Genotype × environment interaction effects on carcass traits in Japanese Black cattle[1]

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ABSTRACT: The importance of genotype × environment (region or management system) interactions for carcass traits in Japanese Black cattle was investigated using both univariate and multivariate animal models. The univariate approach was used mainly to test the significance of interaction effects. The multivariate approach was used to estimate genetic correlations, which indicated the magnitude of genotype × environment (GE) interactions. The more a genetic correlation deviates from 1, the larger the interaction. From the univariate approach, the addition of genotype × environment (region or management system) interaction (co)variance components resulted in an improved fit of the model for all traits in both cases ($P < 0.001$). However, estimates of genetic correlation between regions obtained from the multivariate approach for hot carcass weight, LM area, rib thickness, s.c. fat thickness, and marbling score were 0.97, 0.95, 0.93, 0.97, and 0.93, respectively. The corresponding estimates between management systems were 0.84, 0.92, 0.84, 0.90, and 0.97, respectively. These results indicate that GE interaction effects on carcass traits of Japanese Black cattle may be biologically unimportant. Therefore, breeding values obtained using the multivariate method would rank sires similarly in all environments. Consequently, carcass traits measured in these two different regions or management systems can be treated as the same traits.

Key Words: Carcass Traits, Genotype × Environment Interaction, Japanese Black

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Introduction

The Japanese Black cattle breed is the predominant beef breed in Japan, with a population of 560,000 breeding cows (MAFF, 2003). The breed has recently received greater interest not only in Japan but also in beef-exporting countries because of its excellent meat quality, especially its high degree of (i.m.) marbling. Well-marbled beef is expensive in Japan, and marbling is important in North America and Australia, especially for beef destined for Japan.

Beef production in Japan generally is practiced under a variety of environmental conditions. Although genetic evaluation and selection for Japanese Black cattle have been conducted within each prefecture for a long time, interest in nationwide genetic evaluation schemes has increased. In such situations, the same genotype may perform differently depending on environment (regions or management systems), and therefore the presence of genotype × environment (**GE**) interactions would hamper the usefulness of such an evaluation. There are several reports that have investigated the effect of GE interaction for growth traits using a univariate approach (Tess et al., 1979; Bertrand et al., 1985, 1987; Notter et al., 1992); however, studies on the GE interaction for carcass traits of beef cattle are limited.

As suggested by Falconer (1952), the expression of the same trait in two environments can be considered as two different characters, and the genetic correlation between them can be estimated in the same way as for any two correlated traits. To estimate the genetic correlation between the same traits in two different environments, a multivariate approach may be applied.

The objective of this study was to evaluate the importance of GE (region or management system) interactions for carcass traits in Japanese Black cattle and to compare genetic correlations estimated using multivariate and univariate animal models.

Materials and Methods

Animals and Data

Data were collected from consigned farms under the Agura Farm umbrella, which is the largest cooperative

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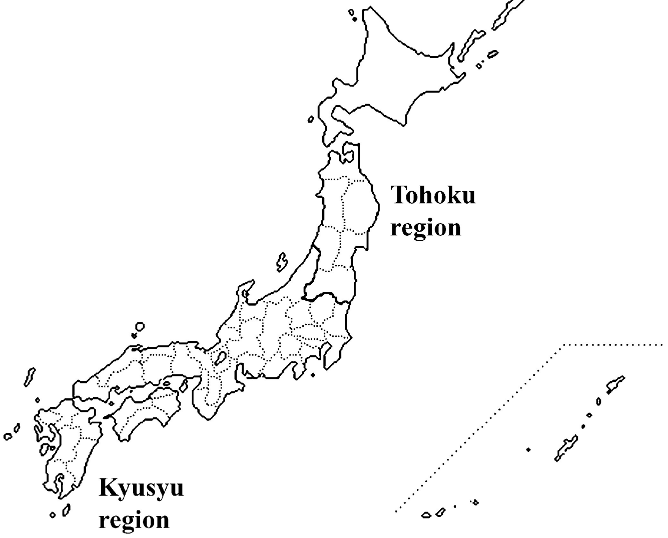

Figure 1. Boundary definitions for the Tohoku region and the Kyusyu region of Japan.

