

## Genetic Parameters for Traits in Performance and Progeny Tests and Their Genetic Relationships in Japanese Black Cattle

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**ABSTRACT :** Genetic parameters for performance traits on 409 bulls and growth and carcass traits on 591 of their steer progeny were estimated in Japanese Black cattle with Gibbs sampling. Traits of bulls included body weight at the start (BWS) and finish (BWF) of test, daily gain (DG), concentrate, roughage and TDN intake, and TDN conversion ratio. Progeny traits were BWS, BWF, DG, rib eye area, marbling score (MSR), dressing percentage and subcutaneous fat thickness (SFT). In bulls, heritabilities were high for BWS (0.50) and BWF (0.63) and moderate for concentrate (0.48) and TDN intake (0.45), while in progeny, the heritability for all the studied traits was moderate to high (ranging from 0.30 to 0.73), highlighting the potential for genetic improvement of these traits. Genetic correlations between TDN intake and growth traits (BWS, BWF and DG) in bulls were highly positive (ranging from 0.77 to 0.94). The weak but negative genetic correlation (-0.20) between MSR and SFT in progeny indicated that improvement of beef marbling without increasing subcutaneous fat deposition could be possible. The estimated genetic correlations of roughage intake of bulls with body weights (BWS and BWF) and MSR of their progeny were moderate (ranging from 0.35 to 0.52). On the basis of the selection for bulls, growth traits and TDN intake correlated positively with SFT (ranging from 0.43 to 0.53) of their progeny, suggesting the necessity of controlling the increase of SFT in selection programs. (*Asian-Aust. J. Anim. Sci.* 2006. Vol 19, No. 5 : 611-616)

**Key Words :** Beef Cattle, Carcass Quality, Genetic Parameters, Performance Test

### INTRODUCTION

A two-stage selection using performance tests jointly with progeny tests has been established for the genetic improvement of Japanese Black cattle in Japan since 1972. A sire evaluation program was implemented in Miyagi prefecture for the improvement of Japanese Black cattle in 1979. Bulls with a satisfactory outcome in the performance test later have been progeny-tested to improve carcass characteristics. The joint analysis of carcass traits of progeny and performance traits of bulls could minimize selection bias by using animal models jointly with relationship matrix including pedigree animals (Kennedy et al., 1988). Such joint evaluation could also potentially improve the efficiency of the genetic evaluation of bulls by increasing the number of records, minimizing the effect of bias attributed to a common environment on their progeny and including carcass traits. Thus genetic parameters among tested traits are prerequisite for the genetic evaluation of bulls by joint analysis of performance test records and their progeny carcass records.

Growth is one of the most economically important quantitative traits that affect carcass quality in beef cattle (Chung and Kim, 2005). Several studies have demonstrated moderate to high heritabilities for different carcass traits and a wide range of inter-trait correlations (Mohiuddin,

1993; Marshall, 1994), while fewer studies have been made on the relationships between performance traits of bulls and growth and carcass traits of their progeny (Hoque et al., 2005b). Although the relation between the feed efficiency traits of bulls and carcass traits of their progeny have been estimated by Hoque et al. (2005b), it is necessary to estimate the relationships between growth traits of bulls and carcass traits of their progeny to provide the genetic structure for these traits recorded by two testing programs. Uchida et al. (2001) estimated the genetic parameters for performance traits of bulls and carcass traits of their progeny. However, they did not find out the relationship between performance traits of bulls and carcass traits of progeny, and the present study was mainly focused on this area with the aim of estimating genetic parameters for the performance traits of bulls and carcass traits of their progeny.

### MATERIALS AND METHODS

#### Source of data

The performance test for bulls and the progeny test for their steer progeny were carried out on Japanese Black cattle at the test station of Miyagi Prefecture, Japan. The data set contains records of tests covering the period from 1978 to 2000. The pedigrees of the recorded bulls were traced back to three generations and, including the tested animals, totaled 4,272. Bulls selected on the outcome of performance test were test-mated with commercial cows to produce steer progeny for progeny test. The data structure is presented in Table 1.

