



## Sire-maternal Grand sire Model and Sire Model in Estimation of Genetic Parameters for Average Daily Gain and Carcass Traits of Japanese Black Cattle

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**ABSTRACT :** The objectives of this study were to estimate genetic parameters and sire breeding values for average daily gain (ADG) and carcass traits using sire-maternal grandsire model with REML approach, sire model with REML approach, sire model without relationships among sires and with REML and ANOVA approach, and to investigate advantages and disadvantages of these methods. Data were collected from 42,325 Japanese Black steers and heifers finished and slaughtered from 1991 to 2004. Traits analyzed in this study were average daily gain (ADG) during the fattening period, live weight at slaughter (LW), cold carcass weight (CW), estimated lean yield percentage (LYE), longissimus muscle area (LMA), subcutaneous fat thickness (SFT), rib thickness (RT), and marbling score (BMS). Bivariate analyses were also performed to obtain genetic and phenotypic correlation coefficients among traits. Estimated breeding values were obtained from each model, and simple and rank correlations among breeding values from each model were calculated. Estimates of heritability using the four models ranged from 0.25 to 0.31 in ADG, from 0.21 to 0.24 in LW, from 0.23 to 0.27 in CW, from 0.10 to 0.17 in DP, from 0.40 to 0.42 in LYE, from 0.19 to 0.31 in LMA, from 0.31 to 0.34 in SFT, from 0.26 to 0.33 in RT, and from 0.18 to 0.44 in BMS. The differences in heritability estimates using the four models seemed to be feasible in ADG, CW, DP, LMA, RT, and BMS. Genetic correlation coefficients of ADG with CW, SFT, RT and BMS were moderate to high and positive while the genetic correlation coefficients between ADG and LYE was low and negative. Correlation coefficients of BMS with SFT were negligible for both genetic and phenotypic correlations. The correlations of estimates evaluated from sire models with those from sire-maternal grandsire model were not large enough to convincing that breeding values using a sire model were corresponding to those using a sire-maternal grand sire model. If information of maternal grand sires are not available, the sire model with incomplete pedigree information included only sire of sire (Model 2) is optimal among the sire models evaluated in this study. (**Key Words :** Sire-maternal Grand Sire Model, Sire Model, Heritability, Japanese Black Cattle)

### INTRODUCTION

Japanese black cattle, a major beef breed in Japan, have been famous for its high meat quality with high marbling. Recently, they have been utilized as genetic sources for improving meat quality even outside of Japan such as USA, Australia and Canada (Barker et al., 1995; Mir et al., 1999; Pitchford et al., 2002). Although the Japanese black cattle is a local breed, they are genetically quite heterogeneous. They could be divided into sub populations on a prefecture

basis, and the genetics of each subpopulation depends on which European breed used in the early stage of breed formation and on breeding program adopted by each prefecture (Sasaki, 1992). The subpopulations have been reported to have various migration rates (Honda et al., 2002) and heritabilities (Sasaki et al., 2006). After the liberalization of beef import restriction in 1991, emphasis on high-quality beef production for domestic consumption was the reason for intensive use of limited sires with a genetic merit of high marbling over the Japan. This might lead to reduction of the effective population size, increase of the inbreeding coefficient, and decline of the genetic diversity (Nomura et al., 2001; Honda et al., 2002). Therefore, genetic parameters could be correspondingly changed, and there have been a need to assess them more accurately.

Currently, animal models with restricted maximum

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**Table 1.** Descriptive statistics for traits and covariates

Variable	n	Mean	SD	CV	Min.	Max.
AS (d)	42325	889.4	50.4	57.7	470	1,255
ADG (kg/d)	42291	0.65	0.11	17.3	0.10	1.20
LW (kg)	42274	669.9	71.7	10.7	370	965
CW (kg)	42295	415.0	50.2	12.1	168.8	635.4
DP (%)	42054	61.99	2.17	3.50	47.8	75.7
LVE	42323	72.78	1.35	1.9	66.70	78.80
LMA (cm <sup>2</sup> ) <sup>a</sup>	42322	49.17	6.93	14.1	19.0	83.0
SFT (cm <sup>2</sup> ) <sup>a</sup>	42324	3.05	0.89	29.0	0.10	7.40
RT (cm) <sup>a</sup>	42320	7.37	0.85	11.5	3.20	11.50
BMS <sup>ab</sup>	42319	5.41	1.90	35.1	1	12

<sup>a</sup> Measured at sixth-seventh rib section.

