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Genetic Parameters for Growth and Carcass Traits in Japanese Brown Cattle Estimated from Field Records

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ABSTRACT: Field records from 14,380 Japanese Brown steers by 92 sires were used to estimate genetic parameters for growth and carcass traits. Multiple-trait restricted maximum likelihood (REML) procedures accounting for relationships among sires were used in estimating (co)variance components among average daily gain during fattening periods (ADG), carcass weight (CWT), longissimus muscle area

(LMA), rib thickness (RT), marbling score (MS), and subcutaneous fat thickness (SFT). Heritability estimates on an age-constant basis were .22, .37, .38, .26, .40, and .35 for ADG, CWT, LMA, RT, MS, and SFT, respectively. Estimated genetic correlations (r_g) among ADG, CWT, and RT were positive and moderately high (.48 to .85). The r_g between MS and SFT was -.12.

Key Words: Japanese Brown, Carcass, Traits, Heritability, Genetic Correlation

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Introduction

Since the liberalization of beef import restrictions in 1991, domestic production of high-quality beef has been receiving much emphasis in Japan. In Japan, carcass value is determined by meat quality, primarily degree of (intramuscular) marbling. Imported beef is usually sold at a much lower price than beef from domestic breeds. However, interest in exporting beef to Japan has been growing in the United States, Australia, and Canada (Klein and Kagatsume, 1990; Wahl et al., 1991; Hopkins and Roberts, 1993). In the United States, researchers have investigated growth and carcass characteristics of cattle with genetic material from Japanese breeds (Lunt et al., 1993; Harris et al., 1995). Production of domestic Japanese beef is competitive only because of its outstanding meat quality. Japanese Brown (especially the Kumamoto strain) has larger mature size and growth rate than other domestic breeds, but meat quality is lower relative to Japanese Black (Namikawa, 1992). The potential for improving carcass traits, and especially meat quality, in Japanese Brown by selection needs to be evaluated.

A (single trait) sire evaluation program was implemented in Kumamoto prefecture (province) for

the Japanese Brown in 1983. Growth and carcass records are collected from calf and carcass markets. Accurate genetic parameter estimates using such records are required for accurate sire evaluation. The most recent estimations of heritabilities for growth and carcass traits in Japanese Brown steers were done by Sasaki (1991), using Henderson method 3 to analyze field data collected from 1983 to 1986. Literature estimates for genetic correlations are not available for Japanese Brown Cattle. The objective of this study was to estimate heritabilities and genetic correlations for growth and carcass traits, including meat quality, in Japanese Brown steers, using MT-REML procedures.

Materials and Methods

There are four domestic beef breeds in Japan: Japanese Black, Japanese Brown, Japanese Poll, and Japanese Shorthorn. Japanese Brown is the second most common breed after Japanese Black. Historically, native cows of the Japanese Brown were upgraded by Simmental and Korean cattle in the period of crossbreeding with foreign breeds from 1868 to 1910. No crossbreeding with other breeds has occurred since then. In 1944, the Japanese Brown was considered an established breed, characterized by brown coat color. At present, the breed is mainly reared in Kumamoto and Kouch prefectures, and was recently introduced into the Hokkaido area. Because breeding has been within each prefecture, there are

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two distinct strains in the Japanese Brown (i.e., the Kumamoto strain and the Kouch strain). The total population size is 163,000 animals, about 10% of the Japanese domestic beef population (Namikawa, 1992). The Japanese Brown was used as a foundation breed to develop the American Wagyu (Lunt et al., 1993).

In Japan, beef production systems are generally divided into two operations, a cow-calf operation and feedlot (fattening) operation. Cow-calf operations generally involve only a few cows. Steers are sold at 8 to 10 mo of age at calf markets and purchased by feedlot farmers. The size of feedlot operations ranges from small (fewer than five animals) to large (more than 1,000 animals). In the feedlot operations, steers are given free access to concentrates throughout the whole feedlot period. Concentrates mainly consist of ground barley, ground yellow corn, and wheat bran.

