

## Genetic correlation between live body measurements and beef cutability traits in Hanwoo steers

Yun Ho Choy<sup>1,\*</sup>, Jae Goo Lee<sup>1</sup>, Alam Mahboob<sup>1</sup>, Tae Jeong Choi<sup>1</sup>, and Seung Hee Rho<sup>2</sup>

\* **Corresponding Author:** Yun Ho Choy  
**Tel:** +82-41-580-3354, **Fax:** +82-41-582-1248,  
**E-mail:** ychoy000@korea.kr

<sup>1</sup> Division of Animal Breeding & Genetics, National Institute of Animal Science, Cheonan 31000, Korea  
<sup>2</sup> Hanwoo Improvement Center, National Agricultural Cooperative Federation, Seosan 31948, Korea

Submitted Sept 13, 2016; Revised Dec 1, 2016;  
Accepted Feb 25, 2017

**Objective:** The growth, carcass and retail cut yield records on 1,428 Hanwoo steers obtained through progeny testing were analyzed in this study, and their heritability and genetic relationships among the traits were estimated using animal models.

**Methods:** Two different models were compared in this study. Each model was fitted for different fixed class effects, date of slaughter for carcass traits and batch of progeny test live measurement traits, and a choice of covariates (carcass weight in Model 1 or backfat thickness in Model 2) for carcass traits.

**Results:** The differences in body composition among individuals were deemed being unaffected by their age at slaughter, except for carcass weight and backfat thickness. Heritability estimates of body size measurements were 0.21 to 0.36. Heritability estimates of retail cut percentage were high (0.56 from Model 1 and 0.47 from Model 2). And the heritability estimates for loin muscle percentage were 0.36 from Model 1 and 0.42 from Model 2, which were high enough to consider direct selection on carcass cutability traits as effective. The genetic correlations between body size measurements and retail cut ratio (RCR) were close to zero. But, some negative genetic correlations were found with chest girths measured at yearling (Model 1) or at 24 months of age or with chest widths. Loin muscle ratio (LMR) was genetically negatively correlated with body weights or body size measurements, in general in Model 1. These relationships were low close to zero but positive in Model 2. Phenotypic correlation between cutability traits (RCR, LMR) and live body size measurements were moderate and negative in Model 1 while those in Model 2 were all close to zero.

**Conclusion:** Therefore, the body weights or linear body measurements at an earlier age may not be the most desirable selection traits for exploitation of correlated responses to improve loin muscle or lean meat yield.

**Keywords:** Hanwoo; Linear Measurement; Carcass; Retail Cut; Heritability; Genetic Correlation

### INTRODUCTION

Current bull selection programs of Hanwoo focus on the improvement of beef carcass yield and quality, with a higher emphasis on marbling score, which make the final products to be produced at high costs through an elongated feeding period. The greater demands, on the other hand, for loins and sirloins for grilling reflecting Korean beef consumers' choices also influence the wholesale prices of beef retail cuts. Therefore, this often attracts beef retailers in obtaining beef carcass of higher cut proportions instead of the value of whole carcass itself. In the past, several reports were published on the prediction of retail cut production using different approaches, such as ultrasound trait measures [1-5] or direct linear measurements on live animals [6-8]. The linear measurements are particularly useful to understand the growth and frame size of the animals. Therefore, it raises a possibility for a further investigation on how they might contribute genetically to an indirect selection if targeted to a more efficient retail cut production, and thus could

facilitate a selection earlier than the period of progeny testing.

The objective of this study was to estimate the genetic correlation between linear body measurements at different ages (12 and 24 mo) and retail beef cut production of Hanwoo steers.

## MATERIALS AND METHODS

### Data

A total of 1,428 steer records of beef retail cuts collected by Hanwoo Improvement Center of Nonghyup, Korea were analyzed in this study. The steers were born between 2008 and 2012 and slaughtered at 24 months of age after the completion of corresponding (46th to 54th) Hanwoo progeny testing batches. These progeny test steers represented 145 young bulls in the National Hanwoo Improvement System of the Republic of Korea. Live body measures such as body weight (BWT) and 10 linear traits were taken at their yearling (12 mo) and slaughter (24 mo) ages.