<sup>b</sup> Beef marbling standard classes (scored on a scale 1 (poor) to 12 (best)).

AS: age at slaughter, ADG: average daily gain during the feedlot period.

LW: live weight at slaughter, CW: cold carcass weight, LVE: estimated lean yield percentage.

LMA: longissimus muscle area, SFT: subcutaneous fat thickness, RT: rib thickness, BMS: marbling score.

likelihood (REML) method are favored for breeding value evaluation and genetic parameter estimation by animal breeders because of its relative insensitivity to unbalance designs in data set and usefulness for reducing the biases from selection in populations with known pedigrees (Banik and Gandhi, 2006). The method is, however, hardly applied for genetic parameter estimation in some situations when the average number of breeding cows per farm is small and the percentage of artificial insemination (AI) for reproduction is high (Kim and Lee, 2000; Sasaki, 2001). In Japan, the farmers with small herd size tend to have less interest in keeping the pedigree information of breeding cows. That is one of the reasons for the deficiency of pedigree information from maternal side. Furthermore, although farmers have kept the pedigree of cows, pedigree information gathered from small individual farms are hard to be standardized. Therefore, a large number of Japanese black cattle often require genetic evaluations using paternal pedigree.

The objectives of this study were to estimate genetic parameters and sire breeding values for average daily gain (ADG) and carcass traits using sire-maternal grandsire model with REML approach, sire model with REML approach, sire model without relationships among sires and with REML and ANOVA approach, and to investigate advantages and disadvantages of these methods.

## MATERIALS AND METHODS

Data were collected from 42,325 Japanese Black steers and heifers finished and slaughtered from 1991 to 2004. Data with less than 5 records per sire were not incorporated in the analyses. Traits analyzed in this study were average daily gain (ADG) during the fattening period, live weight at slaughter (LW), cold carcass weight (CW), estimated lean yield percentage (LVE), longissimus muscle area (LMA), subcutaneous fat thickness (SFT), rib thickness (RT), and

marbling score (BMS). The LMA, SFT and BMS were measured at the sixth-seventh rib section. The RT was defined as the distance between latissimus muscle and pleura membrane and measured at the mid-point of seventh rib. The BMS was classified based on the Beef Marbling Standards with scores 1 (poor) to 12 (best). The LVE for a carcass was calculated by the following equation first, and an extra value for a beef breed, 2.049, was added finally (JMGA, 1988).

$$\text{LVE (\%)} = 69.419 + (0.130 \times \text{LMA}) + (0.667 \times \text{RT}) - (0.025 \times \text{LSCW}) - (0.896 \times \text{SFT})$$

Where LSCW is a cold left-side carcass weight.

The four analytical models were utilized for estimation of heritability and sire breeding values for each trait. The first model (Model 1) was a sire-maternal grandsire model with pedigree information. The second model (Model 2) was a sire model with incomplete pedigree information included only sire of sire. The third model (Model 3) was a sire model ignoring relationships among sires. Here, sires were assumed to be unrelated. The fourth model (Model 4) was a paternal half-sib model. The fixed effects in the four models included year-month of slaughter (166 levels), slaughter house (9 levels), farm (111 levels), and sex of animal (2 levels, steer and heifer), and age at slaughter was fitted as linear and quadratic covariates in the models. Sire, maternal grand sire, and residual effects were fitted as random effects in the Model 1, and sire effect and residuals were fitted in the Model 2, 3, and 4 as random effects. Variance components on Model 1, Model 2, and Model 3 were estimated by single-trait analyses with derivative-free REML using MTDFREML programs of Boldman et al. (1995). The program was run with a convergence criterion of simplex variance less than  $10^{-10}$ . Variance components on Model 4 were estimated by an analysis of variance (ANOVA) treating random effects as fixed but their

**Table 2.** Frequency of progeny per sire

No. of progeny per sire	No. of sires	Total no. of records
5-10	46	337
11-50	54	1,246
51-100	18	1,273
101-200	13	1,837
201-500	15	3,842
501-1000	8	5,611
>1,000	13	28,179
Total	167	42,325

expectations as random, using the GLM procedure in SAS (SAS Institute, Inc. 1985). Direct genetic variances were obtained by four times sire variance estimated for each model and the corresponding heritabilities were calculated. Bivariate analyses with the Model 2 were also performed to obtain genetic and phenotypic correlation coefficients among traits. Estimated breeding values were obtained from each model, and simple and rank correlations among breeding values from each model were computed by CORR procedure (SAS Institute, Inc. 1985).

