Genetic Relationship between Ultrasonic and Carcass Measurements for Meat Qualities in Korean Steers

D. H. Lee* and H. C. Kim[1]

Department of Animal Life and Resources, Hankyong National University, Korea

ABSTRACT : Real time ultrasonic measurements for 13th rib fat thickness (LBF), longissimus muscle area (LEMA) and marbling score (LMS) of live animal at pre-harvest and subsequent carcass measurements for fat thickness (BF), longissimus muscle area (EMA), marbling score (MS) as well as body weight of live animal, carcass weight (CW), dressing percentage (DP), and total merit index (TMI) on 755 Korean beef steers were analyzed to estimate genetic parameters. Data were analyzed using multivariate animal models with an EM-REML algorithm. Models included fixed effects for year-season of birth, location of birth, test station, age of dam, linear and quadratic covariates for age or body weight at slaughter and random animal and residual effects. The heritability estimates for LEMA, LBF and LMS on RTU scans were 0.17, 0.41 and 0.55 in the age-adjusted model (Model 1) and 0.20, 0.52 and 0.55 in the weight-adjusted model (Model 2), respectively. The Heritability estimates for subsequent traits on carcass measures were 0.20, 0.38 and 0.54 in Model 1 and 0.23, 0.46 and 0.55 in Model 2, respectively. Genetic correlation estimate between LEMA and EMA was 0.81 and 0.79 in Model 1 and Model 2, respectively. Genetic correlation estimate between LBF and BF were high as 0.97 in Model 1 and 0.98 in Model 2. Real time ultrasonic marbling score were highly genetically correlated to carcass MS of 0.89 in Model 1 and 0.92 in Model 2. These results indicate that RTU scans would be alterative to carcass measurement for genetic evaluation of meat quality in a designed progeny-testing program in Korean beef cattle. *(Asian-Aust. J. Anim. Sci. 2004. Vol 17, No. 1 : 6-12)*

Key Words : Real-time Ultrasound, Korean Beef Cattle, Carcass, Genetic Parameters

INTRODUCTION

Real time ultrasound (RTU) has been used to assess meat quality of live animal in beef cattle. Assessment for meat qualities of live animal is considered the time- and cost-effective method for genetic evaluation of carcass merit in beef cattle (Wilson, 1992). The potential of this technology has been well reported by many authors (Herring et al., 1998; Moser et al., 1998; Reverter et al., 2000; Devitt and Wilton, 2001). Since 1992, actual carcass data from well designed progeny-testing program in Korean beef cattle have been used to estimate expected progeny differences (EPD) for carcass traits. However, these programs are required costly and timely endeavor and consumption. If meat quality in live animal were well determined by ultrasound scans and ultrasound EPD were accurately predicted, these criteria could be used for selecting superior bulls. Prerequisite is that reliable heritability and genetic relationships among steer ultrasound and the subsequent carcass traits must be determined. Thus, the objective of this study was to estimate the genetic and environmental relationships between carcass traits from live animal RTU and subsequent real carcass traits from slaughter in Korean steers.

* Corresponding Author: D. H. Lee. Tel: +82-31-670-5091, Fax: +82-31-676-5091, E-mail: dhlee@hnu.hankyong.ac.kr

1 National Livestock Research Institute, RDA, Korea.

MATERALS AND METHODS

Data and analysis

Real-time ultrasonic scans were assessed and carcass measures investigated from 755 heads randomly selected from steers which were born at 1999 through 2000 and involved on the well designed progeny-testing program of Korean cattle in Korea. Real-time Ultrasounds of 755 steers were scanned at 7-14 d before slaughter (average 24 mo) by expert technicians.