Traits studied were yearling weight (YWT), BWT, chest girth (CG), body length (BL), chest depth (CD), chest width (CW), hip width (HW), rump width (RW), retail cut ratio (RCR), loin muscle ratio (LMR), cold carcass weight (CWT), and carcass backfat thickness (BFT). Trait details are presented in Table 1. The CG, BL, CD, HW, and RW traits were included in this study as an account for frame size which was associated with muscle mass growth. Cold carcass measurements were collected post-mortem after an overnight chilling of the hot carcass. Beef carcass grading was performed at the same time. Ten primal cuts were obtained from all carcass samples according to the regulations

once they were sent to a processing plant after completion of beef grading (see details in Choi et al [9]). The primal cut weights were recorded accordingly. The ratio of loin and sirloin together, also expressed as LMR, were calculated as the weight ratio of each cut to the total weight of retail cuts. However, the ratio of the retail cut indicates the ratio of sum weight of primal cuts to the respective carcass weight of the slaughtered animals in this study.

In Hanwoo progeny testing, each batch of animals is measured at an approximate 90 days interval when all animals attain a target test age on average. Therefore, as some animals differ from an exact test age during each test period, all BWT measures were pre-adjusted linearly from their previous live measurements. For YWT and BWT at 24 months of age, they were adjusted by a linear growth function of average daily gain through multiplying days and average daily gain from weight at 6 mo and 18 mo measures, respectively. A brief on the datasets and pedigree structure is shown in Table 2.

**Table 2.** General statistics on data and pedigree structure

Item	No. of records/ levels
Total phenotypic records	3,383
Number of animals in the pedigree	16,022
Number of inbred animals in the pedigree	2,497
Average inbreeding coefficient of inbred animals (%)	1.8223
Contemporary group (batches of progeny) size for live body measures	19
Contemporary group (date of slaughter) size for carcass traits	175

**Table 1.** Summary statistics of live body measurements and beef carcass cut ratios

Trait	Age (mo)	Abbr <sup>1)</sup>	N	Mean	SD	CV	Min	Max
Body weight (kg) <sup>2)</sup>	12	YWT	10,516	350.00	39.79	11.37	157.37	535.90
	24	BWT	3,373	672.12	74.62	11.10	370.50	1,002.4
Body length (cm)	12	BL12	9,837	132.25	6.47	4.89	109	146
	24	BL24	3,420	156.02	6.65	4.26	138	171
Chest depth (cm)	12	CD12	9,804	61.49	2.79	4.53	51	68
	24	CD24	3,430	76.11	3.02	3.96	68	84
Chest width (cm)	12	CW12	43	55.63	6.15	11.06	49	67
	24	CW24	3,432	50.56	3.91	7.73	41	60
Rump width (cm)	12	RW12	9,892	39.20	2.84	7.23	31	46
	24	RW24	3,438	48.67	3.27	6.71	40	57
Chest girth (cm)	12	CG12	9,869	165.21	8.25	5.00	131	183
	24	CG24	3,418	213.64	8.03	3.76	191	234
Hip width (cm)	12	HW12	9,918	21.12	2.54	12.01	14	27
	24	HW24	3,447	25.55	2.11	8.26	20	31
Retail cut (%)	24	RCR	1,425	78.66	3.09	3.92	59.83	89.47
Loin muscle cut (%)	24	LMR	1,425	15.29	1.19	7.79	11.58	21.09
Carcass weight (kg)	24	CWT	5,220	340.97	45.42	13.32	158	518
Backfat thickness (mm)	24	BFT	5,221	8.60	3.74	43.50	1	35

SD, standard deviation; CV, coefficient of variation.

<sup>1)</sup> YWT, yearling weight; BWT, body weight at 24 mo; BL12, body length at 12 mo; BL24, body length at 24 mo; CD12, chest depth at 12 mo; CD24, chest depth at 24 mo; CW12, chest width at 12 mo; CW24, chest width at 24 mo; RW12, rump width at 12 mo; RW24, rump width at 24 mo; CG12, chest girth at 12 mo; CG24, chest girth at 24 mo; HW12, hip width at 12 mo; HW24, hip width at 24 mo; RCR, retail cut ratio; LMR, loin muscle ratio; CWT, cold carcass weight; BFT, backfat thickness.