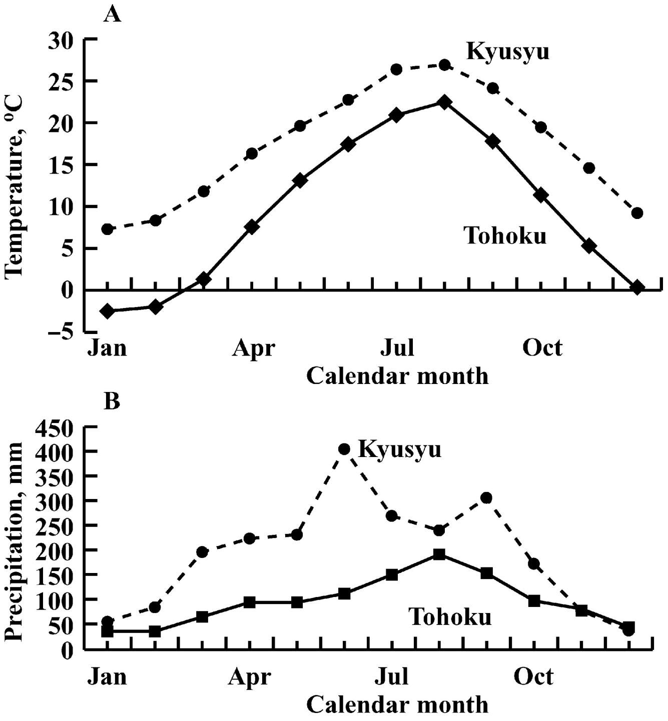

Figure 2. Climate situation in each region. A) Average temperature by month; B) total precipitation by month (Jan = January; Apr = April; Jul = July; Oct = October).

farming company for Japanese Black cattle in Japan. Animals were raised under a feedlot management system. Throughout the feedlot period, the animals were given free access to concentrates, which consisted of ground barley, ground yellow corn, and wheat bran. Roughage was supplied by restricted access to rice straw. Proportions of concentrate and roughage were approximately 80:20 on an as-fed basis.

The original data comprised 58,305 carcass records collected from April 1997 to December 2002 at the Agura Farm. The following carcass traits were analyzed: hot carcass weight (HCW); LM area (**LMA**); rib thickness (**RT**); s.c. fat thickness (**SFT**); and marbling score (**MS**). Measurements of LMA, RT, SFT and MS were at the 6th- to 7th-rib section. The LMA was measured on the left side of the carcass by grid approximation (i.e., by placing a transparent sheet with grids [1 cm × 1 cm] on a section and counting the number of intersections in LM). The RT was the distance between the latissimus muscle and pleura membrane measured half way between the rib ends. The MS was measured according to the Beef Marbling Standard, with scores of 1 to 12 (a so-called BMS number), with 12 being the best (JMGA, 1988).

Genotype × Region Interaction

In the Agura Farm cooperative, feedlot operations were mainly in the Tohoku and Kyusyu regions (Figure 1). The climate in the Tohoku region is relatively cold, and there are large differences in temperatures between summer and winter. Conversely, in the Kyusyu region, the climate is relatively warm throughout the year, and the annual precipitation is twice that in the Tohoku region (Figure 2). The vegetation in these two regions also is different, with that in the Tohoku region being deciduous broadleaved, and that in the Kyusyu being evergreen broadleaved. Therefore, these two regions experience different climatic conditions.

To investigate the effects of genotype × region interactions, the original data were classified into two groups based on the animal's point of origin (Tohoku or Kyusyu region). As a result of the classification, 3,073 records were excluded because they were from other regions. Only information from abattoirs with more than 50 records and feedlots with more than 25 records within each region were used. This resulted in a total of 20,106 and 34,670 records from the Tohoku and Kyusyu regions, respectively. Table 1 shows the structure of data used for analysis of the effects of genotype × region interaction.

