# Genetic Relationships between Live Animal Measurements at Performance Testing and Field Carcass Traits of Japanese Black Cattle

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Abstract Genetic relationships between ultrasonically measured live animal measurements and carcass traits in Japanese Black cattle were estimated using a two-trait sire and maternal grandsire model with REML procedure. Live animal measurements included longissimus muscle area (7-REAu), subcutaneous fat thickness (SFTu), intermuscular fat thickness (IMFTu), rib thickness (RTu) and beef marbling score (BMSu) at 7th rib, and longissimus muscle area at 13th rib (13-REAu) by ultrasound on 154 performance tested bulls. For carcass traits, carcass weight (CWc), longissimus muscle area (REAc), rib thickness (RTc), subcutaneous fat thickness (SFTc), yield estimate (YEc), and beef marbling score (BMSc) were measured on 4,725 steers and heifers. Heritabilities for live animal measurements, at the end of performance testing, were estimated at 0.20, 0.58, and 0.15 for 7-REAu, SFTu, and BMSu, respectively. For carcass traits, heritabilities of 0.25 for CWc, 0.52 for REAc, 0.55 for SFTc, and 0.56 for BMSc were obtained. Carcass traits were highly heritable and had higher heritability estimates compared to those for ultrasonic measurements. Genetic correlations between ultrasonic longissimus muscle area and REAc ranged from 0.52 to 0.71. Ultrasonic subcutaneous fat thickness correlated negatively to SFTc and BMSu correlated positively to BMSc at the beginning of testing but negatively at the end of testing. Although ultrasonic live animal measurements concerning fat deposition did not correlate consistently to corresponding carcass traits, possibilities for improving REAc were indicated by the introduction of ultrasonic techniques into performance testing.

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In Japanese Black cattle, the main beef breed in Japan, individual sires have large genetic influences in the population because more than 90% of progeny are produced by artificial insemination. Selection of sires of Japanese Black cattle is practiced by two-stage selection, namely, performance and progeny testing at official stations. As the testing capacity in the station is limited, bulls are selected with relatively strong selection intensity using growth characteristics at performance testing. Bulls with favorable carcass merit, especially meat quality, might be culled before progeny testing because of their poor growth characteristics.

To overcome these kinds of problems, the techniques for estimating carcass characteristics in live animals have been developed. WILSON<sup>15</sup> reviewed the role of ultrasound for genetic improvement. In addition, increased computer facilities and developments in computing strategies allow the widespread genetic

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evaluation of livestock using mixed model methods. Attempts to clarify genetic relationships of ultrasonic measurements to carcass traits using these statistical procedures are reported by ARNOLD *et al.*<sup>1)</sup> and ROBINSON *et al.*<sup>11)</sup>.

The objectives of this study were to evaluate the genetic relationships between ultrasonic live animal measurements of performance tested bulls and carcass traits recorded in the field and to examine the efficiency of applying ultrasound at performance testing for improvement of carcass characteristics.

#### **Materials and Methods**

Ultrasonic Measurements : Bulls used in this study were those performance tested at Kagoshima Prefectural Animal Experimental Station from November 1988 through May 1992. Every year approximately 30 bulls have been tested for their performance and out of 30 bulls, approximately 10 bulls have been selected for progeny testing. After a 20 days adjustment period, bulls were housed individually in  $2.7 \,\mathrm{m} \times 3.6 \,\mathrm{m}$  pens with approximately 10 m<sup>2</sup> of paddock and were tested for 112 days. They were allowed ad libitum access to roughage and water, but only an hour access to concentrate feed containing 10.5% of DCP, 73% of TDN, minerals, salt, and vitamins each morning and evening. Ultrasonic measurements were recorded twice during the testing period, each at the beginning and at the end of testing. Measurements by ultrasound were rib thickness (RTu), subcutaneous fat thickness (SFTu), intermuscular fat thickness (IMFTu), beef marbling score (BMSu), longissimus muscle area between the 6th and the 7th rib sections (7-REAu), and between the 12th and the 13th rib sections (13-REAu). All the measurements except 13-REAu were interpreted between the 6th and the 7th rib sections.