<sup>2)</sup> Body weights were adjusted for the age (days) at measure.

**Statistical analyses**

The live body measurements and carcass traits were analyzed simultaneously using two different animal models to estimate heritability and genetic correlation coefficients among the traits. Each model differed for a covariate effect, either carcass weight (model 1) or BFT (model 2), fitted to the carcass traits only, which were two cases of slaughter end points tried in the study of Wheeler et al [10] applied over various beef cattle breeds. These covariates were fitted in their first order linear forms. Carcass traits were also fitted with date of slaughter as a fixed effect which defined the effect of contemporary group fed, and the same slaughter and carcass processing environments. For live body measurements, however, respective batches of progeny tests were fitted as a contemporary group irrespective of models. A random animal breeding value effect was fitted with these mixed models as well. The variance and covariance components were estimated using restricted maximum likelihood (REML) based REMLF90 software package [11]. Two mixed model equations for carcass traits and live measurement traits tested for significance of the effects were as follows:

$$\begin{aligned} \text{Model 1} \\ y_{ij} &= \mu + cg_i + BV_j + e_{ij} && \text{(live measurement traits)} \\ y_{ij} &= \mu + cg_i + \beta(CWT_j) + BV_j + e_{ij} && \text{(carcass traits)} \end{aligned}$$

$$\begin{aligned} \text{Model 2} \\ y_{ij} &= \mu + cg_i + BV_j + e_{ij} && \text{(live measurement traits)} \\ y_{ij} &= \mu + cg_i + \beta(BFT_j) + BV_j + e_{ij} && \text{(carcass traits)} \end{aligned}$$

Where,  $y_{ij}$  is the carcass and live measurements of  $j$ th animal of  $i$ th contemporary group. The  $\mu$ ,  $cg$ , are means and fixed contemporary group effects (date of slaughter or batch of progeny test), respectively, The  $CWT$  and  $BFT$  are the covariate terms for  $j$ th animal and  $\beta$  is the partial regression coefficients related to each term. The  $BV_j$  is the random breeding value of  $j$ th animal. The  $e_{ij}$  is the random residual of the model.

The above two models can also be expressed using the same matrix notation for multivariate mixed models:

$$y = X\beta + Zu + r$$

or

$$\begin{bmatrix} y_1 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} X_1 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & X_n \end{bmatrix} \begin{bmatrix} \beta_1 \\ \vdots \\ \beta_n \end{bmatrix} + \begin{bmatrix} Z_1 & \dots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \dots & Z_n \end{bmatrix} \begin{bmatrix} u_1 \\ \vdots \\ u_n \end{bmatrix} + \begin{bmatrix} r_1 \\ \vdots \\ r_n \end{bmatrix}$$

Where  $y$  is a vector of the observations for all  $n$  traits ( $y_1, y_2, \dots, y_n$ )<sup>T</sup>;  $\beta$  is a vector of fixed effect solutions ( $\beta_1, \beta_2, \dots, \beta_n$ )<sup>T</sup> for each trait (date of slaughter for carcass traits and batch of progeny tests for BWT and frame size measurement traits) and covariates (carcass weight in Model 1 and BFT in Model 2);  $u$  is

a vector of random additive genetic effect solutions (breeding values) for all  $n$  traits ( $u_1, u_2, \dots, u_n$ )<sup>T</sup>;  $r$  is a vector of random residuals ( $r_1, r_2, \dots, r_n$ )<sup>T</sup>; and,  $X$  and  $Z$  are incidence matrices that relate observations to fixed and random effects  $\beta$  and  $u$ , respectively.