## RESULTS AND DISCUSSION

### Summary of phenotypes

Mean, SD, coefficient of variation, minimum, and maximum for each variable utilized in this study were calculated in Table 1. A wide range of slaughter age (785 d) was observed. The mean values of CW, LMA, RT, SFT and LYE were corresponded to those reported by Mukai et al. (1995) for Japanese black cattle data collected from 1988 to 1993 in Kagoshima prefecture. The mean of BMS was smaller than that expected. Generally, carcasses of Japanese black cattle have been graded around 6 to 7 on the 12-grade system, finished for long period, and slaughtered at older age, more than 30 month of age (Sasaki, 2001).

The distribution for the number of sires within varying progeny class sizes is presented in Table 2. Out of the evaluated 167 sires, 100 sires had fifty and below progeny records, and 13 sires had more than 1,000 progeny records. The average number of progeny records per sire was 253. The sum of the progeny records from the sires having more than 1,000 progeny records was 28,179, which was about 66% of the total 42,325 records. This showed that a small number of sires had great impact on the herd performance.

### Estimates of genetic parameters

Estimates of heritability using the four models ranged from 0.25 to 0.31 in ADG, from 0.21 to 0.24 in LW, from 0.23 to 0.27 in CW, from 0.10 to 0.17 in DP, from 0.40 to 0.42 in LYE, from 0.19 to 0.31 in LMA, from 0.31 to 0.34 in SFT, from 0.26 to 0.33 in RT, and from 0.18 to 0.44 in BMS (Table 3). The heritability estimates for LYE were

**Table 3.** Estimates of heritability by each model

Traits	Model 1	Model 2	Model 3	Model 4
ADG	0.27	0.31	0.25	0.26
LW	0.23	0.24	0.21	0.23
CW	0.26	0.27	0.23	0.26
DP	0.17	0.16	0.15	0.10
LYE	0.42	0.40	0.41	0.41
LMA	0.31	0.29	0.28	0.19
SFT	0.34	0.33	0.31	0.34
RT	0.26	0.33	0.28	0.26
BMS	0.44	0.40	0.37	0.18

ADG: average daily gain during the feedlot period, LW: live weight at slaughter, CW: cold carcass weight, LYE: estimated lean yield percentage, LMA: longissimus muscle area, SFT: subcutaneous fat thickness, RT: rib thickness, BMS: marbling score.

larger than those for its component traits (CW, LMA, SFT, and RT) regardless of the models. Heritability estimates for DP were tending to be smaller than those for other traits. Heritabilities for carcass traits estimated in the current study ranged from moderate to large, which concurred with the findings from previous studies (Wilson et al., 1993; Koots et al., 1994a; Marshall 1994; Mukai et al., 1995; Hirooka et al., 1996; Pariacote et al., 1998; Crews and Kemp, 1999; Crews and Kemp, 2001; Kemp et al., 2002; Riley et al., 2002; Crews et al., 2004; Koch et al., 2004; Nephawe et al., 2004; Rios-Utrera et al., 2005; Ibi et al., 2005; Sasaki et al., 2006). On the other hand, the heritability estimates for DP were smaller than those reported in most studies where estimates ranged from 0.20 to 0.77 (Veseth et al., 1993; Koots et al., 1994a; Aass, 1996; Wulf et al., 1996; Pariacote et al., 1998; Engelland et al., 1999; Riley et al., 2002; Rios-Utrera et al., 2005; Oikawa et al., 2006). Only Reynolds et al. (1991) reported a negligible heritability (0.01) from non-selected Hereford bull data. The large variation of heritability estimates for DP might be due to differences in management of animals before slaughter and dressing procedures. If the injured parts of carcasses by traumatic events were discarded and only the saleable parts of carcasses were used to calculate dressing percentage, then environmental variance for DP might be inflated, and its heritability could be correspondingly decreased.

### Discrepancy among genetic parameter estimates with four models

The differences in heritability estimates using the four models seemed to be feasible in ADG, CW, DP, LMA, RT, and BMS. Heritability estimate from model 2 was larger than those from models 1, 3, and 4 in ADG. The estimate from model 3 was slightly smaller than those from models 1, 2, and model 4 in CW. The heritability estimate for BMS using model 1 was larger than those using models 2, 3, and 4. Generally, heritability estimated by paternal half-sib analysis with ANOVA method (model 4) tends to be smaller than those with REML method (Models 1, 2 and 3) in DP.