Liquid paraffin was used to ensure acoustic contact and ultrasonic images were recorded using Fujihira Supereye Meat real-time scanner fitted with a 2.0 MHz linear probe. Images were frozen and printed out and interpreted for each measurement. Traces were measured using an electric digitizer. Beef marbling score is a subjective score of the degree of marbling ranging from null (0) to very abundant (5). A summary of age at the end of testing and ultrasonic measurement of 154 bulls are given in Table 1.

Field Carcass Traits: For field carcass traits, steers and heifers that were fed on farms in Kagoshima Prefecture from April 1988 through August 1992 were used. Fattened animals were slaughtered at 5 carcass markets (3 markets in Kagoshima, one in Osaka and the other in Kyoto). Traits measured were cold carcass weight (CWc), longissimus muscle area (REAc), rib thickness (RTc), subcutaneous fat thickness (SFTc), yield estimate for percentage of trimmed whole sale cuts (YEc), and beef marbling score (BMSc). All the traits except YEc were measured between the 6th and the 7th rib sections by certificated graders of the Japan Meat Grading Association and YEc was calculated by the following equation :

 $YEc(\%) = 69.419 + 0.130 \times REAc + 0.667 \times$ 

 $RTc-0.025 \times CWc'-0.896 \times SFTc.$ 

In the equation, CWc' means cold left-side carcass weight.

After a removal of abnormal records (>3 sd) and due to the reason of poor connectedness between random sire effect and fixed effects (carcass market and feeding place), records of 980 heifers and 3,745 steers were available for analysis. Means and ranges of slaughter age and carcass traits of 4,725 animals are reported in Table 2.

Analytical Model : A two-trait sire and maternal grand sire model was applied for the estimation of variance components (SCHAEFFER et al.<sup>12)</sup>; EVERETT et al.<sup>4)</sup>).

In matrix notation, the mixed linear models can be written as follows :

#### Relationships between Ultrasonic and Carcass Traits

Trait	Mean	SD	Min.	Max.	h <sup>2</sup> ±SE
End of test age, month	11.5	0.51	10.3	12.2	
Beginning of performance testing					
7–REAu, cm <sup>2</sup>	21.0	2.32	15.6	26.2	0.17±0.258
13–REAu, cm²	39. 2	4.40	28.7	50.5	0.12±0.253
RTu, mm	32.4	4,46	19.7	46.1	0.22±0.264
SFTu, mm	4.9	1,82	1.1	10.2	0.12±0.253
IMFTu, mm	14.1	4.13	5.9	27.0	0.11±0.232
BMSu	0.02	0.079	0.00	0.67	0.18±0.260
End of performance testing					
7-REAu, cm <sup>2</sup>	32.4	2.87	25.6	40.7	0.20±0.262
13–REAu, cm²	54.5	4.98	43.9	68.6	0.18±0.259
RTu, mm	47.9	6,21	30.7	67.4	0.51±0.288
SFTu, mm	8.7	2.39	3.7	15.9	0.58±0.293
IMFTu, mm	19.7	5, 03	10.9	36.6	0.15±0.256
BMSu	0.64	0.364	0.00	2.00	0.15±0.257

Table 1. Basic statistics and heritability estimates  $(h^2)$  of ultrasonic measurements (n=154)

7-REAu : longissimus muscle area at 7 th rib. 13-REAu : longissimus muscle area at 13 th rib. RTu : rib thickness. SFTu : subcutaneous fat thickness. IMFTu : intermuscular fat thickness. BMSu : beef marbling score.