Ultrasound measurements were obtained from the Pie 200 SLC Scanner unit, which used the 18 cm, 3.5 MHz linear array transducer (Pie medical systems, Model ASP-18). This transducer allowed the entire longissimus muscle to be scanned in a single image. Single image by this equipment on 13th rib rump scanned were interpreted and assessed by an experienced technician. Data on individual longissimus muscle area and fat thickness were obtained by assessment by way of imaging software program. Otherwise, data of marbling scores were obtained by comparing to standard references, which described the score according to degree of marbling, by an expert technician. All animals represented in the data set had both carcass and ultrasound measurements. Carcass data represented for meat quality and grade were measured and assessed by meat grade technicians on 13th rib site of bisect chilled carcass at abattoir. Carcasses were weighed after chilling of carcasses for 12 h. Dressing percentages were calculated carcass weights divided by weights of live animals before

Table 1. Simple statistics of real-time ultrasound measure and carcass measures for meat quality in Korean steers

	Mean	SD	Min.	Max.
Age at slaughter (days)	724.84	20.08	652	772
BW24 (kg)	520.55	54.40	320	690
CW (kg)	301.91	34.81	183	443
DP (%)	57.97	2.15	47	77
EMA (cm²)	74.74	8.30	50	103
BF (mm)	7.22	3.29	2	26
MS (score)	3.07	1.61	1	7
TMI ($/kg)	8.93	1.80	5.14	13.67
LEMA (cm²)	74.08	7.57	51	101
LBF (mm)	6.87	2.67	2.3	23.1
LMS (score)	3.31	1.43	1	7

slaughter. Meat price ($) per unit of carcass weight determined by a successful bidder at abattoir was regarded to total merit index. All slaughtering processes and measures of carcass quality and grade were performed in accordance with the guideline for meat grading system provided by ministry of agriculture in Korea. Data were edited according to the progeny-testing program of Korean cattle. Pedigree was traced back up to 4 generation to find the known ancestors. Animals disconnected through pedigree and year-season were deleted from the analyses. The final data sets consisted of RTU and carcass measurement of 755 steers.

Variance component estimation

Heritabilities and genetic correlations were estimated for nine traits: carcass weight (CW), dressing percentage (DP), longissimus muscle area (EMA), fat thickness (BF), marbling score (MS), total merit index (TMI), RTU longissimus muscle area (LEMA), RTU fat thickness (LBF), RTU marbling score (LMS). Data were analyzed with two multivariate animal models using software that used an EM-REML algorithm (REMLF90; Misztal, 2001) to obtain the (co)variance component estimates. The first model (Model 1) possessed all nine traits with fixed effects for location at birth, progeny-testing station, year-season, age of dam, covariates of linear and quadratic effects for slaughtering ages, and a random direct additive genetic effect due to animal. The second model (Model 2) included with corresponding nine traits maintained same fixed and random effects with those on Model 1 except pre-harvest live weights rather than slaughtering ages as covariates. This was an effort to view potential changes in either heritabilities or genetic correlations for any trait that may be highly weight dependent. There were 3,387 animals represented in the resulting relationship matrix, consisting of 755 slaughter progeny and 2,632 parents and ancestors without records. The models were expressed as
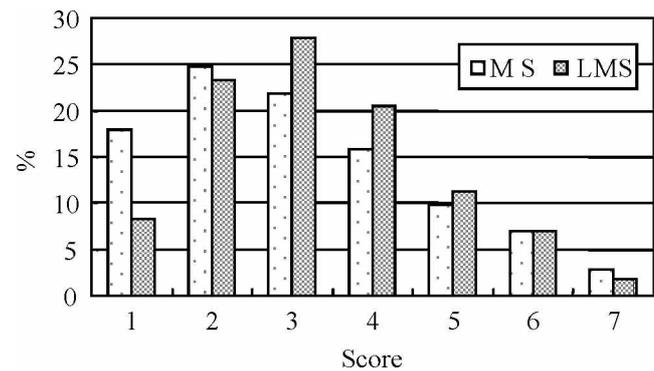
$$y_i = X_i\beta_i + Z_i a_i + e_i$$

Figure 1. Proportions of marbling scores measured by ultrasound in live animal (LMS) and carcass (MS) in Korean steers.