Average age and weight of the steers at the start of the feedlot period in this study were 295 d and 314 kg, respectively. Average slaughter age and weight were 724 d and 685 kg, respectively. These figures indicate the specificity of beef production in Japan, aiming at the production of highly marbled beef. In carcass markets, carcass value is primarily determined by marbling score at the sixth–seventh rib section.

Carcass data were collected from 14,380 Japanese Brown steers sold in five carcass markets in Kumamoto prefecture from 1989 to 1993. Growth and carcass traits considered in this study are average daily gain during the feedlot period (**ADG**), carcass weight (**CWT**), longissimus muscle area (**LMA**), rib thickness (**RT**), marbling score (**MS**), and subcutaneous fat thickness (**SFT**). Measurement of LMA, MS, and SFT was at the sixth–seventh rib section. The RT is a measurement adopted in the new carcass grading system starting in 1988. The trait is measured at the mid-point of the seventh rib. Marbling was classified using Beef Marbling Standards with scores 1 to 12 (so-called BMS number), with number 12 being best (JMGA, 1988). Table 1 shows the number of records, unadjusted means, standard deviations, and extreme values per trait.

Only sires ($n = 92$) having at least five progeny were included in the analyses (Table 2). Average

number of progeny per sire was 156. (Co)variance components were estimated using multiple-trait restricted maximum likelihood (**MT-REML**) analyses, including relationships among sires (Groeneveld, 1993). The sire model was chosen over alternative models (e.g., animal model) because multiple-trait animal models still require large amounts of computing time and costs. Recently, Lamb et al. (1990), Arnold et al. (1991), Woodward et al. (1992), and Wilson et al. (1993) used a sire model for carcass data analysis. The sire model used in this analysis was

$$Y_{ijklm} = \mu + YM_i + M_j + F_k + s_l + b_1 A_{ijklm} + b_2 A_{ijklm}^2 + e_{ijklm}$$

where Y_{ijklm} is observation $ijklm$ for the trait; μ is the population mean; YM_i is the fixed effect of year-month i (1 to 60); M_j is the fixed effect of market j (1 to 5); F_k is the fixed effect of fattening farm k (1 to 132); s_l is the random effect of sire l (1 to 92); b_1 and b_2 are linear and quadratic partial regression coefficients; A_{ijklm} is slaughter age in days; and e_{ijklm} is the random residual associated with observation $ijklm$. By including linear and quadratic regression for slaughter age in the model, age-constant (724 d) estimates were obtained.

Standard errors of heritabilities and genetic correlations were approximated according to Falconer (1989).

Results and Discussion

Estimated variance components, heritabilities, and phenotypic and genetic correlations are given in Table 3. Sire effects were important ($P < .01$) sources of variation for all traits.

Estimated heritability for ADG (.22) was lower than in many literature reports in Hereford (Dinkel and Busch, 1973; Benyshek, 1981; Lamb et al., 1990; Veseth et al., 1993) but higher than the estimates of .13 from Hereford steers by Arnold et al. (1991) and .18 from Japanese Black steers and .15 from Japanese Brown steers by Sasaki (1991).

Table 1. Numbers of records, unadjusted means, standard deviations (σ_p), and extreme values (Min–Max) for growth and carcass traits

Trait	No. of records	Mean	σ_p	Min–Max
Daily gain, g/d	14,361	978.7	133.3	467–1,446
Carcass weight, kg	14,380	437.0	41.5	270–592
Longissimus muscle area, cm ^{2a}	11,355	49.5	6.0	26–75
Rib thickness, cm ^a	11,164	7.0	.7	4.0–9.5
Marbling score, unit ^{ab}	11,380	3.7	1.5	1–11
S.C. fat thickness, cm ^a	11,156	2.6	.8	.7–6.0

^aMeasured at sixth–seventh rib section.