Trait	Mean	SD	Min.	Max.	h <sup>2</sup> ±SE
Slaughter age, month	28.3	1.56	23. 0	33. 6	
CWc, kg	408.3	42.55	274.5	541.7	0.25±0.054
REAc, cm <sup>2</sup>	48.4	6.14	30.0	67.0	0.52±0.099
RTc, cm	7.3	0.78	4.9	9.6	0.29±0.062
SFTc, cm	3.1	0.86	0.8	5.7	0.55±0.104
YEc, %	72.7	1.32	68.7	76. 7	0.70±0.125
BMSc	1.75	0. 706	0. 33	5.00	0.56±0.106

Table 2. Basic statistics and heritability estimates  $(h^2)$  of field carcass traits (n=4,725)

CWc:carcass weight. REAc:longissimus muscle area. RTc:rib thickness. SFTc:subcutaneous fat thickness. YEc:yield estimate. BMSc: beef marbling score.

measurements and carcass traits, respectively. The  $\mathbf{y}_i$  (i=1, 2) is an observation vector, and  $\mathbf{X}_i$ and  $\mathbf{Z}_i$  are incidence matrices consisting of elements, 0, 1, and 1/2, referring the fixed effects and sire and maternal grandsire to the observation. The  $\mathbf{b}_i$  and  $\mathbf{u}_i$  are unknown vectors of the fixed effects and effects of sires and maternal grandsires of each trait, respectively. The  $\mathbf{e}_i$  is a residual vector. The fixed effects considered for ultrasonic measurements were birth place(4 levels), testing year (5 levels), and testing season (4 levels). Age at the end of testing was included as a covariable. For carcass traits, slaughter year (5 levels), sex (2 levels), carcass market (5 levels), feeding place (12 levels), and slaughter age as a covariable were considered. The number of evaluated sires and maternal grandsires was 47, of which 29 were identified

as both sire and maternal grandsire, 18 as sire only and no bull served as maternal grandsire only. Numbers of sires in each data set are summarized in Tabel 3, where it should be noticed that out of the evaluated 47 sires, 26 served in both performance testing and field, no bull in performance testing only and 21 in field only. An average inbreeding coefficient of these 47 sires was 7.7% (maximum 37.9%) and an average relationship coefficient among sires was 12.3% (maximum 75.1%).

As both ultrasonic measurements and carcass traits were recorded on different animals in different environments and performance tested bulls used in this study have not yet produced their progeny, only additive genetic relationships among sires connected these 2 types of data sets. The variances and covariances for the model were assumed to be as follows :

$$\mathbf{Var}\begin{bmatrix}\mathbf{u}_{1}\\\mathbf{u}_{2}\\\mathbf{e}_{1}\\\mathbf{e}_{2}\end{bmatrix} = \begin{bmatrix}\mathbf{A\sigma}^{2}_{s_{1}} & \mathbf{A\sigma}_{s_{12}} & \mathbf{0} & \mathbf{0}\\\mathbf{A\sigma}_{s_{21}} & \mathbf{A\sigma}^{2}_{s_{2}} & \mathbf{0} & \mathbf{0}\\\mathbf{0} & \mathbf{0} & \mathbf{D}_{1} & \mathbf{0}\\\mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{D}_{2}\end{bmatrix} = \begin{bmatrix}\mathbf{G} & \mathbf{0}\\\mathbf{0} & \mathbf{R}\end{bmatrix},$$

where **A** stands for the numerator relationship matrix among bulls, which included both sires and maternal grandsires. The  $\sigma^2_{\mathbf{S}_i}$  and  $\sigma_{\mathbf{S}_{ij}}$  are sire variance and covariance between traits, assuming  $\sigma^2_{\mathbf{S}_i} = \sigma^2_{\mathbf{a}_i}/4$ , where  $\sigma^2_{\mathbf{a}_i}$  is an additive genetic variance. Matrix **A** was calculated using all available information from the pedigree file in the Wagyu Registry Association. Matrix **D**<sub>i</sub> is a diagonal matrix with kth element as follows :

$$\begin{aligned} \sigma^2_{e_i} - \sigma^2_{s_i}/4 & \text{if both sire and mater-}\\ & \text{nal grandsire are known}\\ \mathbf{d}_{ik} = & \sigma^2_{e_i} & \text{if only sire is known}\\ & \sigma^2_{e_i} + 3 \sigma^2_{s_i}/4 & \text{if only maternal grand-}\\ & \text{sire is known} \end{aligned}$$

where  $\sigma_{e_i}^2$  is a residual variance. Mixed model equations to be solved were as follows :