**Table 4.** Estimates of genetic( $r_g$ ) and phenotypic( $r_p$ ) correlations among traits for model 2

Traits	Correlation	Traits							
		LW	CW	DP	LYE	LMA	SFT	RT	BMS
ADG	$r_g$	0.92	0.92	0.53	-0.10	0.11	0.28	0.67	0.37
	$r_p$	0.86	0.79	0.17	-0.02	0.37	0.23	0.48	0.13
LW	$r_g$	-	0.97	0.45	-0.14	0.10	0.26	0.64	0.31
	$r_p$	-	0.92	0.17	-0.04	0.39	0.29	0.52	0.12
CW	$r_g$	-	-	0.69	-0.17	0.06	0.31	0.68	0.34
	$r_p$	-	-	0.49	-0.07	0.40	0.32	0.56	0.14
DP	$r_g$	-	-	-	-0.19	0.07	0.26	0.49	0.25
	$r_p$	-	-	-	-0.10	0.16	-0.77	0.32	0.10
LYE	$r_g$	-	-	-	-	0.79	-0.69	0.25	0.20
	$r_p$	-	-	-	-	0.68	-0.32	0.27	0.27
LMA	$r_g$	-	-	-	-	-	-0.09	0.27	0.20
	$r_p$	-	-	-	-	-	-	0.30	0.28
SFT	$r_g$	-	-	-	-	-	-	0.10	0.01
	$r_p$	-	-	-	-	-	-	0.19	-0.04
RT	$r_g$	-	-	-	-	-	-	-	0.42
	$r_p$	-	-	-	-	-	-	-	0.28

ADG: average daily gain during the feedlot period, LW: live weight at slaughter, CW: cold carcass weight, LYE: estimated lean yield percentage, LMA: longissimus muscle area, SFT: subcutaneous fat thickness, RT: rib thickness.

LMA, and BMS.

In the analyses using model 3 (REML) and model 4 (ANOVA), pedigree information was not used. Estimates of heritability using model 3 were larger than that using model 4 in DP, LMA, and BMS while the differences were not considerably large in the other traits. Using either model 3 or model 4 may generate bias caused by ignoring the genetic relationship among animals. In addition, model 4 is not a preferable method for variance component estimation with unbalanced data (Searle, 1989). Aass (1996) reported that, in Norwegian dual-purpose cattle, heritability estimates for ADG during performance test were 0.35 by ANOVA method and 0.30 by REML method, and the estimates for DP were 0.32 by ANOVA and 0.23 by REML. The heritability estimates of ADG, LW, CW, DP, and LMA using model 4 (paternal half-sib analysis) in the current study were mostly smaller than those estimated using the paternal half-sib analysis of Veseth et al. (1993).

The comparison between model 2 and model 3 revealed that heritability estimates from model 2 were larger than those from model 3 in ADG, RT and BMS. This could be due to the failure to account for relationship among sires. This concurred with the finding from Ferreira et al. (1999) where reduced heritability estimate was obtained for 205-day weight using the sire model without genetic relationship.

Compared with model 2, model 1 showed that heritability estimates were increased in BMS and decreased in ADG and RT. They were comparable to the estimates previously reported for Japanese black cattle. Heritability estimates reported by Mukai et al. (1995) for Japanese black cattle in Kagoshima were 0.39 for CW, 0.47 for LMA, 0.41 for RT, 0.55 for SFT, 0.53 for LYE, and 0.52 for BMS using sire-maternal grandsire model. Ibi et al. (2005) reported that

heritabilities estimated by animal model for Japanese black cattle data collected from 1997 to 2002 in Kyushu region were 0.41 for CW, 0.32 for LMA, 0.28 for RT, 0.41 for SFT, and 0.44 for BMS and Oikawa et al. (2006) reported heritability estimates of 0.40 for LMA, 0.52 for BMS, and 0.31 for SFT on the performance and progeny test data collected from 1978 to 2000 for Japanese Black cattle. Heritability estimates using model 1 in the present study were smaller than those estimated by Mukai et al. (1995). One of the possible reasons for the smaller estimates in the present study was an intensive use of a small number of elite sires to calf production. This may reduce the effective population size, increase the chance of inbreeding, and consequently decrease the genetic diversity in Japanese black cattle herd. Nomura et al. (2001) showed that the effective size of the Japanese black cattle population sharply decreased after 1991 because of the intensive use of a few prominent sires with high marbling for the liberalization of beef import restrictions in Japan. The small effective population size might be the reason for the reduction of genetic gain due to decreased genetic diversity and the inbreeding depression of economically important traits (Nomura et al., 2001; Honda et al., 2004).