where, y_i=vector of observations for trait i

X_i=matrix that relates fixed effects to measurements for trait i

β_i=vector of unknown fixed effects for measures of trait i

Z_i=matrix that relates animal of record to measurements for trait i

a_i=vector of random animal effects for measures of trait i

e_i=vector of residual effects for measures of trait i

It was assumed to correlate among the genetic and residual effects of all traits considered.
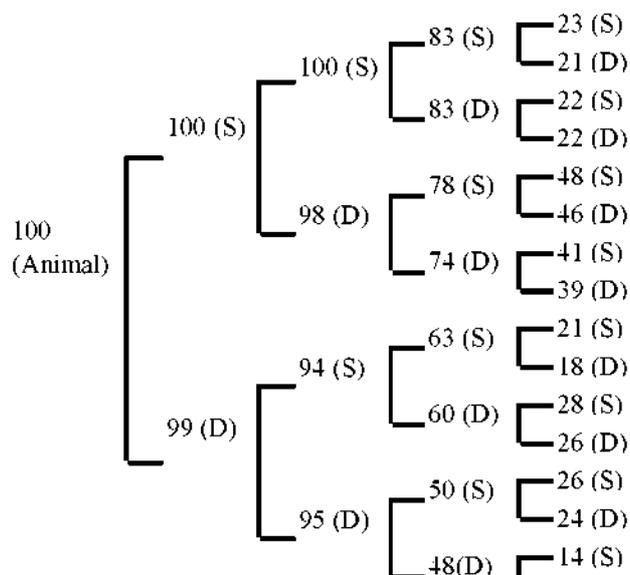
RESULTS AND DISCUSSION

Summary statistics

Table 1 shows the mean, SD, minimum and maximum for each trait and age at slaughter. The average age of steers at the slaughter was 724.8 d (23.8 mo) and all animals tested in present study were scanned within a couple of weeks before slaughter. The average live weight at slaughter was 520 kg with range of 320-690 kg, whereas the average of carcass weight was 302 kg. The average of dressing percentage, longissimus muscle area, fat thickness, and marbling score measured at 13th rib were 57.97%, 74.74 cm², 7.22 mm and 3.07 scores, respectively. Similarly, the average of RTU longissimus muscle area, RTU fat thickness, and RTU marbling score scanned at same point as carcass measures were 74.08 cm², 6.87 mm, and 3.31 scores, respectively. These results showed little change in the average of RTU scans and carcass measurements. The average of total merit index indicated the price offered by a successful bidder at abattoir was $8.93 per carcass kg.

Proportions of each marbling score by RTU scans and carcass measurement were shown in Figure 1. Distribution property for observations of marbling scores would be violated the normal distribution which were generally assumed for genetic evaluation in animal breeding. However, with comparing marbling scores on Korean bull (Lee et al., 2001), distribution of these scores looked like to be shown as much expand and approach to normalize.

Table 2. F-statistics and significant level for each trait by effects in Korean steers

Source	DF	CW	DP	EMA	BF	MS	TMI	LBF	LEMA	LMS
Year-Season	6	7.19**	7.45**	10.66**	4.66**	12.34**	175.3**	7.13**	13.38**	8.19**
Loc. at birth	8	3.16**	0.83	1.53	2.28*	0.97	1.13	2.26*	2.05*	0.99
Loc. at test	1	6.25*	8.42**	0.07	18.75**	9.23**	1.89	20.7**	2.09	3.14***
Age of dam	9	0.98	1.12	1.71***	0.78	0.84	0.53	0.81	1.83***	0.60
Age at slaughter.	1	29.35**	4.01*	13.61**	0.82	2.99***	0.08	2.62	15.14**	2.09

* p<0.05, ** p<0.01, *** p<0.10.

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                                           ┌─ 23 (S)
                               ┌─ 83 (S) ──┤
                    ┌─ 100 (S)─┤           └─ 21 (D)
                    │          │           ┌─ 22 (S)
          ┌─ 100 (S)┤          └─ 83 (D) ──┤
          │         │                      └─ 22 (D)
          │         │          ┌─ 78 (S) ──┬─ 48 (S)
          │         └─ 98 (D) ─┤           └─ 46 (D)
  100     │                    │           ┌─ 41 (S)
 (Animal) ┤                    └─ 74 (D) ──┤
          │                                └─ 39 (D)
          │                    ┌─ 63 (S) ──┬─ 21 (S)
          │         ┌─ 94 (S) ─┤           └─ 18 (D)
          │         │          │           ┌─ 28 (S)
          └─ 99 (D) ┤          └─ 60 (D) ──┤
                    │                      └─ 26 (D)
                    │          ┌─ 50 (S) ──┬─ 26 (S)
                    └─ 95 (D) ─┤           └─ 24 (D)
                               └─ 48(D) ───┬─ 14 (S)
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Furthermore, scoring system here represented the degree of intramuscular fat are categorized 1 (lowest marbling) to 7 (highest marbling).