$\mathbf{X}_{1}^{'}\mathbf{D}^{1}\mathbf{X}_{1}$	0	$\mathbf{X}_{1}^{'}\mathbf{D}^{1}\mathbf{Z}_{1}$	ך 0
0	$X_{2}^{'}D^{2}X_{2}$	0	$X_{2}D^{2}Z_{2}$
$\mathbf{Z}_{1}^{'}\mathbf{D}^{1}\mathbf{X}_{1}$	0	$Z_1^{'}D^1Z_1 + s^{11}A^{-1}$	s <sup>12</sup> A <sup>-1</sup>
-0	$\mathbf{Z}_{2}^{'}\mathbf{D}^{2}\mathbf{X}_{2}$	$s^{21}A^{-1}$	$\mathbf{Z}_{2}^{'}\mathbf{D}^{2}\mathbf{Z}_{2} + \mathbf{s}^{22}\mathbf{A}^{-1}$
۲ĵ	יין ר <u>א</u>	$\mathbf{D}^{1}\mathbf{y}_{1}$	
b	$ _2  _   X_2$	$\mathbf{D}^2 \mathbf{y}_2$	
ũ	$\mathbf{z}_{1} = \mathbf{z}_{1}$	$\mathbf{D}^{1}\mathbf{y}_{\mathbf{I}}$	
Lũ	,」 LZ,	$\mathbf{D}^2 \mathbf{y}_2 \rfloor$	

where  $s^{ij}$  is the element of the inverse matrix of sire variance and covariance matrix, and  $\mathbf{D}^i$  is the inverse of  $\mathbf{D}_i$ . Estimation of variance and covariance components was carried out between all pairwise combinations of ultrasonic measurements and carcass traits. We had 12 different ultrasonic measurements and 6 different carcass traits, so 72 analyses were conducted to find all the combinations of genetic correlations. As such, heritability was calculated 6 times for each ultrasonic measurement and 12 times for each carcass trait. Heritability estimates were expressed as averages of these 6 estimates for each ultrasonic measurement and 12 for each carcass trait.

Variance and covariance components were estimated iteratively by restricted maximum likelihood (REML) procedure (PATTERSON and THOMPSON<sup>10</sup>; HENDERSON<sup>7</sup>); SCHAEFFER<sup>13</sup>). The quadratic form for estimation of the residual

Ultrasonic S				+		S-										
mea- surements	;	М	+			М	-			M	[+			M		
Field	S	+	S		S	+	S	_	S	+	S		S	+	S	-
traits	M +	M —	M+	M-	M +	M —	M+	M	M+	M	M+	M –	M+	M-	M+	M-
No. of sires	9	0	1	0	2	6	0	0	8	0	0	0	9	12	0	_

Table 3. Number of evaluated sires in data set

S+, S-: served or not served as sire in each trait, respectively.

M+, M-: served or not served as MGS in each trait, respectively.

was as follows :

### $\operatorname{tr}(\mathbf{P}_{i}\mathbf{R}) = \tilde{\mathbf{e}}'\mathbf{P}_{i}\tilde{\mathbf{e}} + \operatorname{tr}(\mathbf{P}_{i}\mathbf{W}\mathbf{C}\mathbf{W}'),$

where  $\mathbf{P}_i = \mathbf{R}^{-1}\mathbf{D}_i\mathbf{R}^{-1}$  (i=1, 3),  $\mathbf{W} = [\mathbf{X} : \mathbf{Z}]$ , and C is the inverse of the coefficient matrix, respectively. The quadratic form necessary for between sire variances and covariances was as follows:

#### $\operatorname{tr}(\mathbf{Q}_{i}\mathbf{G}) = \tilde{\mathbf{u}}'\mathbf{Q}_{i}\tilde{\mathbf{u}} + \operatorname{tr}(\mathbf{Q}_{i}\mathbf{C}^{*}),$

where  $\mathbf{Q}_i = \mathbf{G}^{-1}\mathbf{G}_i\mathbf{G}^{-1}$  (i=1, 3), and tr ( $\mathbf{Q}_i\mathbf{C}^*$ ) is the trace of the product of  $\mathbf{Q}_i$  and  $\mathbf{C}^*$ , which is a random part of the inverse of the coefficient matrix.