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**Table 1.** Description of data structures

Data sets	Traits	Animals	Sires	Years	Cohort
Performance test	7	409	23	22 (1978-1999)	91
Progeny test	7	591	62	18 (1983-2000)	62

### Performance test for bulls

The bull calves, collected from cooperative farms, were within the age limit of 7 to 8 months and body weight of 200-300 kg. Each year, 20-30 bull calves were selected on the basis of heavier body weight for performance test from approximately 200 bulls. After three weeks of being introduced to the feed, the animals were entered into the testing program for the test period of 112 days. The animals were given access to roughage (green forage, silage or hay) and water *ad libitum*; however, feeding of concentrate was restricted to 1 h twice a day during the test period. The concentrate consisted of 20 parts ground barley, 35 parts ground yellow corn, 20 parts wheat bran, 17 parts defatted rice bran, 6 parts soybean meal, 1 part NaCl and 1 part calcium carbonate with 15.5% DCP and 73% TDN. The cohort was a group of animals of the same age maintained under a uniform environment during the test period. The traits studied included body weight at the start of the test (BWS), body weight at the finish (BWF), average daily gain (DG), concentrate intake (CON), roughage intake (ROU), total digestible nutrient (TDN) intake (TIT), and TDN conversion (TCV) expressed as TDN consumption (kg) per weight gain (kg). Values of the mean, standard deviation (SD) and coefficient of variation (CV) for the traits are presented in Table 2 together with age at the start of the test (AGS).

### Progeny test for steers

From 20 to 30 bulls tested in performance test, 3 to 4 bulls were selected for progeny test each year. The first selection was primarily based on the growth performance of the bulls at performance test. Steer calves (eight to 10 animals) sired by the same bulls (selected) at cooperative farms were transferred to the test station at 7 to 8 months of

age and housed together in a feedlot (45 to 50 m<sup>2</sup>) with an adjacent paddock (36-40 m<sup>2</sup>) for exercise. Three weeks after being introduced to the new environment, the animals were entered into the testing program. Over the test period of 364 days, the animals were given access to the concentrate mixed with chopped rice straw (10% by weight), and *ad libitum* water. Thus cohort in station progeny test was a group of half-sibs of almost same age and managed them in the same feedlot. The traits studied were BWS, BWF, DG, rib eye area (REA), marbling score (MSR), dressing percentage (DRS) and subcutaneous fat thickness (SFT). The REA, MSR and SFT were measured at the 6<sup>th</sup> to 7<sup>th</sup> rib section by grid approximation as described (Oikawa et al., 2000). The MSR was measured according to the Beef Marbling Standard (JMGA, 1988) of 12 categories, with the numeral 5.0 being the highest (0.0 to 3.0 with increments of 0.33, and 4.0, 5.0). The weight of the carcass was determined by weighing the carcass of slaughtered steers after removing the skin, lungs, heart, liver, intestine, ancillary organs, bladder, reproductive organs and blood. The DRS was calculated as the weight of the carcass divided by the live weight at slaughter.

### Statistical analysis

The (co)variance components and heritabilities were estimated by the Gibbs sampling method with the variance component estimation computer program (Neumaier and Groeneveld, 1998). The sample size and burning period of Gibbs sampling were twenty thousands and one hundred, respectively. Only effects which were found to be significant by analysis of variance (ANOVA) were included in the model. ANOVA were made by General Linear Model procedure of Statistical Analysis System (SAS, 1994). Significant fixed effects and covariates were a cohort and AGS or age at finish (AGF). The fixed effect of dam at calving was excluded from the model because of statistical insignificance.