#### Analysis of multiple traits

Genetic correlation coefficients of ADG with CW, SFT, RT and BMS were moderate to high and positive while the genetic correlation coefficients between ADG and LYE was low and negative (Table 4). The large positive genetic correlation coefficients among ADG, LW, and CW were concurred with the findings from previous studies. Reynolds et al. (1991) reported genetic correlation of 0.97 between LW and CW in Herefords bulls. In Riley et al. (2002), genetic correlation coefficients were 0.98 between

**Table 5.** Pearson(P) and Spearman(S) correlation coefficients among estimates of sire breeding values(BV) from various models

Traits	Correlation	BV1:BV2	BV1:BV3	BV1:BV4	BV2:BV3	BV2:BV4	BV3:BV4
ADG	P	0.95	0.95	0.88	0.99	0.92	0.91
	S	0.95	0.95	0.92	0.99	0.96	0.96
LW	P	0.96	0.95	0.85	0.99	0.89	0.87
	S	0.96	0.95	0.92	0.98	0.95	0.96
CW	P	0.97	0.95	0.87	0.99	0.90	0.89
	S	0.97	0.95	0.93	0.98	0.96	0.97
DP	P	0.97	0.95	0.82	0.97	0.82	0.85
	S	0.96	0.93	0.90	0.94	0.90	0.95
LYE	P	0.97	0.96	0.92	0.99	0.95	0.95
	S	0.97	0.96	0.94	0.99	0.97	0.97
LMA	P	0.98	0.96	0.90	0.98	0.91	0.91
	S	0.97	0.95	0.93	0.98	0.95	0.97
SFT	P	0.96	0.95	0.90	0.99	0.92	0.93
	S	0.97	0.96	0.93	0.99	0.96	0.97
RT	P	0.91	0.84	0.84	0.90	0.92	0.80
	S	0.89	0.78	0.85	0.85	0.97	0.83
BMS	P	0.96	0.96	0.92	1.00	0.94	0.95
	S	0.94	0.94	0.93	0.99	0.96	0.97

BV1, BV2, BV3 and BV4; sire breeding values and ranks evaluated from model 1, model 2, model 3 and model 4, respectively.

ADG: average daily gain during the feedlot period, LW: live weight at slaughter, CW: cold carcass weight, LYE: estimated lean yield percentage.

LMA: longissimus muscle area, SFT: subcutaneous fat thickness, RT: rib thickness, BMS: marbling score.

ADG and LW, 0.84 between ADG and CW, and 0.90 between LW and CW. Veseth et al. (1993) reported that genetic correlation coefficients among ADG, LW, and CW were all close to 1 in the Brahman young bull data. While Eriksson et al. (2003) showed that genetic correlation coefficients between post weaning daily gain and CW were 0.56 in Charolais breed, 0.76 in Hereford breed, and 0.86 in Simmental breed.

The estimates of genetic and phenotypic correlation coefficients were comparable to the estimates reported previously. Hirooka et al. (1996) reported that genetic correlation of ADG during fattening period with CW, LMA, SFT, RT, and BMS were 0.85, 0.24, 0.31, 0.48, and 0.11, respectively, in Japanese Brown cattle. Koots (1994b) reported that genetic correlation estimates for post weaning gain (PWG) with SFT, LYE, CW, DP, BMS, LW, and LMA were 0.19, 0.18, 0.87, 0.16, 0.11, 0.87, and 0.32 and phenotypic correlation estimates were 0.18, 0.16, 0.68, 0.01, 0.13, 0.75, and 0.28. These results suggested that single trait selection for growth rate would lead to production of heavier carcass with favorable marbling and slightly increased SFT. However, Oikawa et al. (2006) showed negative genetic correlation of average daily gain during progeny test with SFT in Japanese Black cattle.

Genetic correlation coefficient estimate between ADG and DP was 0.53. This concurred with the result from Engelland et al. (1999) where 0.52 of genetic correlation coefficient was estimated between the traits in German Gelbvieh bull data, but not with the finding from Aass (1996) where no genetic relationship was observed between the traits.