Iteration was stopped at  $(\mathbf{k}+1)^{\text{th}}$  iteration round when  $\|\mathbf{\tilde{u}}_{i}^{k+1}-\mathbf{\tilde{u}}_{i}^{k}\|/\|\mathbf{\tilde{u}}_{i}^{k+1}\| < 1.0^{-8}$  was satisfied.

Approximate standard errors of heritability estimates were calculated as suggested by SWIGER *et al.*<sup>14)</sup> and of genetic correlations were as suggested by FALCONER<sup>5)</sup>.

#### **Results and Discussion**

Table 1 contains heritability estimates of ultrasonic measurements. Most of the heritability estimates of ultrasonic measurements were higher at the end of testing than at the beginning. The estimates were low to moderate except for SFTu and RTu at the end of testing. At the end of testing heritabilities of 0.20 for 7 -REAu, 0.18 for 13-REAu, 0.58 for SFTu, and 0.15 for BMSu were obtained. Our results for REAu were similar to the value of 0.21 estimated from various breeds by ROBINSON et al<sup>11)</sup>. ARNOLD et al.<sup>1)</sup> reported heritability estimates of ultrasonic measurements in Hereford at an average of 369 days of age. In their study, heritability of longissimus muscle area and backfat thickness adjusted to constant age were estimated at 0.28 and 0.26, respectively. Compared with their study, heritability of REAu was lower and SFTu was much higher in our study, although their estimates were from both bulls and heifers. A higher heritability estimate for SFTu indicates that large genetic variability exists in fat deposition even for yearlings and thus Japanese Black seems to

be a comparatively early-maturing breed.

Heritability estimates of field carcass traits are shown in Table 2. Heritability of CWc, REAc, SFTc and BMSc were estimated at 0.25, 0.52, 0.55, and 0.56, respectively. In this study, heritabilities of carcass traits were higher than those of ultrasonic measurements. ARNOLD et al.<sup>1)</sup> also found higher heritabilities of carcass traits than those of ultrasonic measurements. Although the reason for this is not clear, it may be due to the fact that performance tested bulls that were ultrasonically measured were not old enough to fully express their genetic potentials. In other words, they were still growing in terms of muscle and fat content. This is especially true for those measurements concerning fat deposition like marbling score. However, as we could observe, they showed fairly large phenotypic differences among individual bulls. ROBINSON et al.<sup>11)</sup> reported that measurements of longissimus ultrasonic muscle area were not as accurate as careful carcass measurements, so some reduction in heritability might be expected. Heritability of CWc was similar to the values of 0.31 reported by LAMB et al.<sup>9)</sup> and 0.24 reported by ARNOLD et  $al^{(1)}$ . But the value of 0.56 for BMSc in our study was higher compared to other literature, 0.40 by Koch et al.<sup>8)</sup> or 0.23 by Woodward et  $al.^{16}$ . This indicates that in Japanese Black cattle a large genetic variability still remains, which may be utilized for the improvement of marbling score.

In Table 4 genetic correlations between ultrasonic measurements at the beginning of performance testing and carcass traits, and in Table 5 the correlations between the measurements at the end of testing and carcass traits are shown.

From Table 4 REAu at both 7th and 13th rib sections at the beginning of performance testing had high genetic correlations (0.71 and 0.70, respectively) to REAc. Also at the end of performance testing (Table 5), those ultrasonically measured REAu were highly correlated with

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REAc (0.52 and 0.66, respectively). This suggests some possibilities of the improvement for longissimus muscle area by the introduction of

ultrasound into performance testing. Most Japanese consumers prefer marbled beef, so beef with a higher degree of marbling has

Table 4. Genetic correlations between ultrasonic measurements at the beginning of testing and field carcass traits