And the covariance structure of random effects assumed was

$$\begin{bmatrix} u_1 \\ \vdots \\ u_n \\ r_1 \\ \vdots \\ r_n \end{bmatrix} = \begin{bmatrix} g_{11}A & \dots & g_{1n}A & 0 & \dots & 0 \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ g_{n1}A & \dots & g_{nn}A & 0 & \dots & 0 \\ 0 & \dots & 0 & r_{11} & \dots & r_{1n} \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ 0 & \dots & 0 & r_{n1} & \dots & r_{nn} \end{bmatrix}$$

Where,  $g_{ii}$ 's are the genetic variances of the  $i$ th trait and  $r_{ii}$ 's are the residual variances of the  $i$ th trait. And  $g_{ij}$ 's are the genetic covariances of  $i$ th and  $j$ th traits and  $r_{ij}$ 's are the residual covariances of  $i$ th and  $j$ th traits.  $A$  is the numerator relationship matrix among animals.

Sampling standard deviations of the (co)variances were estimated using AIREMLF90 package written by Shogo Tsuruta which uses the algorithm of Meyer and Houle [12].

**RESULTS AND DISCUSSION**

**Descriptive statistics of traits and Pearson's correlation**

The descriptive statistics of live body measurements and beef carcass cut ratios are shown in Table 1. It is observed that individual variation for BWT in Hanwoo cattle increased noticeably between 12 and 24 mo of age period. For frame size measurements (CG, BL, CD, HW, and RW), the changes in amount of variation were somewhat low to negligible with animal aging. However, the scalar increases of BL and CG deemed larger as compared to other frame size measures *i.e.*, widths and depths. The coefficient of variation (CV) of live body measurements slightly decreased over time. The CV of BFT was relatively larger than those of CWT, RCR, and LMR. The lower phenotypic variation in RCR suggests that the selection progress for beef cut ratios could be slower over generations [13]. In this study, the average of YWT (350.00±39.79 kg), CWT (340.97±39.79 kg), and BFT (8.6±3.74 mm), and their CV estimates were greatly similar to those reported by Choi et al [9], though our obtained phenotypic ranges were slightly greater than their reports. Choi et al [14] also reported similar YWT from Hanwoo males. The CWT found in this study was in line with Moon et al [15] and Baik et al [16]. The averages of different loin cuts (tenderloin: 1.63%, striploin: 9.95%, and sirloin: 1.99%) reported by Choi et al [9] was somewhat lower than the present study. They also reported a total primal-cut average of 78.95%, which coincided greatly with RCR in this study. However, a study on Hanwoo steers by Lee et al [17] reported slightly lower meat yield (65.3%) than our study.

Table 3 illustrates the Pearson's correlation coefficients between carcass and live body measurements. Most live body measurements

**Table 3.** Pearson's correlation coefficients among observed values of carcass measures, retail cuts and live body measurements

Trait	Abbr <sup>1)</sup>	Retail cut ratio	Loin muscle ratio	Cold carcass weight	Backfat thickness
Yearling weight	YWT	-0.26	-0.08	0.73	0.21
Body length	BL12	-0.23	-0.11	0.59	0.17
	BL24	-0.14	-0.15	0.52	0.09
Chest depth	CD12	-0.22	-0.18	0.60	0.24
	CD24	-0.25	-0.23	0.59	0.22
Chest width	CW12	-	-	0.79	0.18
	CW24	-0.33	-0.23	0.54	0.28
Rump width	RW12	-0.23	-0.12	0.57	0.13
	RW24	-0.19	-0.08	0.45	0.02
Chest girth	CG12	-0.28	-0.16	0.66	0.27
	CG24	-0.42	-0.17	0.81	0.35
Hip width	HW12	-0.16	-0.07	0.48	0.20
	HW24	-0.19	-0.11	0.42	0.20
Body weight	BWT	-0.15	0.07	0.67	0.13
Retail cut ratio	RCR	-	0.56	-0.32	-0.52
Loin muscle ratio	LMR	-	-	-0.03	-0.31
Cold carcass weight	CWT	-	-	-	0.41

<sup>1)</sup> YWT, yearling weight; BL12, body length at 12 mo; BL24, body length at 24 mo; CD12, chest depth at 12 mo; CD24, chest depth at 24 mo; CW12, chest width at 12 mo; CW24, chest width at 24 mo; RW12, rump width at 12 mo; RW24, rump width at 24 mo; CG12, chest girth at 12 mo; CG24, chest girth at 24 mo; HW12, hip width at 12 mo; HW24, hip width at 24 mo; BWT, body weight at 24 mo; RCR, retail cut ratio; LMR, loin muscle ratio; CWT, cold carcass weight.