Genotype × Management System Interaction

In the Agura Farm cooperative, there were two main management systems. Figure 3 shows the management

Table 1. Data structure for analysis of genotype × region interaction

Item	Total	Tohoku	Kyusyu	Both[a]
Records	54,776	20,106	34,670	—
Feedlot farms	120	41	79	—
Abattoirs	28	17	19	8
Sires	728	524	402	198

[a] Records in both regions.

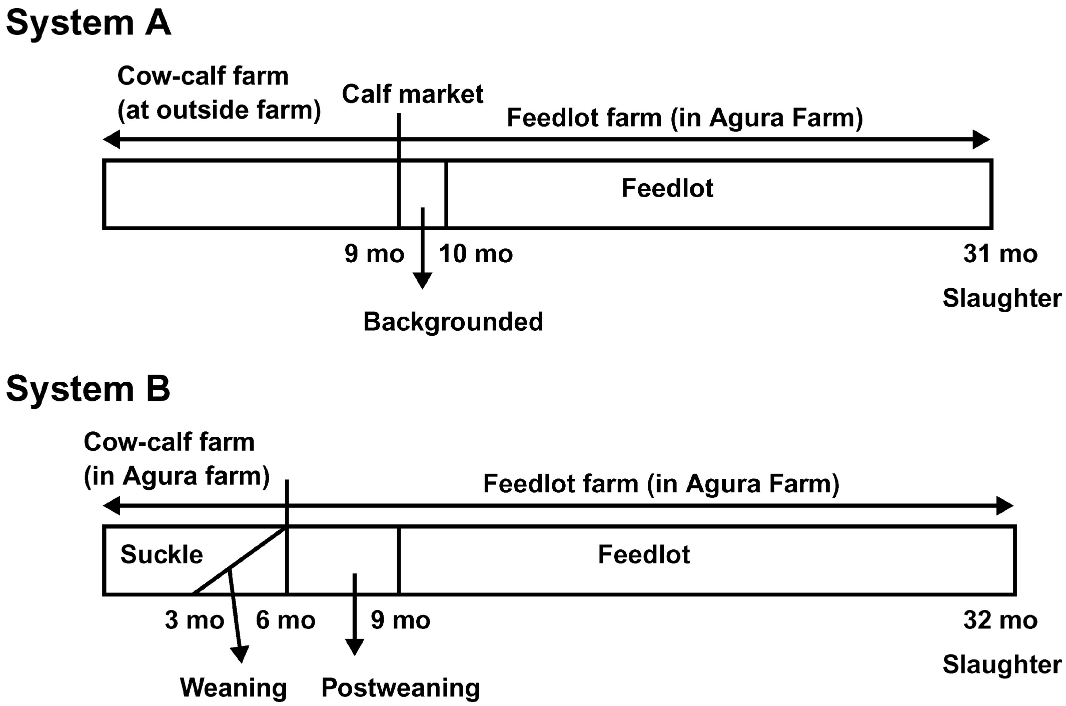

Figure 3. Management system for fattening animals at the Agura Farm.

systems used for fattening animals in the Agura Farm cooperative. In System A, calves were purchased from calf markets when they were 8 to 10 mo of age and placed in the feedlot farms. They were later backgrounded for 1 mo in drylot. Animals were fed mainly roughage during this period before being placed in the actual feeding program. In System B, the calves were born and raised on cow-calf farms under the Agura cooperative until they were approximately 6 mo old, at which time they were moved to a feedlot farm. The difference between the two systems was in the number of months the calves were placed in the feedlot operation and in the subsequent slaughter age. Calves in System A spent 3 mo less time in the feedlot and were 1 mo younger at slaughter than those in System B.