	Field carcass trait <sup>a</sup>									
	CWc	REAc	RTc	SFTc	YEc	BMSc				
Ultrasonic measur	rement <sup>b</sup>									
7-REAu	0.18	0.71	0.48	-0.75	0.54	0.27				
	(0.400)°	(0.190)	(0.316)	(0.168)	(0.267)	(0.357)				
13-REAu	0.08	0. 70	0.24	-0.21	0.50	-0.19				
	(0.482)	(0. 234)	(0.452)	(0.431)	(0.328)	(0.435)				
RTu	0.59	0.26	0.72	0. 23	0. 15	0.90				
	(0.234)	(0.313)	(0.171)	(0. 316)	(0. 317)	(0.062)				
SFTu	-0.38	0.06	-0.72	0.33	0.08	-0.68				
	(0.416)	(0.453)	(0.232)	(0.402)	(0.437)	(0.242)				
IMFTu	0. 37	-0.53	0.07	-0.00	—0. 29	0.69				
	(0. 435)	(0.336)	(0.494)	(0.468)	(0. 416)	(0.245)				
BMSu	0. 25	0. 29	-0.00	-0.15	0.35	0. 25				
	(0. 370)	(0. 338)	(0.388)	(0.359)	(0.314)	(0. 343)				

<sup>a</sup> CWc : carcass weight, REAc : longissimus muscle area, RTc : rib thickness, SFTc : subcutaneous fat thickness, YEc : yield estimate, BMSc : beef marbling score.

<sup>b</sup>7-REAu : longissimus muscle area at 7th rib, 13-REAu : longissimus muscle area at 13th rib, RTu : rib thickness, SFTu : subcutaneous fat thickness, IMFTu : intermuscular fat thickness, BMSu : beef marbling score.

° Standard errors.

*Table 5.* Genetic correlations between ultrasonic measurements at the end of testing and field carcass traits

	Field carcass trait <sup>a</sup>									
	CWc	REAc	RTc	SFTc	YEc	BMSc				
Ultrasonic measu	rement <sup>b</sup>									
7-REAu	0.10	0.52	0.05	-0.21	0.35	0.39				
	(0.372)°	(0.257)	(0.370)	(0.334)	(0.298)	(0.296)				
13-REAu	0. 29	0.66	0. 55	-0.75	0,56	0.51				
	(0. 367)	(0.213)	(0. 276)	(0.165)	(0,251)	(0.276)				
RTu	0. 39	0.11	0.48	-0.02	0.07	0.11				
	(0. 212)	(0.231)	(0.191)	(0.232)	(0.225)	(0.230)				
SFTu	-0.75	0.30	-0.37	-0.54	0. 40	0.35				
	(0.102)	(0.199)	(0.199)	(0.156)	(0, 179)	(0.191)				
IMFTu	-0.03	-0.07	-0.20	-0.30	0.06	0.48				
	(0.436)	(0.406)	(0.414)	(0.369)	(0.394)	(0.313)				
BMSu	0.14	0. 12	-0.29	0.64	0. 12	-0.31				
	(0.421)	(0. 397)	(0.390)	(0.235)	(0. 384)	(0.361)				

<sup>a</sup> CWc : carcass weight, REAc : longissimus muscle area, RTc : rib thickness, SFTc : subcutaneous fat thickness, YEc : yield estimate, BMSc : beef marbling score.

<sup>b</sup>7-REAu : longissimus muscle area at 7th rib, 13-REAu : longissimus muscle area at 13th rib, RTu : rib thickness, SFTu : subcutaneous fat thickness, IMFTu : intermuscular fat thickness, BMSu : beef marbling score.

°Standard errors.

higher economic merits on the market. Consequently it is most important to improve marbling ability of sires. The ultrasonic measurements, which were highly correlated with marbling score of carcass measurement, were SFTu, IMFTu, RTu at the beginning of testing, and 13-REAu at the end of testing. Of these measurements, a genetic correlation of 0.90 was obtained between RTu at the beginning of testing and BMSc. However, the correlations concerning about fat deposition indicators such as SFTu or BMSu at different testing stages did not indicate favorable or consistent relationships with SFTc or BMSc during performance testing. For example SFTc correlated negatively to SFTu both at the beginning and the end of performance testing. Carcass beef marbling score correlated positively to BMSu at the beginning of testing and negatively at the end of testing. One reason to explain this phenomenon is the ability of ultrasonic equipment. BRETHOUR<sup>2)</sup> reported that ultrasonic measurements on marbling score was about 80% accurate in grade classification if borderline cattle were omitted and BRETHOUR<sup>3)</sup> also reported that ultrasonic estimates for backfat were at least equal to and perhaps more accurate and precise than the carcass measure. However Japanese Black cattle have a generally superior marbling ability compared with other European breeds. As such, it is more difficult to estimate marbling score in detail by ultrasound in Japanese Black cattle.