^bScored on a scale of 1 to 12.

Table 2. Distribution of sires by number of progeny

No. of progeny per sire	No. of sires	Total no. of records
5 to 10	13	94
11 to 100	49	2,198
101 to 300	17	2,940
> 300	13	9,148
Total	92	14,380

Estimated heritability for CWT (.37) corresponds with estimates by Koch et al. (1982) for crossbred steers, by Lamb et al. (1990) and Veseth et al. (1993) for Hereford bulls, by Wilson et al. (1993) for Angus steers and heifers, by Benyshek (1981) for Hereford steers under field conditions, and by Mukai (1994) for Japanese Black steers. However, the present estimate is considerably higher than the estimates of .14 from Japanese Black steers by Fukuhara et al. (1989) and .17 from Japanese Brown steers by Sasaki (1991).

Estimated heritability for LMA (.38) was within the range (.28 to .46) in the literature (Benyshek, 1981; Fukuhara et al., 1989; Lamb et al., 1990; Arnold et al., 1991). The heritability estimate of .26 for RT was similar to .23 from Japanese Black steers by Fukuhara et al. (1989).

Estimated heritability for MS (.40) corresponds with an average estimate (.35) from a literature summary by Marshall (1994) and .33 for Hereford bulls reported by Lamb et al. (1990) and .46 for Japanese Black steers by Mukai (1994) using MT-REML. Estimated heritability for SFT (.35) was also within the literature range (.26 to .68) (Marshall, 1994). However, considerably lower estimates of .19 and .13 for MS and SFT were reported by Fukuhara et al. (1989) for Japanese Black steers.

Heritability estimates may vary with methods of analysis. There are a few cases in which carcass traits were analyzed on a constant slaughter weight basis (Arnold et al., 1991). When data from the present study were analyzed by including slaughter weight as a covariate instead of slaughter age, slaughter weight-constant heritabilities were .42, .27, .42, and .33 for

LMA, RT, MS, and SFT, respectively. These estimates were about the same as those in the analyses represented in Table 3, indicating that choices of covariates in the model (slaughter age vs slaughter weight) had little effect on heritability estimates. Benyshek (1981) found that combinations of covariates in the model altered the estimates of heritability for carcass traits only slightly. More recently, using many literature values, Koots et al. (1995a) showed that heritability estimates for carcass traits did not significantly differ for different adjustments.

In recent years, REML (Patterson and Thompson, 1971) has generally been used to estimate variance components and heritabilities, whereas until the 1980s Henderson's method 3 (Henderson, 1953) was used. Sasaki (1991) analyzed Japanese Brown data from this same population, but different years (from 1983 to 1986), using Henderson's method 3. Sasaki's (1991) heritability estimates were .15, .17, and .15 for ADG, CWT, and MS, respectively, all lower than results from the present study. When data from the present study were analyzed using Henderson's method 3, heritability estimates were .17, .28, .31, .18, .27, and .32 for ADG, CWT, LMA, RT, MS, and SFT, respectively, also all lower than those obtained using MT-REML. Henderson's method 3 resulted in smaller sire variance component estimates. Mukai (1994) estimated heritabilities of .44, .45, .38, .46, and .35 for CWT, LMA, RT, MS, and SFT in Japanese Black steers using the MT-REML procedure, whereas Fukuhara et al. (1989) estimated heritabilities of .14, .32, .23, .19, and .13 for the corresponding traits from data for the same breed and sex using Henderson's method 3. The higher estimates by the MT-REML than those by Henderson's method 3 correspond to the results in the present study.