Pedigree information

The 755 steers in the final data set were produced by 132 different sires averaging 5.72 progeny per sire. Figure 2 presented the proportions of known ancestors up to four generation according to paternal and maternal lineage. As shown Figure 2, 74-83 percentages of ancestors up to 3 generations were known in paternal lines and 48-63 percentages of ancestors up to 3 generation were known in maternal lines. These results illustrate good record keeping system on lineage with taking into account of history for a progeny-testing program of Korean beef cattle in Korea.

Fixed effects

Individual year-season of birth was highly significant (p<0.01) for all traits considered. Location of birth was highly significant (p<0.01) for CW and moderately significant (p<0.05) for BF and LBF. Otherwise, Test station was significant for CW, DP, BF, MS and LBF. This would be due to the difference of management and environmental conditions. The effects of age of dam were not significantly affected for all traits. The highly significant differences (p<0.01) among regression coefficients of traits for quadratic effects of age of slaughter were for CW, EMA, and LEMA. Otherwise, no difference for linear regression of age at slaughter was for all traits.

Heritabilities

Table 3 summarizes age-adjusted estimates of heritability, genetic and environmental correlation in Model 1. Table 4 also showed weight-adjusted estimates of corresponding parameters in Model 2. Heritability estimates for CW of 0.28 in Model 1 and 0.25 in Model 2 are comparable to other reports. Kemp et al. (2002) cited heritability estimates for carcass weight of 0.48. Lee and Bertrand (2001) reported heritability estimates for carcass weight of 0.22 on Korean bull. The heritability estimate for DP was 0.21 in Model 1 and 0.23 in Model 2. These estimates were lower than estimates of 0.41 by Gibbs sampling (Lee et al., 2001) and 0.34 by REML (Lee and Bertrand, 2001) when used station data of Korean bulls.

The heritability estimate for EMA was 0.20 in Model 1 and 0.23 in Model 2. These estimates were much lower than the estimate of 0.45 in an age-adjusted model reported by Kemp et al. (2002) and Devitt and Wilton (2001) and higher

Table 3. Age-adjusted heritability (diagonal), genetic correlation (upper diagonal), and environmental correlation (below diagonal) estimates for carcass traits measured by real time ultrasound on live animals and carcass measurement in Korean steers

	CW	DP	EMA	BF	MS	TMI	LEMA	LBF	LMS
CW	0.28	0.21	0.43	0.08	0.39	0.37	0.55	0.12	0.10
DP	0.43	0.21	-0.10	0.57	0.05	-0.12	0.35	0.60	-0.23
EMA	0.55	0.35	0.20	-0.50	0.16	0.43	0.81	-0.44	0.20
BF	0.50	0.14	0.28	0.38	0.18	-0.21	-0.17	0.97	-0.08
MS	0.04	0.12	0.24	0.03	0.54	0.89	0.28	0.31	0.89
TMI	0.06	0.22	0.27	-0.01	0.55	0.57	0.43	-0.07	0.91
LEMA	0.55	0.29	0.74	0.34	0.14	0.14	0.17	-0.09	0.17
LBF	0.52	0.13	0.31	0.78	-0.04	-0.01	0.35	0.41	0.05
LMS	0.04	0.09	0.07	0.19	0.55	0.11	0.07	0.05	0.55

Table 4. Weight-adjusted heritability (diagonal), genetic correlation (upper diagonal) and environmental correlation (below diagonal) estimates for carcass traits measured by real time ultrasound on live animals and carcass measurement in Korean steers