As the pooled data set tends to have a weak connectedness between the records of performance and progeny test, and a bias attributed to the selection at performance test is expected in the records of progeny test,

**Table 2.** Means, standard deviations (SD) and coefficient of variations (CV) for traits of the performance and the progeny test

Trait <sup>1</sup>	AGS (day)	BWS (kg)	BWF (kg)	DG (kg)	CON (kg)	ROU (kg)	TIT (kg)	TCV	REA (cm <sup>2</sup> )	MSR	DRS (%)	SFT (mm)
Performance test												
Mean	231.4	260.8	392.0	1.17	618.7	323.2	606.5	4.69	-	-	-	-
SD	18.5	32.7	39.4	0.16	79.7	49.3	60.6	0.62	-	-	-	-
CV	8.0	12.5	10.1	13.7	12.9	15.3	10.0	13.2	-	-	-	-
Progeny test												
Mean	264.9	256.2	547.8	0.80	-	-	-	-	48.0	2.9	58.4	17.1
SD	17.3	30.4	52.2	0.10	-	-	-	-	6.1	0.9	2.5	5.5
CV	6.5	11.9	9.5	12.5	-	-	-	-	12.7	31.0	4.3	32.2

<sup>1</sup> AGS and BWS, age and body weight at the start of the test, respectively; BWF, body weight at finish; DG, daily gain; CON, concentrate intake; ROU, roughage intake; TIT, total digestible nutrient intake; TCV, total digestible nutrient conversion; REA, rib eye area; MSR, marbling score; DRS, dressing percentage; SFT, subcutaneous fat thickness.

**Table 3.** Estimates of heritabilities ( $h^2$ ) (on the diagonal), genetic correlations ( $\pm$ SE) (above the diagonal) and phenotypic correlations (below the diagonal) among traits of bulls at performance test

Trait <sup>1</sup>	BWS	BWF	DG	CON	ROU	TIT	TCV
BWS	0.50 $\pm$ 0.13	0.97 $\pm$ 0.02	0.76 $\pm$ 0.12	0.75 $\pm$ 0.10	0.72 $\pm$ 0.14	0.77 $\pm$ 0.10	-0.35 $\pm$ 0.42
BWF	0.87	0.63 $\pm$ 0.12	0.87 $\pm$ 0.05	0.78 $\pm$ 0.10	0.71 $\pm$ 0.15	0.81 $\pm$ 0.11	-0.22 $\pm$ 0.40
DG	0.11	0.59	0.23 $\pm$ 0.06	0.93 $\pm$ 0.04	0.63 $\pm$ 0.18	0.94 $\pm$ 0.03	-0.25 $\pm$ 0.30
CON	0.01	0.58	0.65	0.48 $\pm$ 0.10	0.41 $\pm$ 0.21	0.98 $\pm$ 0.01	0.42 $\pm$ 0.32
ROU	0.24	0.37	0.33	0.29	0.21 $\pm$ 0.08	0.68 $\pm$ 0.14	0.05 $\pm$ 0.42
TIT	0.34	0.59	0.63	0.92	0.50	0.45 $\pm$ 0.11	-0.10 $\pm$ 0.61
TCV	0.14	-0.28	-0.80	-0.06	-0.06	-0.04	0.06 $\pm$ 0.02

<sup>1</sup> BWS, body weight at the start of the test; BWF, body weight at finish; DG, daily gain; CON, concentrate intake; ROU, roughage intake; TIT, total digestible nutrient intake; TCV, total digestible nutrient conversion.

we sought a common trait among DG, BWS and BWF before analyzing the pooled data set. According to preliminary results, heritabilities for DG in performance and progeny test were 0.33 $\pm$ 0.06 and 0.44 $\pm$ 0.17, respectively, with a genetic correlation of 0.89 $\pm$ 0.05. The corresponding values were 0.32 $\pm$ 0.16 and 0.59 $\pm$ 0.12 with 0.54 $\pm$ 0.11 for BWS, and 0.41 $\pm$ 0.16 and 0.40 $\pm$ 0.07 with 0.64 $\pm$ 0.06 for BWF. Since the estimate of genetic correlation was close to unity for DG, the DG of both tests was included as a common trait.