There are many comparisons between Henderson's method 3 and REML from theoretical points of view (e.g., Henderson, 1985; Searle, 1989) or using computer simulation (e.g., Lin and McAllister, 1984). However, there are few reports directly comparing estimates for variance components by different procedures using the same real data. Recently, Mielenz et al. (1994) reported that heritability estimates ob-

Table 3. Estimated sire (σ_s^2) and residual (σ_e^2) variance components, heritabilities (h^2), and phenotypic (below diagonal), and genetic correlations (above diagonal) among traits

Trait	σ_s^2	σ_e^2	h^2 ^a	Correlations ^a					
				ADG	CWT	LMA	RT	MS	SFT
Daily gain (ADG), g/d	747	12,787	.22		.85	.24	.48	.11	.31
Carcass weight, (CWT), kg	126	1,246	.37	.64		.23	.66	-.05	.39
Longissimus muscle area (LMA), cm ²	3.2	30.6	.38	.31	.36		.14	.12	-.12
Rib thickness (RT), cm	.030	.428	.26	.44	.60	.26		.25	.33
Marbling score (MS), unit	.198	1.772	.40	.08	.20	.16	.30		-.12
S.C. fat thickness (SFT), cm	.055	.566	.35	.21	.36	-.05	.33	.03	

^aApproximated standard errors of heritabilities range from .02 to .03 and of genetic correlations from .02 to .06.

tained by MT-REML were substantially different from those obtained by Henderson's method 3 using data from a selected population of White Leghorns. They concluded that differences between the methods may be caused by the fact that the REML gives parameter estimates for the base population, whereas Henderson's method 3 yields estimates averaged over generations. This may also explain the results found in the present study. Lower estimates of heritability by Henderson's method 3 ignoring relationships among sires might result from ignoring a decrease in additive genetic variance due to selection since the base generation.

Genetic correlations (r_g) among ADG, CWT, and RT were moderately high (Table 3). Lamb et al. (1990) reported a much higher genetic correlation between ADG and CWT (.94) in Hereford bull data. Results indicate that selection for increased ADG would increase CWT and RT. The low genetic correlation (.09) between ADG and MS is in agreement with the correlations of .15 reported by Dinkel and Busch (1973) for Hereford steers and Koch et al. (1982) for crossbred steers, although Lamb et al. (1990) reported a higher estimate of .48. The genetic correlation (.24) between CWT and LMA was moderate. The estimates vary widely across studies. Lamb et al. (1990) and Wilson (1993) reported moderately high estimates (.58 and .47) in Hereford and Angus data, respectively, but Fukuhara et al. (1989) reported a similar estimate (.15) in Japanese Black steers from field data.

A negative correlation (-.12) between MS and SFT was found. Many reports show moderately positive genetic correlations of marbling with subcutaneous fat thickness. For example, Dinkel and Busch (1973) and Lamb et al. (1990) reported genetic correlations of .38 and .21 in Hereford data. Koots et al. (1995b) reported a weighted mean genetic correlation of .36 in their review paper. However, Wilson et al. (1993) recently reported a negative genetic correlation of -.13 in Angus field data. For Japanese Black steers, Fukuhara et al. (1989) and Yang et al. (1985) reported a negative genetic correlation (-.04 and -.10) between MS and SFT.

In Japan, the official performance and progeny testing programs in testing stations started in 1968. As pointed out by Namikawa (1992), however, there are unexpected problems in the present programs, when improvement of carcass traits is emphasized. The first step of selection is based on performance tests, having no progeny information on carcass traits. Therefore, bulls of potential merit for carcass traits may be culled in the performance tests. Moreover, numbers of bulls that are progeny-tested in stations cannot be increased dramatically due to limited testing capacity. Therefore, accurate genetic parameter estimates and efficient breeding programs using field progeny records are required to overcome these problems.

Implications

Growth and carcass traits in Japanese Brown Cattle are moderately heritable. Results indicate opportunities for genetic improvement of meat quality by selection. In particular, the low, negative genetic correlation between marbling and subcutaneous fat thickness encourages the farmers who aim to produce high-quality beef without increasing external fat. Establishment of recording systems under field conditions and accurate genetic parameter estimates using the records will be valuable in efficient breeding programs.

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