(BL, CD, RW, CG, and HW), regardless of age, were negatively correlated with RCR and LMR at different magnitudes. Their correlations with LMR were relatively weak (-0.07 to -0.17) as compared to those with RCR (-0.14 to -0.42). These results deemed in agreement with Ort et al [8]. These live body measurements, on the contrary, revealed positive correlations with BFT and CWT where correlations were mostly low (0.02 to 0.27) and moderate to strong (0.42 to 0.81), respectively. The YWT and BWT also showed similar correlation trends with RCR, LMR, CWT, and BFT mostly (Table 3), as showed by body frame measures with others. Among the 24-month carcass measures, the correlation between RCR and LMR or between CWT and BFT was moderate and positive, by 0.56 or 0.41, respectively. However, the former two traits also showed negative correlations with latter two traits in most cases. Above results indicate that these body growth indicators in Hanwoo steers such as BWTs, carcass weight or carcass volume might have rather trivial relationships with compositional growth (BFT) that appears late in life.

### Heritability estimates, genetic and phenotypic correlations

The heritability ( $h^2$ ) estimates of all traits using model 1 and 2 are presented in Table 4. Estimated  $h^2$  for body measurement traits were very similar from both models, although varied slightly at different ages. The  $h^2$  estimates for BL, CW, CD, CG, RW, and HW were 0.23 to 0.25, 0.21 to 0.29, 0.28 to 0.31, 0.27 to 0.36, 0.26

to 0.27, and 0.20 to 0.22, respectively. Heritability estimates for YWT and BWT remained similar with different covariates in the models. Our  $h^2$  estimate of YWT (0.27) lies within the previously reported range, 0.18 to 0.39, in Hanwoo and other breeds [14,6, 18-20]. For RCR, a moderate to high heritability range was obtained in this study, where  $h^2$  estimates using model 1 and 2 were 0.56 and 0.47, respectively. The LMR tended to be somewhat more heritable with model 2 (0.42) than with model 1 (0.36). Earlier Choi et al [9] in Hanwoo males showed  $h^2$  for particular loin cuts (tenderloin: 0.41; sirloin: 0.60; striploin: 0.64) instead of our estimate for overall LMR (0.36) which found to be seemingly in an overall agreement with the present estimate. Similar overall agreeable ranges for heritability were observed with Pabiou et al [21], which also estimated  $h^2$  for sirloin, tenderloin, striploin and percentage of retail product. The  $h^2$  reported for loins (0.07 to 0.48) by Cundiff et al [22] also deemed in close agreement with our figure. Nonetheless, the  $h^2$  range of RCR in this study (0.47 to 0.56) was greatly supported by the total primal-cut heritability (0.52) in Choi et al [9], reviewed adjusted carcass lean percentage (0.47 to 0.55) in Koots et al [18], and predicted percentage retail cuts (0.49) in Benyshek [23]. Thus, our results indicate that selection for both RCR and LMR directly are likely to be effective in Hanwoo cattle because of their high heritability. Based on differences in  $h^2$  for individual primal-cuts showed by Choi et al [9] and our estimates, our study also indicated that predicting genetic merit for particular meat-cuts rather than gross meat-cut proportions *i.e.* LMR or RCR could be a good alternative for effective selection improvement. However, the differences between models estimates could be caused by some genetic variations of carcass compositions remained hidden by the variations of body fat reserves in different forms and localities [24, 13, 25-27].

The genetic correlation ( $r_G$ ) estimates of all live body measurements with RCR were generally low negative to low positive across the models such as -0.32 to 0.13 (model 1) and -0.21 to 0.19 (model 2). Genetically, RCR showed almost none to very low positive or low negative correlations with BL, CD, RW, and HW regardless of models or ages of animals. The LMR also expressed similar genetic relationships with these body measurement traits except for their magnitude. Either CWT or BFT fitted as covariates, CG deemed genetically more negatively correlated with RCR at older age. The correlations between LMR and some linear traits (BL, CW, CD, and CG), with CWT or BFT fitted models were somewhat similar but with opposite trends.

