of date at the finish of test (for body measurements and carcass traits) or age of month at parturition (only for reproductive traits) of the ijk^{th} animal (\bar{T} is the mean of age); t_1 and t_2 are the partial linear and quadratic regression coefficient

Table 2. Mating structures in three categories of traits

Traits ¹		Number of ²		Full-sib % ³
		piglet	mate	
BMR	Sire	18.41	4.07	99.54
	Dam	4.52	1.00	
RPR	Sire	4.19	2.81	60.35
	Dam	1.49	1.00	
CCS	Sir	6.83	3.92	84.30
	Dam	1.74	1.00	

¹ BMR: body measurements; RPR: reproductive traits; CCS: carcass traits.

² Average number of piglets and mate.

³ Percentage of full-sib progeny.

on age; F_{ijk} is the inbreeding coefficient of the ijk^{th} animal (\bar{F} is the mean of inbreeding coefficient); b is the partial linear regression coefficient on inbreeding coefficient; a_{ijk} , d_{ijk} and e_{ijk} are the random additive, dominance and residual effects of the ijk^{th} animal, respectively. Models A and D include regression on inbreeding coefficient as a covariate to take into account inbreeding depression (Kennedy et al., 1988). The inbreeding coefficients were calculated based on the algorithm of Meuwissen and Luo (1992) using all pedigree information available. In order to accelerate REML convergence, the Aitken acceleration method (Gerald, 1970) with faster EM-alike REML formula (VanRaden, 1986) was used. The iteration was stopped when

$$\frac{|\hat{\sigma}_i^2 - \hat{\sigma}_{i-1}^2|}{\hat{\sigma}_i^2} \leq 1.0E-6$$

was attained, where $\hat{\sigma}_i^2$ is estimated additive or dominance variance at i^{th} iteration. After convergence, the EM-REML procedure without acceleration method was run again to confirm the convergence.

RESULTS AND DISCUSSION

Degree of inbreeding and relationships

An average inbreeding coefficient and additive and dominance relationships for the three categories of traits were shown in table 3. In this study, additive or dominance relationship was the average of the elements of additive or dominance relationship matrices, **A** or **D**, respectively.

Because these categories of traits were measured on the same population selected by the same line breeding, there were no large differences among three categories of traits although relatively lower values were observed for reproductive traits (RPR). This is because RPR were measured up to sixth generation of selection, as opposed to seven generation for body measurements (BMR) and carcass traits (CCS).

The average inbreeding coefficient of 1.77% and additive relationship of 6.77% were observed for BMR. In addition, the percentages of inbred pigs and combination of pigs with additive relationships were 52.6% and 77.5%, respectively. Because inbreeding was avoided deliberately at the design of mating plan in this line breeding, the inbreeding and relationships were relative low. The degree of dominance relationship was much lower than additive relationship. The percentages of combination of pigs with dominance relationships were 56.9% with the average relationship of 0.37% in BMR. Although the percentages of full-sib progeny were very high as given in table 2, an avoidance of full-sib mating has resulted in lower dominance relationship.

Estimated variance components

Estimated variance components for body measurements and reproductive traits were shown in table 4, and for carcass traits in table 5. The estimates of additive genetic variances for NP and NW corresponded with those reported for Landrace population (Southwood and Kennedy, 1990; Roche and Kennedy, 1995). On the other hand, the estimates of additive variance for DG and ABF were considerably lower than those reported by Ferraz and Johnson (1993) and Kennedy et al. (1985) using ultrasonic measurements. Although it was not significant, additive genetic variances for most traits studied were slightly overestimated by Model A compared with Model D. These overestimations were also reported by Wei and van der Werf (1993) and Ishida et al. (2000) in poultry, van der Werf and de Boer (1989a, b) and Tempelman and Burnside (1991) for milk production of dairy cattle, and Rodríguez-Almeida et al. (1995) for body measurements of beef cattle.

The estimated components of residual variances for most traits were also overestimated by Model A compared with Model D, taking account of the sampling error of estimate. This was due primarily to the confounding of dominance genetic variance with residual variances and partially to the confounding of dominance with additive genetic variances under Model A.

Since both components from Model A tended to be overestimated and then the biases might cancel out, the estimates of narrow-sense heritabilities by Model A were in the range of 0.07 to 0.46 for body measurements, 0.05 to 0.14 for reproductive traits, and 0.05 to 0.68 for carcass traits. The results for DG, NP, NW and ABF were in agreement with those reported in literature (Kennedy et al., 1985; Southwood and Kennedy, 1990; Ferraz and Johnson, 1993; Roche and Kennedy, 1995).