The original data were classified by management system to investigate the effects of the genotype × management system interaction. As a result, 562 records were excluded because they were from other management systems. Only information from abattoirs with more than 50 records and feedlots with more than 25 records within each management system were used, which resulted in a total of 19,385 and 35,461 records from the Systems A and B, respectively. Table 2 shows the structure of data used for the analysis of the effects of genotype × management system interaction.

Statistical Model

In this study, pedigree information was traced back two generations. An animal model that included all relationships among all animals was used as a statistical model for all analyses. The fixed effects included sex, farm, abattoir, and the combination of slaughter year and month. In the investigation of the effects of the genotype × region interaction, the management system was included as an additional fixed effect. On the other hand, region was not included as a fixed effect for the investigation of the genotype × management interaction because the effect of farm was nested within region. Days in the feedlot and slaughter age were fitted as linear and quadratic covariables.

Genetic parameters were estimated using MTDFREML programs (Boldman et al., 1993). Convergence was considered to have been reached when the variance of the –2 log likelihoods in the simplex was less than 10^{-4}. After initial convergence, cold restart was terminated when the variance of the –2 log likelihoods in the simplex fell below 10^{-8}.

Table 2. Data structure for analysis of genotype × management system interaction

Item	Total	System A[a]	System B[a]	Both[b]
Records	54,846	19,385	35,461	—
Feedlot farms	126	100	103	77
Abattoirs	27	23	26	22
Sires	728	564	348	184

[a] In System A, calves were purchased from calf markets when they were 8 to 10 mo of age and placed in the feedlot farms. They were later backgrounded for 1 mo before being placed in the actual feeding program. In System B, the calves were born and raised on cow-calf farms under the Agura cooperative until they were approximately 6 mo old, at which time they were moved to a feedlot farm. Calves in System A spent 3 mo less time in the feedlot and were 1 mo younger at slaughter than those in System B.

[b] Records occurred in both systems.

In this study, the magnitude of the GE interaction was evaluated using genetic correlations. These correlations were equal to 1 if there were no interactions. The more they deviated from 1, the larger the interactions. A problem in estimating these correlations is that the observations of a genotype in different environments are taken on different individuals. Therefore, the observations are not paired and a simple covariance analysis cannot be used; however, several methods can be used to estimate this genetic correlation (Mathur, 2002). In this study, genetic correlations were estimated using multivariate and univariate approaches.

Multivariate Approach. As suggested by Falconer (1952), the expression of the same trait in two environments can be considered as two different traits, and the genetic correlation between them can be estimated in the same way as for any two correlated traits. The model can be described in matrix notation as follows:

$$\begin{bmatrix} \mathbf{y_1} \\ \mathbf{y_2} \end{bmatrix} = \begin{bmatrix} \mathbf{X_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{X_2} \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z_2} \end{bmatrix} \begin{bmatrix} \mathbf{a_1} \\ \mathbf{a_2} \end{bmatrix} + \begin{bmatrix} \mathbf{e_1} \\ \mathbf{e_2} \end{bmatrix} \quad [1]$$

where $\mathbf{y_1}$ and $\mathbf{y_2}$ are the vectors of observations in Environments 1 and 2, respectively; β_1 and β_2 are the vectors of the fixed effects and covariates in Environments 1 and 2, respectively; $\mathbf{a_1}$ and $\mathbf{a_2}$ are the vectors of the random additive genetic effects in Environments 1 and 2, respectively; $\mathbf{e_1}$ and $\mathbf{e_2}$ are the vectors of random residual effects for Environments 1 and 2, respectively; and $\boldsymbol{X_1}$ and $\boldsymbol{X_2}$ are known incidence matrices relating the observations to the respective fixed effects in Environments 1 and 2, respectively, whereas $\boldsymbol{Z_1}$ and $\boldsymbol{Z_2}$ relate the observations to the random effects in the two environments. The variance and covariance structures for random components can be described as:

$$\mathbf{var}\begin{bmatrix} \mathbf{a_1} \\ \mathbf{a_2} \\ \mathbf{e_3} \\ \mathbf{e_4} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma^2_{\mathbf{a1}} & \mathbf{A}\sigma_{\mathbf{a12}} & \mathbf{0} & \mathbf{0} \\ \mathbf{A}\sigma_{\mathbf{a12}} & \mathbf{A}\sigma^2_{\mathbf{a2}} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_{\mathbf{e1}} & \mathbf{I}\sigma_{\mathbf{e12}} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_{\mathbf{e12}} & \mathbf{I}\sigma^2_{\mathbf{e2}} \end{bmatrix} \quad [2]$$

where $\mathbf{A}$ is the numerator relationships matrix; $\mathbf{I}$ is the identity matrix; σ^2_{a1} and σ^2_{a2} are the additive genetic variances for Environments 1 and 2, respectively; σ^2_{e1} and σ^2_{e2} are the environmental variances for Environments 1 and 2, respectively; and σ_{a12} and σ_{e12} are additive genetic and environmental covariances between Environments 1 and 2, respectively.

Univariate Approach. This approach can estimate GE interaction variance directly (Lee and Pollak, 1997; Maniatis and Pollott, 2002; Mathur, 2002). The full model can be described in matrix notation as follows:

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Z_A a} + \mathbf{Z_i i} + \mathbf{e} \quad [3]$$

where $\mathbf{y}$ and β are the vectors of observations and of fixed effects, respectively; $\mathbf{a}$ and $\mathbf{e}$ are the vector of additive genetic and environment effects, respectively; $\mathbf{i}$ is the vector of sire × environment interaction effects; and $\mathbf{X}$, $\mathbf{Z_A}$, and $\mathbf{Z_I}$ are known incidence matrices relating observations to β, $\mathbf{a}$, and $\mathbf{i}$, respectively. Likelihood ratio tests were used to test the significance of GE interaction effects. The variance and covariance structure for random components can be described as:

$$\mathbf{var}\begin{bmatrix} \mathbf{a} \\ \mathbf{i} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma^2_{\mathbf{a}} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma^2_{\mathbf{i}} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_{\mathbf{e}} \end{bmatrix} \quad [4]$$

where $\sigma_{\mathrm{a}}{}^2$ and σ^2_{i} are the variance components due to genetic and GE interaction effects, respectively.

Using this approach, several methods have been suggested to estimate genetic correlations. Robertson (1959) suggested the use of mean squares due to genotype, GE interaction, and error to estimate genetic correlations. Dickerson (1962) proposed a formula based on variance components instead of the mean squares, as well as an adjustment for differences among the genetic variances within environments. Yamada (1962) discussed the nature of the statistical models and expectations of mean squares used by these methods and provided a formula for random and mixed models considering environments as either random or fixed effects. In this study, genetic correlations ($\mathrm{r_g}$) were estimated using the following equation:

$$r_g = \frac{\sigma_a^2 - \frac{1}{2}\sigma_i}{\sigma_a^2 + \frac{1}{2}\sigma_i - \frac{1}{2}(\sigma_{a1} - \sigma_{a2})^2} \quad [5]$$

where σ_{a1} and σ_{a2} are genetic SD estimated from separate data for Environments 1 and 2, respectively.

Fernando et al. (1984) pointed out that direct application of the method in Yamada (1962) gives biased estimates of genetic covariances if the data are unbalanced. However, Yamada et al. (1988) claimed that the criticism was inappropriate, and used an alternative method that also was applicable to unbalanced data. In addition, using a mixed model approach, Itoh and Yamada (1990) suggested that the formulas by Yamada (1962) can be used for unbalanced data given specific assumptions and restrictions. Estimates of genetic correlation from the univariate approach were used mainly for comparisons with the multivariate approach in this study because the genetic correlation from a univariate approach is only justified if many assumptions and restrictions are met (Mathur, 2002).