The statistical model used in the analysis was as follows:

$$Y_{ij} = F_{ij} + a_{ij} + e_{ij}$$

with  $F_{ij} = CH_i + b(AGF_{ij} - \overline{AGF})$  for BWF, DG, CON, ROU, TIT, TCV, REA, MSR, DRS, SFT or

$$F_{ij} = CH_i + b(AGS_{ij} - \overline{AGS}) \text{ for BWS}$$

where  $CH_i$  = the fixed effect of  $i$ th cohort of the test;  $b$  = the linear regression coefficient of the observation on age;  $AGX_{ij}$  = the age of  $j$ th animals in  $i$ th cohort at either the start (S as X) or the finish (F as X);  $\overline{AGX}$  = the mean age of the animals;  $Y_{ij}$  = the phenotypic value for  $j$ th animals in  $i$ th cohort;  $a_{ij}$  = the additive genetic effect for  $j$ th animals in  $i$ th cohort;  $e_{ij}$  = the random residual. The (co)variances for the traits in the performance test and the traits in the progeny test were estimated by two-trait analyses. The covariances between the traits of performance and progeny test were estimated by three-trait (pooled DG was common with one performance test trait and one progeny test traits) analyses except for correlations including DG itself. The covariance structure for additive genetic effects of animals and residual effects is described below:

$$E \begin{bmatrix} a_1 \\ a_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \quad \text{Var} \begin{bmatrix} a_1 \\ a_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a1}^2 & A\sigma_{a12} & 0 & 0 \\ A\sigma_{a2}^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_{e1}^2 & I\sigma_{e12} \\ 0 & 0 & I\sigma_{e12} & I\sigma_{e2}^2 \end{bmatrix}$$

where  $a_1$  and  $a_2$  are the vectors of additive genetic effects of animals for trait 1 and trait 2, respectively and  $e_1$  and  $e_2$  are the residual effects for them.  $A$  is the numerator relationship matrix in which diagonal elements consist of 1.0 plus coefficient of inbreeding and off-diagonal elements consist of the genetic relationships between animals. The symbols,  $\sigma_{a1}^2$  and  $\sigma_{a2}^2$  are the additive genetic variances for trait 1 and trait 2, respectively and  $\sigma_{a12}$  is the additive genetic covariance for them.  $\sigma_{e1}^2$  and  $\sigma_{e2}^2$  are the residual variances for trait 1 and trait 2, respectively and  $\sigma_{e12}$  is the residual covariance for them. This model was assumed while the two traits were recorded on the same animal. When the two traits were recorded on different animals the  $\sigma_{e12}$  was assumed to be zero. This two-trait model for variance structure can be extended for three-trait model straightforwardly, including  $a_3$  and  $e_3$  for third trait. The estimated genetic variances, heritabilities and their standard errors (SE) were the averages of the estimates.

## RESULTS AND DISCUSSION

### Genetic parameters for traits in performance test

Estimates of heritabilities and correlations (genetic and phenotypic) among different traits of bulls are presented in Table 3. The heritabilities for BWS and BWF were slightly higher than 0.38 and 0.37, respectively, (Oikawa et al., 2000) but closer to 0.54 and 0.58, respectively (Uchida et al., 2001). Weaning weight is influence by maternal effect in general (Choi et al., 2005) but the additive genetic variance of BWS seems to have little maternal effect because of early practice of weaning in this breed. The heritability for DG was close to 0.20 (Oikawa et al., 2000) and 0.15 (Uchida et al., 2001) for Japanese Black steers, and 0.22 (Hirooka et al., 1996) for Japanese Brown steers. A considerable number of heritability estimates have been published for growth and carcass traits for different breeds of beef cattle. A comprehensive review (Koots et al., 1994a) of these estimates indicates that the growth traits are all moderately heritable, and that the weighted averages of heritabilities for the traits are 0.33 for yearling body weight and 0.31 for post-weaning growth rate. Thus the

**Table 4.** Estimates of heritabilities ( $h^2 \pm \text{SE}$ ) (on the diagonal), genetic correlations ( $\pm \text{SE}$ ) (above the diagonal) and phenotypic correlations (below the diagonal) among traits of progeny at progeny test