Dominance genetic variances by Model D could not be estimated for NW in reproductive traits, and BWS, CWT, CL, MLL and MLW in carcass traits. However, the proportion of dominance variance to total phenotypic variance by Model D for body measurements and reproductive and carcass traits were in the range of 0.03 to 0.90, 0.20, and 0.01 to 0.53, respectively, and large differences among traits were found. Wei and van der Werf (1993) also expressed the proportion of the dominance variance to total genetic variance, in order to detect the dominance effect. The ranges of dominance proportion were 0.11 to 0.91 for body measurements, 0.65 for reproductive trait and 0.03 to 0.86 for carcass traits. These two kinds of proportion for ABF were considerably higher than those reported by Culbertson et al. (1998) for Yorkshire population using ultrasonic measurements.

The proportion mentioned above can be compared with the theoretical values for a single-locus, two-allele model given below (Falconer, 1981):

$$d_s^2 = \frac{2pqd^2}{2pqd^2 + [a + d(q-p)]^2}$$

where p and q stand for the frequency of a favorable and recessive allele, respectively. The genotypic value of the favorable homozygote (a) is assumed to be 1.0,

and d is the genotypic value of the heterozygote. In the case of $d=0.5$, that means a degree of dominance (d/a) is 0.5, the value of d_s^2 reaches its maximum at 0.1429 for $p=0.75$, and d_s^2 reaches its maximum at 0.0870 for $d=0.4$ and $p=0.7$. If d is smaller than 0.7, d_s^2 cannot be larger than 0.33. In this study, d_s^2 for all traits except for SW and HH in body measurements, NP in reproductive traits, and BLI, PS, PH, MLA, ABF, AGF, KFW and NVT in carcass traits were

Table 3. Average inbreeding coefficients and additive and dominance relationships in three categories of traits

Trait ¹	No.	Inbc. ²	% ³	Add.Rel. ²	% ³	Dom.Rel. ²	% ³
BMR	1595	1.77	52.6	6.77	77.5	0.37	56.9
RPR	376	1.09	41.5	6.27	67.7	0.28	43.0
CCS	977	1.50	46.9	6.29	72.1	0.32	50.1

¹ BMR: body measurements; RPR: reproductive traits; CCS: carcass traits.

² Inbc.: inbreeding coefficient (%); Add.Rel.: additive relationship (%), Dom.Rel.: dominance relationship (%).

³ %: percentage of inbred pigs, and percentage of combination of pigs with additive or dominance relationship.

Table 4. Estimates of variance components using two different models for body measurements and reproductive traits

Trait ¹	Model	$\sigma_a^2 \pm se$	σ_d^2	$\sigma_e^2 \pm se$	σ_y^2	$h_N^2 \pm se$	d^2	d_s^2
Body measurements								
BL	A	5.32 ± 0.85		7.07 ± 0.54	12.39	0.43 ± 0.05		
	D	4.66 ± 0.87	2.37	5.28 ± 0.55	12.30	0.38 ± 0.07	0.19	0.34
HG	A	0.88 ± 0.22		3.47 ± 0.19	4.35	0.20 ± 0.05		
	D	0.71 ± 0.22	0.68	2.94 ± 0.19	4.33	0.16 ± 0.06	0.16	0.49
CC	A	$9.43 \times 10^{-2} \pm 1.74 \times 10^{-2}$		$1.84 \times 10^{-1} \pm 0.12 \times 10^{-1}$	2.78×10^{-1}	0.34 ± 0.05		
	D	$7.65 \times 10^{-2} \pm 1.76 \times 10^{-2}$	0.07	$1.29 \times 10^{-1} \pm 0.12 \times 10^{-1}$	2.77×10^{-1}	0.28 ± 0.07	0.26	0.48
WH	A	1.63 ± 0.29		2.53 ± 0.19	4.16	0.39 ± 0.06		
	D	1.33 ± 0.30	1.15	1.64 ± 0.19	4.13	0.32 ± 0.08	0.28	0.46
CD	A	0.09 ± 0.04		1.26 ± 0.06	1.35	0.07 ± 0.03		
	D	0.06 ± 0.04	0.14	1.15 ± 0.06	1.35	0.04 ± 0.03	0.10	0.71
SW	A	0.36 ± 0.09		1.27 ± 0.07	1.63	0.22 ± 0.05		
	D	0.35 ± 0.09	0.04	1.24 ± 0.07	1.63	0.21 ± 0.05	0.03	0.11
CW	A	0.26 ± 0.09		1.95 ± 0.09	2.21	0.12 ± 0.04		
	D	0.15 ± 0.08	0.41	1.64 ± 0.09	2.20	0.07 ± 0.04	0.18	0.72
HW	A	0.55 ± 0.11		1.30 ± 0.08	1.85	0.30 ± 0.05		
	D	0.32 ± 0.11	0.72	0.78 ± 0.08	1.81	0.18 ± 0.08	0.39	0.69
HH	A	2.43 ± 0.39		2.82 ± 0.24	5.25	0.46 ± 0.06		
	D	2.18 ± 0.40	0.99	2.05 ± 0.24	5.22	0.42 ± 0.07	0.19	0.31
DG	A	722.90 ± 141.66		1708.35 ± 105.72	2431.25	0.30 ± 0.05		
	D	210.35 ± 124.87	2138.32	19.08 ± 94.99	2367.75	0.09 ± 0.41	0.90	0.91
Reproductive traits								
NP	A	0.73 ± 0.59		4.45 ± 0.61	5.18	0.14 ± 0.11		
	D	0.57 ± 0.58	1.04	3.57 ± 0.61	5.18	0.11 ± 0.14	0.20	0.65
NW	A	0.24 ± 0.44		4.34 ± 0.53	4.58	0.05 ± 0.10		
	D	0.24 ± 0.44	0.00	4.34 ± 0.53	4.58	0.05 ± 0.10	0.00	0.00