Results

Table 3 shows basic statistics of the final carcass trait data in each region. Differences ($P < 0.01$) between regions were found for all traits except for LMA. The feedlot period in the Tohoku region was shorter, but

Table 3. Basic statistics of the final data for each region

Traits	Region	Mean	SD	Minimum	Maximum
Feedlot period, d	Tohoku	633.6**	69.71	319	1,023
	Kyusyu	711.4*	89.59	390	1,147
Slaughter age, d	Tohoku	935.4**	80.79	532	1,410
	Kyusyu	963.8*	73.57	616	1,377
HCW, kg	Tohoku	410.1**	59.00	176.0	653.0
	Kyusyu	404.8*	54.70	137.3	637.4
LM area, cm^2	Tohoku	49.3*	7.02	18	87
	Kyusyu	49.2*	7.05	10	90
Rib thickness, cm	Tohoku	7.4**	0.96	1.3	13.0
	Kyusyu	7.0*	0.90	1.4	11.0
Subcutaneous fat thickness, cm	Tohoku	2.4**	0.83	0.4	8.6
	Kyusyu	2.6*	0.88	0.2	8.6
Marbling score[a]	Tohoku	4.5**	1.79	1	12
	Kyusyu	4.1*	1.61	1	12

**Difference between regions, $P < 0.001$.

[a] Measured according to the Beef Marbling Standard on a 1 to 12 scale; a score of 12 is best (JMGA, 1988).

carcasses had greater rib thickness and marbling score. Table 4 shows basic statistics for the final carcass trait data for each management system. The effect of management system was different ($P < 0.01$) for all traits. The feedlot period was shorter for System A, but the carcass weight, LMA, and rib thickness were greater than for System B.

Genotype × Region Interaction

Multivariate Approach. Table 5 shows estimates of genetic variance components for carcass traits of animals in the Tohoku and the Kyusyu regions obtained using multivariate and univariate approaches. Genetic and residual variances for MS in the Tohoku region were 22 and 35% as large as corresponding estimates in the Kyusyu region. The estimates of heritability were moderately high (0.28 to 0.48) for all traits. The higher heritability estimates for HCW and SFT in the Tohoku region resulted from larger genetic variances and smaller residual variances. There was no difference in the estimates of heritability for MS between regions. Estimates of genetic correlations between regions for HCW, LMA, RT, SFT, and MS were 0.97, 0.95, 0.93, 0.97, and 0.93, respectively.

Univariate Approach. Estimates of genetic variance components using the univariate approach indicated mostly intermediate values between regions (Table 5). Sire × region interaction terms were highly significant ($P < 0.001$) for all traits; however, the sire × region interaction variance (σ_i^2) expressed as a proportion of phenotypic variance (i^2) was very small (0.007 to 0.026), which resulted in high estimates of genetic correlation between regions that ranged from 0.94 to 0.99 for all

Table 4. Basic statistics of the final data for each management system

Traits	System[a]	Mean	SD	Minimum	Maximum
Feedlot period, d	A	632.2**	65.68	319	901
	B	710.4*	90.95	339	1147
Slaughter age, d	A	926.7**	70.56	621	1349
	B	968.0*	77.38	532	1410
HCW, kg	A	419.8**	53.10	206.4	643.0
	B	399.6*	56.81	137.3	653.0
LM area, cm^2	A	49.6**	6.89	18	84
	B	49.0*	7.11	10	90
Rib thickness, cm	A	7.3**	0.91	1.3	13.0
	B	7.0*	0.93	1.4	11.5
Subcutaneous fat thickness, cm	A	2.8**	0.93	0.3	8.6
	B	2.3*	0.80	0.2	8.6
Marbling score[b]	A	4.2**	1.65	1	12
	B	4.3*	1.71	1	12

**Difference between management systems, $P < 0.01$.

[a] In System A, calves were purchased from calf markets when they were 8 to 10 mo of age and placed in the feedlot farms. They were later backgrounded for 1 mo before being placed in the actual feeding program. In System B, the calves were born and raised on cow-calf farms under the Agura cooperative until they were approximately 6 mo old, at which time they were moved to a feedlot farm. Calves in System A spent 3 mo less time in the feedlot and were 1 mo younger at slaughter than those in System B.