Other reasons may be the age at scanning and differences in feeding systems. Performance tested bulls were fed mainly by roughage to avoid deposition of excess fat compared to the fattened animals used for carcass traits. This may disturb the expression of marbling in bulls. As mentioned earlier fat, as a tissue, tends to be fully developed lately, which makes its genetic relationships with other traits dependent on age at measurement. HARADA *et*  $al.^{6}$ , using multiple regression analysis that included not only ultrasonic but body measurements as independent variables, reported ultrasonic longissimus muscle area at 12 months of age explained 74.5% of total phenotypic variation in measurements at 22 months of age, but in the case of ultrasonic beef marbling score only 29.3% of total phenotypic variation was explained by measurements at 12 months of age. Our study also showed that beef marbling score at same age of 12 months was not closely related to beef marbling score at 28 months of age. It was not clear if age at ultrasonic scanning was optimal. These may cause difficulties for screening superior bulls on the basis of marbling ability during the performance testing period.

To maximize genetic improvement using ultrasound, it is necessary to initially clarify the genetic relationships that exist between those live animal measurements and the end products in beef industry, carcass characteristics. In this respect the application of ultrasound in beef cattle production becomes important. One problem at performance testing is the lack of any selection criteria on carcass characteristics. As the capacity for progeny testing in the station is limited, a strong selection has to be applied at performance testing. It is difficult to expect enough improvement from the selection with high intensity and without criteria because only station tested bulls, at least performance tested, are used in the field. Ultrasound has the potential to solve these problems. The results obtained in this study indicate that longissimus muscle area is a suitable trait, on which selection pressure can be applied at the time of performance testing. Additional studies are needed to estimate genetic parameters accurately and to determine the most effective way to utilize this technology for the genetic improvement of carcass characteristics.

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Relationships between Ultrasonic and Carcass Traits

## 黒毛和種における直接検定時の超音波推定値と現場 枝肉形質との遺伝的関連性

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黒毛和種の直接検定時における超音波推定値と,肥育現場から収集された枝肉形質問の遺伝的関連性 を推定した.超音波測定には鹿児島県畜産試験場において直接検定を受検した154頭の雄牛を用い,直 接検定の開始時および終了時に第6-7肋骨間ロース芯面積(7-REAu),第12-13肋骨間ロース芯面積 (13-REAu),バラの厚さ(RTu),皮下脂肪厚(SFTu),筋間脂肪厚(IMFTu)および脂肪交雑評点 (BMSu)を測定した.現場枝肉形質は同県下から収集された4,725頭の枝肉格付成績のうち枝肉重量 (CWc),ロース芯面積(REAc),皮下脂肪厚(SFTc),バラの厚さ(RTc),推定歩留(YEc)および 脂肪交雑評点(BMSc)の6形質を用い,2形質の種雄牛・母方祖父モデルによるREML法により,分 散・共分散成分の推定を行なった.検定終了時の遺伝率は、7-REAuで0.20,SFTuで0.58および BMSuで0.15,CWcで0.25,REAcで0.52,SFTcで0.55およびBMScで0.56と推定された.REAu とREAcとの遺伝相関は0.52から0.71と高い正の係数を示したが、SFTに関しては両者間に負,また BMSに関しては直接検定開始時には正,終了時には負の遺伝相関が認められた.以上のように検定期間 中を通じて一定の遺伝的関連性を示さない形質も認められたが,直接検定時に超音波測定を導入するこ とにより,現場枝肉形質のロース芯面積を改良できる可能性が示された.

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