¹ Abbreviations of the traits are same as table 1.

² σ_a^2 : additive genetic variance; σ_d^2 : dominance genetic variance; σ_e^2 : residual variance; σ_y^2 : phenotypic variance; h_N^2 : narrow-sense heritability (σ_a^2/σ_y^2); d^2 : dominance variance as a proportion of phenotypic variance (σ_d^2/σ_y^2); d_s^2 : proportion of dominance variance to total genetic variance ($\sigma_d^2/(\sigma_a^2 + \sigma_d^2)$).

Table 5. Estimates of variance components using two different models for carcass traits

Trait ¹	Model	$\sigma_a^2 \pm se$		σ_d^2	$\sigma_e^2 \pm se$		σ_f^2	$h_N^2 \pm se$	d^2	d_e^2	
Carcass traits											
BWS	A	0.28 ±	0.42			5.81 ±	0.51	6.09	0.05 ± 0.07		
	D	0.28 ±	0.42	0.00		5.81 ±	0.51	6.09	0.05 ± 0.07	0.00	0.00
CWT	A	0.59 ±	0.39			4.14 ±	0.40	4.73	0.12 ± 0.08		
	D	0.59 ±	0.39	0.00		4.14 ±	0.40	4.73	0.12 ± 0.08	0.00	0.00
CL	A	2.88 ±	0.76			2.93 ±	0.56	5.81	0.50 ± 0.11		
	D	2.88 ±	0.76	0.00		2.93 ±	0.56	5.81	0.50 ± 0.11	0.00	0.00
CWD	A	$2.58 \times 10^{-1} \pm 1.08 \times 10^{-1}$			$7.34 \times 10^{-1} \pm 0.94 \times 10^{-1}$	9.91×10^{-1}		0.26 ± 0.10			
	D	$2.56 \times 10^{-1} \pm 1.08 \times 10^{-1}$		6.60×10^{-3}	$7.29 \times 10^{-1} \pm 0.94 \times 10^{-1}$	9.91×10^{-1}		0.26 ± 0.10	0.01	0.03	
BLI	A	1.87 ±	0.62			3.06 ±	0.49	4.94	0.38 ± 0.11		
	D	1.59 ±	0.58	1.16		2.16 ±	0.46	4.91	0.32 ± 0.14	0.24	0.42
BLII	A	1.56 ±	0.56			3.19 ±	0.46	4.75	0.33 ± 0.11		
	D	1.46 ±	0.55	0.42		2.86 ±	0.45	4.74	0.31 ± 0.11	0.09	0.23
PS	A	$4.23 \times 10^{-2} \pm 3.05 \times 10^{-2}$			$3.26 \times 10^{-1} \pm 0.32 \times 10^{-1}$	3.68×10^{-1}		0.11 ± 0.08			
	D	$3.44 \times 10^{-2} \pm 2.96 \times 10^{-2}$		4.64×10^{-2}	$2.87 \times 10^{-1} \pm 0.31 \times 10^{-1}$	3.68×10^{-1}		0.09 ± 0.09	0.13	0.57	
PH	A	$4.12 \times 10^{-2} \pm 2.31 \times 10^{-2}$			$1.89 \times 10^{-1} \pm 0.22 \times 10^{-1}$	2.30×10^{-1}		0.18 ± 0.10			
	D	$1.68 \times 10^{-2} \pm 1.94 \times 10^{-2}$		1.07×10^{-1}	$1.05 \times 10^{-1} \pm 0.19 \times 10^{-1}$	2.29×10^{-1}		0.07 ± 0.15	0.47	0.86	
MLA	A	5.35 ±	1.54			5.87 ±	1.15	11.22	0.48 ± 0.12		
	D	3.56 ±	1.35	5.41		2.02 ±	1.02	10.99	0.32 ± 0.20	0.49	0.60
MLL	A	0.90 ±	0.41			3.37 ±	0.38	4.27	0.21 ± 0.09		
	D	0.90 ±	0.41	0.00		3.37 ±	0.38	4.27	0.21 ± 0.09	0.00	0.00
MLW	A	$1.42 \times 10^{-2} \pm 0.65 \times 10^{-2}$			$5.58 \times 10^{-2} \pm 0.61 \times 10^{-2}$	7.00×10^{-2}		0.20 ± 0.09			
	D	$1.42 \times 10^{-2} \pm 0.65 \times 10^{-2}$		0.00	$5.58 \times 10^{-2} \pm 0.61 \times 10^{-2}$	7.00×10^{-2}		0.20 ± 0.09	0.00	0.00	
ABF	A	$4.18 \times 10^{-2} \pm 1.32 \times 10^{-2}$			$5.52 \times 10^{-2} \pm 1.01 \times 10^{-2}$	9.70×10^{-2}		0.43 ± 0.12			
	D	$3.18 \times 10^{-2} \pm 1.20 \times 10^{-2}$		2.72×10^{-2}	$3.66 \times 10^{-2} \pm 0.93 \times 10^{-2}$	9.56×10^{-2}		0.33 ± 0.15	0.28	0.46	