[b] Measured according to the Beef Marbling Standard on a 1 to 12 scale; a score of 12 is best (JMGA, 1988).

Table 5. Estimates of additive genetic (σ_a^2) and residual variances (σ_e^2), sire × region interaction variances (σ_i^2), heritabilities (h^2), σ_i^2 as a proportion of phenotypic variance (i^2), log likelihood expressed as a deviation from the reduction model (ΔlogL), and correlations (r_g) between the Tohoku and Kyusyu region

Traits[a]	Approach[b]	σ_a^2	σ_e^2	σ_i^2	h^2	i^2	ΔlogL	r_g
HCW, kg	T	1,064.4	1,134.7	—	0.48	—	—	0.97
	K	829.8	1,176.2	—	0.41	—	—	
	U	928.9	1,171.3	24.6	0.44	0.012	33***	0.99
LMA, cm^2	T	15.03	30.27	—	0.33	—	—	0.95
	K	14.17	29.52	—	0.32	—	—	
	U	14.34	30.13	0.33	0.32	0.007	15***	0.98
RT, cm	T	0.225	0.514	—	0.30	—	—	0.93
	K	0.181	0.455	—	0.28	—	—	
	U	0.201	0.481	0.007	0.29	0.010	28***	0.97
SFT, cm	T	0.284	0.337	—	0.46	—	—	0.97
	K	0.247	0.350	—	0.41	—	—	
	U	0.260	0.352	0.016	0.41	0.026	87***	0.94
MS	T	1.309	1.769	—	0.43	—	—	0.93
	K	1.004	1.286	—	0.44	—	—	
	U	1.194	1.424	0.030	0.45	0.011	33***	0.98

***Difference in log likelihood, $P < 0.001$.

[a] LMA = LM area; RT = rib thickness; SFT = s.c. fat thickness; and MS = marbling score.

[b] T and K show the Tohoku region and the Kyusyu region from the multivariate approach, respectively, and U shows the univariate approach.

traits. Estimates of genetic correlation using the univariate approach were higher than those using multivariate approach for all traits except for SFT.

Genotype × Management System Interaction

Multivariate Approach. Estimates of genetic variance components for carcass traits of animals in Management Systems A and B obtained using multivariate and univariate approach are shown in Table 6. Genetic and residual variances of MS for the System A were 10% larger and 29% smaller than corresponding estimates for System B. Estimates of genetic correlations between management systems for HCW, LMA, RT, SFT, and MS were 0.84, 0.92, 0.84, 0.90, and 0.97, respectively. The genetic correlations between management systems for all traits except MS were lower than those between regions.

Table 6. Estimates of additive genetic (σ_a^2) and residual variances (σ_e^2), sire × management system interaction variances (σ_i^2), heritabilities (h^2), σ_i^2 as a proportion of phenotypic variance (i^2), log likelihood expressed as a deviation from the reduction model (ΔlogL), and correlations (r_g) between management systems

Traits[a]	Approach[b]	σ_a^2	σ_e^2	σ_i^2	h^2	i^2	ΔlogL	r_g
HCW, kg	A	821.5	963.9	—	0.46	—	—	0.84
	B	1,029.2	1,185.7	—	0.46	—	—	
	U	916.4	1,174.4	38.2	0.43	0.018	74***	0.97
LMA, cm^2	A	14.54	27.57	—	0.35	—	—	0.92
	B	15.14	30.08	—	0.33	—	—	
	U	14.35	30.05	0.36	0.32	0.008	26***	0.98
RT, cm	A	0.201	0.431	—	0.32	—	—	0.84
	B	0.199	0.490	—	0.29	—	—	
	U	0.195	0.484	0.009	0.28	0.013	51***	0.96
SFT, cm	A	0.262	0.377	—	0.41	—	—	0.90
	B	0.246	0.331	—	0.43	—	—	
	U	0.261	0.352	0.019	0.41	0.031	80***	0.93
MS	A	1.337	1.142	—	0.54	—	—	0.97
	B	1.199	1.476	—	0.45	—	—	
	U	1.186	1.431	0.028	0.45	0.011	14***	0.98

***Difference in log likelihood, $P < 0.001$.

[a] LMA = LM area; RT = rib thickness; SFT = s.c. fat thickness; and MS = marbling score.