	CW	DP	EMA	BF	MS	TMI	LEMA	LBF	LMS
CW	0.25	0.99	0.16	0.53	0.03	-0.10	0.58	0.61	-0.18
DP	0.98	0.23	0.13	0.52	0.05	-0.09	0.58	0.60	-0.17
EMA	0.28	0.31	0.23	-0.47	-0.07	0.24	0.79	-0.36	0.11
BF	0.13	0.12	0.08	0.46	0.09	-0.31	-0.08	0.98	-0.14
MS	0.12	0.11	0.27	0.01	0.55	0.88	0.03	0.20	0.92
TMI	0.17	0.18	0.29	-0.02	0.55	0.55	0.16	-0.18	0.94
LEMA	0.23	0.24	0.66	0.14	0.16	0.17	0.20	0.04	0.04
LBF	0.08	0.08	0.07	0.72	-0.05	-0.01	0.12	0.52	-0.02
LMS	0.07	0.06	0.08	0.22	0.51	0.09	0.09	0.08	0.55

than the estimate of 0.18 by Baik et al. (2002). In addition, Lee and Bertrand (2001) reported the estimate of 0.34 for carcass longissimus muscle area by REML methodology on Korean bulls.

The heritability estimate of 0.34 for BF in Model 1 is similar or slightly low with comparing to other reports. Hassen et al. (1999) and Arnold et al. (1991) cited heritability estimates for carcass fat thickness of 0.42 and 0.49, respectively. Lee and Bertrand (2001) also reported the heritability estimate of 0.43 for carcass fat thickness in an age-adjusted model. Additionally, Wilson et al. (1999) reported a heritability estimate for carcass fat thickness of 0.44 and Koots et al. (1994) summarized 26 studies and reported a weighted average of heritability estimates to be 0.44. Moser et al. (1998) used Brangus field data to estimate a heritability of 0.27 for carcass fat thickness. Kemp et al. (2002) reported the estimate of 0.35 for carcass fat thickness and Wilson et al. (1993) reported an estimate of 0.26 derived from Angus field data.

The heritability estimate of 0.54 for MS is also reported in Table 3. This estimate is within the ranges reported in the literature (Pariacote et al., 1998, 0.88; Crews and Kemp, 2001, 0.55; Devitt and Wilton, 2001, 0.35; Riley et al., 2002, 0.44; Kemp et al., 2002, 0.42). Otherwise, our estimate for MS was higher than the estimate of 0.36 for same trait in Korean bulls reported by Lee and Bertrand (2001). The heritability estimate for TMI that indicated total genetic merit affect to meat unit price was high as 0.57. Total merit index are apparently not heritable trait. However, these index are implied to primary traits affected to meat price by means of indirect selection.

The heritability estimate for LEMA in an age-adjusted model (0.17) was lower than the estimates in literature (Moser et al., 1998, 0.29; Devitt and Wilton, 2001, 0.48; Kemp et al., 2002, 0.29). Crews and Kemp (2001) also reported that heritability estimates for RTU longissimus muscle area were 0.61 and 0.52 in bulls and 0.49 and 0.47 in heifers at 12 and 14 mo. respectively.

For LBF measured at 13th-rib rump, the heritability estimate of 0.41 in an age-adjusted model of this study is close to the estimate of carcass fat thickness in the same

model and comparable to estimate in literature. Moser et al. (1998) estimated heritability of 0.11 for 13th-rib fat thickness on Brangus and Brangus-sired fed steers and heifers. Crews and Kemp (2001) also reported heritability estimates of 0.50 and 0.35 in bulls and 0.44 and 0.49 in heifers for RTU fat depth at 12 and 14 mo. respectively. Additionally, Kemp et al. (2002) also estimated heritability of 0.39 for 13th-rib RTU fat thickness on yearling Angus steers.