Traits <sup>1</sup>	BWS	BWF	DG	REA	MSR	DRS	SFT
BWS	0.49 $\pm$ 0.12	0.78 $\pm$ 0.11	0.58 $\pm$ 0.14	0.41 $\pm$ 0.19	-0.13 $\pm$ 0.21	0.23 $\pm$ 0.17	0.71 $\pm$ 0.45
BWF	0.66	0.73 $\pm$ 0.09	0.87 $\pm$ 0.04	0.23 $\pm$ 0.16	-0.09 $\pm$ 0.15	0.41 $\pm$ 0.16	0.55 $\pm$ 0.19
DG	0.18	0.86	0.30 $\pm$ 0.09	0.37 $\pm$ 0.24	-0.20 $\pm$ 0.16	0.40 $\pm$ 0.24	0.49 $\pm$ 0.23
REA	0.30	0.44	0.59	0.40 $\pm$ 0.09	0.12 $\pm$ 0.30	0.46 $\pm$ 0.17	0.40 $\pm$ 0.20
MSR	0.03	0.08	-0.09	0.29	0.52 $\pm$ 0.13	-0.16 $\pm$ 0.17	-0.20 $\pm$ 0.26
DRS	0.25	0.28	0.40	0.24	0.05	0.58 $\pm$ 0.15	0.25 $\pm$ 0.29
SFT	0.19	0.30	0.32	0.17	0.04	0.28	0.31 $\pm$ 0.14

<sup>1</sup> BWS, body weight at the start of the test; BWF, body weight at finish; DG, daily gain; REA, rib eye area; MSR, marbling score; DRS, dressing percentage; SFT, subcutaneous fat thickness.

heritabilities of weight gain estimated for Japanese breeds are lower than the average of published estimates.

For the traits of feed utilization, estimated heritabilities for CON and TIT were moderate and that for ROU was low. However, a higher heritability for ROU (0.71), a lower one for CON (0.18), and a slightly lower one for TIT (0.36) than the present estimates have been reported (Oikawa et al., 2000). The present heritability for feed intake was consistent with the moderate mean value by Koots et al. (1994a) who reported the weighted means of heritabilities for feed intake and feed conversion to be 0.34 and 0.32, respectively, in their review article. Low heritability for TCV was observed in the present study, which was in agreement with the reported estimate of 0.11 by Oikawa et al. (2000). This low heritability value for TCV suggesting that inclusion of TCV in selection programs seems unlikely and an alternative approach needs to be investigated for the improvement of feed efficiency.

Genetic and phenotypic correlations among the traits of bulls were positive with the exception of those between TCV and the others. Genetic correlations between BWS and BWF and those between CON and TIT were close to unity, whereas the corresponding phenotypic correlations were highly positive but lower than unity. Genetic correlations between DG and body weights (BWS and BWF) were highly positive. The high genetic correlation between DG and BWF was expected because BWF is a trait that comprises BWS and weight gain during the fixed testing period. These genetic and phenotypic correlations between live weight and DG were comparable to those reported at 0.69 and 0.60, respectively (Arthur et al., 2001), 0.97 and 0.64 (Oikawa et al., 2000), 0.59 and 0.49 (Hoque et al., 2005a).

Genetically, high correlations were observed between TIT and bull traits other than TCV. The positive correlations between TIT and growth traits can be partly explained by the heavier animals having larger-capacity digestive organs and generally eats more; also their intake and digestibility lead to greater carbohydrate, protein and fat deposition. Arthur et al. (2001) have estimated genetic and phenotypic correlations between feed intake and live weight at 0.83 and

0.54, respectively, and between feed intake and DG at 0.39 and 0.47, respectively. Moderate to high correlations of these traits for growing bulls have been reported by Bishop (1992) and Nieuwhof et al. (1992). The genetic and phenotypic correlations between TCV and growth traits were favorably negative and consistent with the estimates by Oikawa et al. (2000).