Genetically, RCR deemed almost independent of BWT and YWT, irrespective of covariates fitted. In this regards, Choi et al [9] showed similar none or low correlation ( $0.17 \pm 0.16$ ) between YWT and total primal-cut yield. The LMR, on the contrary, was either negatively ( $r_G$ : -0.31; model 1) or positively ( $r_G$ : 0.11; model 2) related to BWT based on slaughter endpoints. Both models also revealed similar trends between LMR and YWT showing  $r_G$  of -0.18 and 0.29 with CWT and BFT as slaughter endpoints,

**Table 4.** Estimates of genetic and phenotypic correlation between live body measurements and carcass cut ratio, and loin muscle ratio from two animal models, and their heritability ( $h^2$ ) estimates

Item <sup>1)</sup>	Model 1 <sup>2)</sup>						Model 2 <sup>2)</sup>					
	$(h^2)$	SE <sup>3)</sup>	Correlation with				$(h^2)$	SE <sup>3)</sup>	Correlation with			
			Genetic		Phenotypic				Genetic		Phenotypic	
			RCR	LMR	RCR	LMR			RCR	LMR	RCR	LMR
YWT	0.27	0.01	-0.01	-0.18	-0.21	-0.38	0.27	0.02	0.08	0.29	-0.09	0.05
BWT	0.36	0.01	-0.02	-0.31	-0.22	-0.37	0.36	0.01	0.04	0.11	-0.12	0.07
CG12	0.27	0.01	-0.17	-0.22	-0.23	-0.36	0.27	0.02	-0.09	0.17	-0.12	0.01
CG24	0.36	0.01	-0.32	-0.44	-0.43	-0.52	0.36	0.01	-0.19	0.12	-0.27	0.00
BL12	0.23	0.01	-0.05	-0.14	-0.13	-0.30	0.23	0.01	-0.03	0.17	-0.06	0.00
BL24	0.25	0.01	0.08	-0.27	-0.08	-0.27	0.25	0.01	0.05	0.00	-0.02	0.03
CD12	0.28	0.01	-0.05	-0.18	-0.16	-0.33	0.28	0.01	0.02	0.08	-0.05	-0.03
CD24	0.31	0.01	-0.07	-0.26	-0.23	-0.42	0.30	0.01	0.03	0.13	-0.12	-0.06
CW12	0.21	0.01	-0.29	-0.28	-0.17	-0.25	0.21	0.02	-0.21	0.01	-0.11	-0.02
CW24	0.29	0.01	-0.28	-0.41	-0.28	-0.33	0.29	0.01	-0.17	0.11	-0.17	0.03
HW12	0.20	0.01	0.05	-0.23	-0.10	-0.20	0.20	0.01	0.19	0.12	-0.03	-0.02
HW24	0.22	0.01	0.12	-0.11	-0.10	-0.20	0.21	0.02	0.16	0.15	-0.05	0.02
RW12	0.26	0.01	-0.07	-0.36	-0.16	-0.34	0.26	0.01	0.04	0.06	-0.08	-0.04
RW24	0.27	0.01	0.13	-0.27	-0.11	-0.23	0.27	0.01	0.18	0.10	-0.05	0.07
RCR	0.56	0.01	1	0.64	1	0.60	0.47	0.01	1	0.50	1	0.42
LMR	0.36	0.01		1		1	0.42	0.03		1		1
$\hat{\beta}$			-	-	0.0047	0.0173			-	-	-0.3279	-0.0911
Model statistics												
AIC	196,083.71						196,278.26					
-2logL	194,927.71						195,122.26					

RCR, retail cut ratio; LMR, loin muscle ratio.

<sup>1)</sup> YWT, yearling weight; BWT, body weight at 24 mo; CG12, chest girth at 12 mo; CG24, chest girth at 24 mo; BL12, body length at 12 mo; BL24, body length at 24 mo; CD12, chest depth at 12 mo; CD24, chest depth at 24 mo; CW12, chest width at 12 mo; CW24, chest width at 24 mo; HW12, hip width at 12 mo; HW24, hip width at 24 mo; RW12, rump width at 12 mo; RW24, rump width at 24 mo; CWT, cold carcass weight; BFT, backfat thickness

<sup>2)</sup> Model 1 and 2 were fitted with carcass weight and backfat thickness as linear covariates, respectively.