[b] A and B show System A and B estimates from the multivariate approach, respectively, and U shows estimates from the univariate approach.

Univariate Approach. The addition of genotype × management system interaction (co)variance components resulted in an improved fit of the model for all traits ($P < 0.001$; Table 6). Conversely, the sire × environment interaction variance (σ_i^2) expressed as a proportion of phenotypic variance (i^2) was very small (0.003 to 0.031). Therefore, estimates of genetic correlation between management systems for all traits were very high (0.93 to 0.98). As with the genotype × region data, estimates of genetic correlation using the univariate approach were higher than those using the multivariate approach.

Discussion

The estimates of heritability for carcass traits were almost the same in both approaches. The estimates of heritability for MS were lower than literature values for Japanese Black cattle (Mukai et al., 1995; Oikawa et al., 2000; Kawada et al., 2003). For HCW, the heritability estimates in this study were lower than the estimate of 0.64 reported by Kawada et al. (2003) but higher than the estimate of 0.39 reported by Mukai et al. (1995; Tables 5 and 6).

The multivariate approach with animal model is more complex and computationally more demanding than the univariate approach. Therefore, in earlier studies (Tess et al., 1979; Bertrand et al., 1985, 1987; Notter et al.; 1992), univariate methods with a sire model were used to investigate GE interaction; however, over the past few years, the multivariate method is becoming more and more common because of the computational feasibility of solving large numbers of equations. Moreover, a univariate approach with an animal model has been used in recent years (Lee and Pollak, 1997; Maniatis and Pollott, 2002; Mathur, 2002).

As far as we know, there are no available reports that investigate the differences in the magnitude of GE interaction effects estimated using multivariate and univariate approaches. Cameron (1993) pointed out that the genetic correlation computed from the GE interaction may vary depending on the approaches used. Recently, Ojango and Pollot (2002) estimated the genetic correlation of first-lactation milk yields between the United Kingdom and Kenya for Holstein bulls using a multivariate approach with different models (animal model vs. sire model). They reported a difference in the estimates of genetic correlation between the models used (0.49 ± 0.06 for the animal model evaluation and 0.58 ± 0.1 for the sire model evaluation). Usually, to estimate genetic correlations using a univariate approach, some specific assumptions and restrictions need to be applied (Mathur and Schlote, 1995). However, because the multivariate approach is based on Falconer's definition (Falconer, 1952) of GE interaction, the multivariate approach seems to have more advantages than the univariate approach.

In the current study, the addition of GE (region or management system) interaction (co)variance components resulted in an improved fit of the model for all traits ($P < 0.001$). Nonetheless, the magnitude of the genetic correlations between regions or management systems was large (0.84 to 0.99) in all cases. Robertson (1959) suggested that the GE interaction is of biological and agricultural importance if the genetic correlation for the same trait in different environments is less that 0.80. In this study, all estimates of genetic correlations for carcass traits were above the threshold of biological importance of GE interaction, providing evidence that GE interactions for carcass traits of Japanese Black cattle in both regions and both management systems were not biologically significant enough to cause much reranking of animals based on estimated breeding values. This indicates that information on carcass traits from different regions of Japan different and management systems can be used in nationwide genetic evaluation schemes without important changes in the ranking of sires based on EBV.

Implications

The addition of genotype × environment (region or management system) interaction (co)variance components resulted in an improved fit of the model for all traits. However, the large genetic correlations between regions or management systems (greater than 0.80) provides evidence that combining the carcass data of Japanese Black cattle from different regions and management systems across Japan for the purposes of a nationwide genetic evaluation would allow for correct predictions of breeding values of carcass traits and rank sires in all environments.

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