#### Genetic parameters for traits in progeny test

The genetic parameters for the traits of progeny in progeny test (Table 4) showed a high heritability for BWF, but a moderate one for each of the other traits. The heritabilities for growth traits were close to those of bulls in performance test (Table 3). The heritabilities for BWS and BWF have been reported at 0.36 and 0.31, respectively, for the progeny of performance-tested bulls (Oikawa et al., 2000). The heritability for DG was slightly higher than that in performance test and within the range (0.23-0.46) of published results (Herd and Bishop, 2000; Oikawa et al., 2000; Arthur et al., 2001; Eriksson et al., 2003).

The heritability for REA was within the range (0.20-0.54) of previous reports for Japanese Black (Mukai et al., 1995; Oyama et al., 1996) and Western breeds (Wilson et al., 1993; Splan et al., 2002; Crews et al., 2003). The heritability for MSR was consistent with previous estimates of 0.49 (Oikawa et al., 2000) and 0.40 (Hirooka et al., 1996), and within the range of moderate to high heritabilities (average 0.35) in a review of meat quality traits (Marshall, 1994). The heritability for DRS was higher than a previous estimate of 0.15 (Oikawa et al., 2000), and that for SFT was within the range (0.26-0.68) in the literature (Wilson et al., 1993; Marshall, 1994; Hirooka et al., 1996; Crews et al., 2003). A review by Koots et al. (1994a) of these traits indicates that carcass traits are all moderately heritable, with weighted averages of heritability of 0.42 for REA, 0.38 for MSR, 0.39 for DRS and 0.44 for SFT. The slight differences in these estimates may be due to variation among different populations.

The genetic correlations of growth traits with SFT were positive, whereas those of MSR with growth traits, DRS and SFT were negative and low. The weak genetic

**Table 5.** Estimates of genetic correlations ( $\pm$ SE) between the traits<sup>†</sup> of bulls at the performance test and of progeny at progeny test

	Bulls						
Progeny	BWS	BWF	DG	CON	ROU	TIT	TCV
BWS	0.52 $\pm$ 0.19	0.44 $\pm$ 0.15	0.45 $\pm$ 0.24	0.35 $\pm$ 0.20	0.35 $\pm$ 0.20	0.42 $\pm$ 0.17	0.17 $\pm$ 0.21
BWF	0.34 $\pm$ 0.27	0.54 $\pm$ 0.07	0.56 $\pm$ 0.19	0.64 $\pm$ 0.24	0.54 $\pm$ 0.16	0.43 $\pm$ 0.19	0.26 $\pm$ 0.24
DG	0.47 $\pm$ 0.20	0.78 $\pm$ 0.11	0.90 $\pm$ 0.08	0.59 $\pm$ 0.22	0.67 $\pm$ 0.14	0.40 $\pm$ 0.25	0.34 $\pm$ 0.43
REA	-0.64 $\pm$ 0.21	-0.34 $\pm$ 0.28	0.07 $\pm$ 0.25	0.16 $\pm$ 0.24	-0.16 $\pm$ 0.26	0.17 $\pm$ 0.34	-0.17 $\pm$ 0.33
MSR	0.11 $\pm$ 0.28	-0.42 $\pm$ 0.30	-0.03 $\pm$ 0.33	0.02 $\pm$ 0.23	0.52 $\pm$ 0.27	-0.11 $\pm$ 0.24	-0.56 $\pm$ 0.42
DRS	0.23 $\pm$ 0.29	0.30 $\pm$ 0.24	0.04 $\pm$ 0.20	0.46 $\pm$ 0.21	0.33 $\pm$ 0.29	0.45 $\pm$ 0.22	0.33 $\pm$ 0.29
SFT	0.43 $\pm$ 0.35	0.48 $\pm$ 0.19	0.43 $\pm$ 0.24	0.33 $\pm$ 0.32	0.24 $\pm$ 0.25	0.53 $\pm$ 0.36	0.06 $\pm$ 0.42