AGF	A	$9.46 \times 10^{-2} \pm 2.30 \times 10^{-2}$			$4.38 \times 10^{-2} \pm 1.56 \times 10^{-2}$	1.38×10^{-1}		0.68 ± 0.13			
	D	$6.16 \times 10^{-2} \pm 1.91 \times 10^{-2}$		6.94×10^{-2}	$0.12 \times 10^{-2} \pm 1.31 \times 10^{-2}$	1.32×10^{-1}		0.47 ± 0.21	0.53	0.53	
KFW	A	9286.68 ± 2566.14			7563.44 ± 1836.39		16850.12	0.55 ± 0.12			
	D	7220.74 ± 2332.56		4755.42	4535.51 ± 1687.92		16511.67	0.44 ± 0.16	0.29	0.40	
NVT	A	$4.37 \times 10^{-2} \pm 1.98 \times 10^{-2}$			$1.59 \times 10^{-1} \pm 0.18 \times 10^{-1}$	2.02×10^{-1}		0.22 ± 0.09			
	D	$3.83 \times 10^{-2} \pm 1.91 \times 10^{-2}$		2.81×10^{-2}	$1.36 \times 10^{-1} \pm 0.18 \times 10^{-1}$	2.02×10^{-1}		0.19 ± 0.10	0.14	0.42	

¹ Abbreviations of the traits are same as table 1.

² σ_a^2 : additive genetic variance; σ_d^2 : dominance genetic variance; σ_e^2 : residual variance; σ_f^2 : phenotypic variance; h_N^2 : narrow-sense heritability (σ_a^2/σ_f^2); d^2 : dominance variance as a proportion of phenotypic variance (σ_d^2/σ_f^2); d_e^2 : proportion of dominance variance to total genetic variance ($\sigma_d^2/(\sigma_a^2 + \sigma_d^2)$).

over 0.33, and these values suggested that at least one locus with partial dominance effect might exist. For SW and HH in body measurements and BLII in carcass traits, the size of d_e^2 also suggested the existence of dominance effect. Of course, the amount of dominance variance depends largely on the unknown number of loci concerned and favorable gene frequencies changed due to selection. However, the results indicated that some loci with partial dominance effects might be involved in an expression of the traits under question.

The amount of dominance variance varied among traits. It is not surprising because the variance depends largely on gene frequencies at loci concerned and changes during selection. However, the degree of

dominance relationships in selected lines did not greatly affect the size of dominance genetic variances. The dominance might affect the expression of all body measurements in this study, and PH, MLA, fat thickness (ABF, AGF) and KFW in carcass traits. In addition, NVT was also affected by dominance and therefore back loin length (BLI, BLII), PS and BL might be affected. It needs further investigation of the reason why the dominance effects could not be detected for the number of weaned piglet (NW) and carcass length (CL) although the number of piglet born in total (NP) and body length (BL) were affected. It appears necessary to consider the dominance effects in genetic evaluation of the selected lines.

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