The heritability estimates for LMS were 0.55 in the age- and weight-adjusted models of this study. These estimates were close to estimates for carcass marbling scores. These estimates were higher than estimate of 0.48 by REML in a linear model and lower than it of 0.74 by Gibbs sampling in threshold model on Korean steers presented by Yoon et al. (2002). With comparing to estimates in literature, Kemp et al. (2002) reported the estimate of 0.51 for RTU marbling scores on yearling Angus steers. Otherwise, Devitt and Wilton (2001) reported that the age-constant heritability estimate from yearling bull measurements of RTU percentage of intramuscular fat was 0.23 and it from finished steer measurement of marbling score was 0.35. Reverter et al. (2000) also reported that heritability estimate for percentage of intramuscular fat by ultrasound measurement was 0.33 for Angus and 0.20 for Hereford.

Correlations

As shown Table 3 and Table 4, several genetic and environmental correlation estimates among the traits considered were not significant different from zero. These correlation estimates in the age-adjusted model (Model 1) were comparable to their estimates in the weight-adjusted model (Model 2). Genetic and environmental correlation estimates between CW and DP were 0.21 and 0.43, respectively, in age-adjusted animal model (Model 1). Otherwise, in the weight-adjusted model (Model 2), these estimates were 0.99 and 0.98, respectively. These results implied that there was co-linearity between CW and DP.

Genetic correlation estimates between carcass EMA and carcass BF were -0.50 in Model 1 and -0.47 in Model 2. These estimates were comparable to estimate of -0.16 for

corresponding traits on Shorthorn reported by Pariacote et al. (1998). Estimated genetic correlations of carcass EMA with MS were positive but low (0.16) in Model 1 and close to zero (-0.07) in Model 2. These results agree to estimates in literature (Lee et al., 2001, -0.08; Yoon et al., 2002, 0.05). Genetic correlation estimates for carcass MS with carcass BF were 0.18 in Model 1 and 0.09 in Model 2. These estimates are in the range of other studies (Pariacote et al., 1998, 0.20; Lee et al., 2001, 0.35-0.40; Yoon et al., 2002b, 0.17). Otherwise, Yoon et al. (2002b) estimated genetic correlation of 0.46 in threshold animal model on Korean steers. These results suggest that on a weight-constant basis, marbling could not or little genetically correlated with fat thickness. Most of genetic correlations between composition traits on RTU measures were not significantly different from zero. Given the objective of this study, there were great interest of genetic correlation between the actual carcass measurements and the measures captured via RTU scanning. The genetic correlation estimates between carcass EMA and RTU EMA were 0.81 in Model 1 and 0.79 in Model 2. These estimates were higher than other studies in literature. Reasons of high estimates would be come from high accurate measures to be obtained and pre-harvest RTU measurement. Moser et al. (1998) reported the estimate of 0.66 for corresponding correlation and Kemp et al. (2002) estimated genetic correlation of 0.69. Devitt and Wilton (2001) also estimated age-constant genetic correlation between corresponding traits of 0.66. Genetic correlation estimate between carcass BF and RTU BF were 0.97 in Model 1 and 0.98 in Model 2 in present study. These estimates were higher than estimates of 0.88 by Devitt and Wilton (1998) and 0.82 from Kemp et al. (2002). Estimated genetic correlation between carcass MS and RTU MS were 0.89 in Model 1 and 0.92 in Model 2. These estimates indicated a strong, positive genetic relationship between marbling score assigned by trained personnel in the abattoir and the information derived by an experienced technician using RTU technology. Kemp et al. (2002) reported correlation between carcass marbling score and RTU predicted percentage ether extract of 0.90 and 0.94 in an age-adjusted model and an age- and weight-adjusted model, respectively. The strong, positive genetic correlations resulting in present study exhibit the ability of RTU technology to accurately reflect subsequent carcass merit. Thus, RTU presents an opportunity to reduce the amount of time required to collect pertinent data. Real-time ultrasound may allow for more timely data and be an alternative to carcass data collection in carcass progeny testing programs in Korean cattle.

CONCLUSION

The results represented here indicate that real-time ultrasonic imaging can be a substitute for carcass data in genetic evaluation programs. It is evident to highly genetical correlation between RTU scans and carcass measurements. This technique can allow an alternative to a progeny-testing grogram. For making selection decisions regarding potential replacement bulls and heifers for improvement of carcass merit. ultrasound scans by timely through yearling to harvest are needed and assessed genetically.

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