<sup>†</sup> BWS, body weight at the start of the test; BWF, body weight at finish; DG, daily gain; CON, concentrate intake; ROU, roughage intake; TIT, total digestible nutrient intake; TCV, total digestible nutrient conversion; REA, rib eye area; MSR, marbling score; DRS, dressing percentage; SFT, subcutaneous fat thickness.

relationships between MSR and growth traits were consistent with the averages reviewed by Koots et al. (1994b). They also reported the average of genetic correlations between marbling score and back fat thickness to be positive (0.36). On the other hand, weak negative genetic correlations between MSR and SFT have been reported in Angus field data (-0.13; Wilson et al., 1993), in Japanese Brown steers (-0.12; Hirooka et al., 1996) and in Japanese Black steers (-0.09; Hoque et al., 2005b). The negative and low correlations of MSR with the growth traits and SFT may be more general for Japanese cattle populations. In general, the negative genetic correlation between MSR and SFT is considered a favorable genetic relationship for further improvement of beef marbling, in that improvement can be achieved without the deposition of excessive subcutaneous fat, and it should be appropriately implemented into a genetic evaluation system to produce good carcass to meet public demand. The genetic correlations among REA, the growth traits, the DRS and the SFT were moderately positive. The negative and low genetic correlation observed between MSR and DRS was, however, lower than the reported average of 0.16 (Koots et al., 1994b).

#### Genetic relationship between traits in performance and progeny test

Genetic correlations between the traits of bulls at performance test and those of their progeny at progeny test (Table 5) showed that the correlation between BWF of bulls and MSR of their progeny was moderately negative and within the reported ranges. In a review of parameters for growth and carcass traits, genetic correlations between yearling weight and MSR have ranged from highly negative to slightly positive (Mohiuddin, 1993), and the weighted mean in a review article is -0.37 (Koots et al., 1994b). Selection for growth traits, such as yearling weight has resulted in positive correlated responses in birth weight and post-weaning gain in selection experiments of beef cattle (Mrode, 1988). In the present study, the body weights of bulls correlated moderately with growth traits and DRS of

the progeny, indicating that selection for body weight in performance tests of bulls would be effective in improving carcass production of progeny. The genetic correlation between DG of bulls and of progeny was high (0.90), showing that DG at performance and progeny test are genetically identical, whereas the genetic correlation between DG of bulls at performance test and DG of their progeny at progeny test has reported at 0.62 (Oikawa et al., 2000). This difference indicates that a separate analysis is requisite for each testing station. The correlations of DG of bulls with body weights and the SFT of progeny were lower than the reported estimates of 0.93, 0.74 and 0.98, respectively (Oikawa et al., 2000), but consistent with the averages in a review article (Koots et al., 1994b).

TCV correlated weakly with most of the carcass traits in the progeny at progeny test except with MSR, although the correlation of TCV with other traits is not conclusive because of the large standard error of TCV. A similar tendency has been reported in correlations between TCV of bulls and progeny traits (Oikawa et al., 2000). On the basis of selection at performance test, increases in the thickness of subcutaneous fat need to be controlled because SFT correlated positively with all of the growth traits and feed intake. The moderate genetic relationship between ROU of bulls and MSR of progeny was consistent with reported estimates (Oikawa et al., 2000), indicating a possibility of improving intramuscular fat deposition by introducing ROU into selection programs at performance tests of bulls.

#### CONCLUSION

The moderate to high heritabilities for the carcass traits of progeny and for the body weights, CON and TIT of bulls indicate that a large genetic variability exists and can be used for further improvement of these traits. The slightly negative genetic correlation between MSR and SFT in progeny carcass is considered a favorable indication for further improvement of MSR, which can be achieved without increasing subcutaneous fat. Although the increase in the thickness of subcutaneous fat needs to be carefully

monitored during any selection program, the favorable genetic relationship between the growth traits of bulls and the other carcass traits of progeny suggested that further improvement of progeny carcass merit is possible with a concurrent improvement in the growth performance of bulls in selection programs.

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