Genetic correlation coefficient of LMA with SFT was

-0.32. Moderately negative genetic correlation coefficients were reported by Kemp et al. (2002) for Angus steers, Mukai et al. (1995) for Japanese Black cattle, Koch et al. (2004) for Hereford breed, Pariacote et al. (1998) for American Shorthorn beef cattle, Rios-Utrera et al. (2005) for the steers produced from European beef breeds. Low negative or positive genetic correlations were reported by Hirooka et al. (1996) for Japanese Brown cattle, Koots et al. (1994b) for literature reviews, Riley et al. (2002) for Brahman cattle, Robinson and Oddy (2004) for feedlot finished cattle in Australia, and Rachman et al. (2000) for Japanese brown cattle. On the other hand, moderately positive genetic correlation coefficients were reported by Baik et al. (2002) for Korean cattle ( $r = 0.38$ ) and by Oikawa et al. (2006) for Japanese Black cattle ( $r = 0.40$ ).

Genetic correlation coefficients of LMA with BMS were 0.20. The positive estimate was agreed with 0.12 of genetic correlation reported by Oikawa et al. (2006), with 0.38 reported by Rachman et al. (2000) for Japanese brown cattle and with 0.44 reported by Riley et al. (2002) for Brahman. However, Kemp et al. (2002), Koch et al. (2004), Koots et al. (2004b), Reverter et al. (2000), and Pariacote et al. (1998) reported low to moderate negative genetic correlation coefficients.

Correlation coefficients of BMS with SFT were negligible for both genetic and phenotypic correlations. Negative or close to zero genetic correlation coefficients were reported by Wilson et al. (1993, -0.13), Hirooka et al. (1996, -0.12), Mukai et al. (1995, -0.04), Pariacote et al. (1998, -0.31) and Oikawa et al. (2006, -0.20). These results implied that single trait selection for high marbling could be effective without side effects of increased SFT. Yet, many

reports showed moderately positive genetic correlations of marbling and intramuscular fat percentage with subcutaneous fat thickness (Reverter et al., 2000; Kemp et al., 2002; Riley et al., 2002; Koch et al., 2004; Koots et al., 2004b; Robinson and Oddy, 2004; Rios-Utrera et al., 2005).

Phenotypic correlation of LYE with its component traits, CW, LMA, SFT and RT, were -0.07, 0.68, -0.69, and 0.27, respectively. The LYE was correlated more strongly with LMA and SFT than with CW and RT. Phenotypic correlation coefficients of CW with LMA, SFT and RT were 0.39, 0.26, and 0.52. These positive correlation coefficients suggested that heavier carcasses tended to have larger LMA, SFT, and RT at 6 to 7th rib section. Similar estimates of positive phenotypic correlation of CW with LMA and SFT were reported by Wilson et al. (1993), Hirooka et al. (1996), Mukai et al. (1995), Koch et al. (2004), and Riley et al. (2002). Comparatively large and positive phenotypic correlation estimate between CW and RT (0.60) was, however, obtained by Hirooka et al. (1996) for Japanese brown cattle.

Simple (Pearson) and rank (Spearman) correlation coefficients for estimates of breeding values for sires among the four models were estimated in Table 5. The correlation estimates obtained using sire models (Models 2, 3, and 4) and sire-maternal grandsire model (Model 1) were not large enough to convince the similarity in breeding values obtained by the sire and sire-maternal grand sire models.

Of the simple and rank correlations between estimates using sire models and sire-maternal grandsire model, the correlation estimates were relatively large between model 1 and model 2. The simple correlation coefficients ranged 0.91 to 0.98 and rank correlation coefficients ranged 0.89 to 0.97. The simple and rank correlation coefficients for RT were smaller than those for other traits. The small correlation estimates for RT indicated that discrepancy between breeding values estimated with the different sire models would not be ignored.

The correlation estimates using model 2 and model 3 showed close to unity in ADG, LYE, SFT, and BMS while rank correlation for RT and simple and rank correlations for RT and BMS were relatively small. The correlation coefficients between model 1 and model 3 were larger than those between model 1 and model 4.

## CONCLUSION

Generally, the sire-maternal grandsire models are preferred to the sire model because relationships on the maternal side can be partly utilized (Parkkonen et al., 2000). Statistically, 6.25% of genetic variance was additionally explained with the sire-maternal grandsire model. If information of maternal grandsires is not available, the

model 2 is optimal among the sire models evaluated in this study.

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