<sup>3)</sup> Standard errors of heritability estimates were estimated with AIREMLF90 program.

respectively. As Choi et al [9] studied various loin-cuts, the only correlation they found to be different from zero existed between striploin and YWT ( $0.35 \pm 0.14$ ). This deemed to agree with our study when BFT was fitted as covariate. Perhaps, the adjustment for BFT as covariate might have partitioned some variation in the trait that were unrelated to loin muscles but fat contents, and thus predicted a less biased estimate for LMR. Also, our  $r_G$  estimate greatly coincided with the correlation of YWT and most heritable loin-cut (striploin) in Choi et al [9]. This resemblance between correlations deemed more reasonable when the greater contribution of striploin to the total loin-cut region (73%; [3]) was considered. The genetic relationship between RCR and LMR fitting CWT as slaughter endpoint was 0.64 (Table 4), whereas fitting with BFT estimated an  $r_G$  of 0.50. Again, our correlation estimate (adjusted for BFT) coincided with the  $r_G$  between total primal-cuts and striploin ( $r_G$ : 0.53) as reported by Choi et al [9,3]. Thus, it may suggest that the genetic merit of overall loin cuts ratio or striploin in particular could be better estimated with BFT as slaughter endpoint than with CWT.

The phenotypic correlations of RCR with most body measurements, body growth and carcass measurements were equal or

somewhat strongly negative relative to the  $r_G$  estimates of the same model. Between models, the CWT as covariate revealed relatively higher negative estimates than fitting BFT for above traits. The LMR also revealed very similar lower negative phenotypic correlations than their respective model  $r_G$  estimates, which mostly stand close to zero, with body measurements as well as body growth and carcass traits measures.

From the genetic standpoint, the observed estimates indicate some possible selection scenario. If selection is targeted on populations where animals are to be slaughtered to obtain a certain carcass weight, the smaller body measurements and growth trait measures in all traits at any age for animals would contribute to a better LMR, whereas only a few (CW, CD, CG) might contribute to RCR to a certain proportion. If certain degree of BFT is aimed at slaughter, a selection of seedstock animals for greater weights or frame size measures might not be feasible enough as compared to the direct selection on genetic merit of LMR itself through progeny testing. The moderate to high heritability estimates as well as their correlations between them or with others greatly indicated that a direct selection on carcass traits, LMR in particular would provide more proportional gains to the other



trait, instead of any indirect selection schemes. Nevertheless, the CW might be the only candidate trait for selection of animals at an earlier age with respect to any of the slaughter endpoints.

Our results, as summarized, suggest that the genetic basis for RCR or LMR might rather be less straight forward with regard to other body growth measurement traits. Thus, any direct selection strategy on these traits such as selection of superior animals could be more useful than any indirect approach. Based on previous reports that each individual carcass retail cuts might inherit differently over generations, a prudent selection strategy on each desired cuts other than overall retail-cuts ratio or LMR could ensure more desirable and faster genetic progress. For live body measurements, there exist some complex and functional trade-off relationships among traits as each animal grow older, which may cause selection (at an early age) gains less predictable. Therefore, to conclude, the BWTs or linear body measurements at an earlier age may not be the most desirable selection traits for exploitation of correlated responses to improve loin muscle or lean meat yield. We believe that this study also provides adequate emphasis for further large scale analyses in order to understand the genetic merit and the connectedness of the less studied primal cut or retail-cut traits in Hanwoo cattle.

## CONFLICT OF INTEREST

We certify that there is no conflict of interest with any financial organization regarding the material discussed in the manuscript.

## ACKNOWLEDGMENTS

This study was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project title: Studies on the genetic correlation between reproduction traits and growth or milking traits in Hanwoo and Korean Holstein cattle, Project No. PJ01096801)” Rural Development Administration, Republic of Korea. Authors also thank members of Hanwoo Improvement Center of Nonghyup for their efforts to collect records of performance test and carcass.

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