

Original Article

Estimation of heritability and genetic parameters for carcass traits and primal cut production traits in Hanwoo

Jae Don Oh^{1,2,3,#}, Gwang Hyeon Lee^{1,4,#} and Hong Sik Kong^{1,2,3,4,*}

¹Department of Biotechnology, Hankyong National University, Anseong 17579, Korea

²Gyeonggi Regional Research Center, Hankyong National University, Anseong 17579, Korea

³Genomic Information Center, Hankyong National University, Anseong 17579, Korea

⁴Hankyong and Genetics, Anseong 17579, Korea

Received May 31, 2024

Revised June 12, 2024

Accepted June 12, 2024

*Correspondence

Hong Sik Kong

E-mail: kebinkhs@hknu.ac.kr

#These authors contributed equally to this work.

Author's Position and Orcid no.

Oh JD, Professor,

<https://orcid.org/0000-0001-7756-1330>

Lee GH, Post doctor,

<https://orcid.org/0000-0002-6598-8430>

Kong HS, Professor,

<https://orcid.org/0000-0003-1144-016X>

ABSTRACT

Background: The Hanwoo industry must develop technologies that can increase the production of preferred cuts to match changing consumer trends. In this study, we aimed to estimate the genetic parameters for carcass traits (carcass weight, eye muscle area, back fat thickness, and intramuscular fat) and primal cut traits (tenderloin, loin, strip loin, neck, clod, top round, bottom round, brisket, shank, and rib) in a Hanwoo population to obtain basic data for improving primal cut productivity.

Methods: Data from 1,905 Hanwoo steers, including carcass traits and primal cut weights, were collected. Genetic parameters were estimated using REMLF90 in a multi-trait analysis.

Results: High heritability was found for carcass weight (0.52) and strip loin yield (0.63). Genetic correlations between carcass weight and primal cut weights ranged from 0.52 to 0.93.

Conclusions: This study demonstrates the significant potential for genetic improvement in Hanwoo cattle through selective breeding, particularly for traits with high heritability and genetic correlations. These findings provide crucial insights into optimizing breeding programs to improve Hanwoo cattle production efficiency.

Keywords: carcass traits, genetic correlation, Hanwoo, heritability, primal cut traits

INTRODUCTION

Currently, the Hanwoo cattle (Korean cattle) industry is improving by selecting superior sires and distributing semen to farms for artificial insemination. This method is highly effective at the national level and has significantly contributed to the development of the Hanwoo industry (Kim et al., 2010). The Hanwoo Improvement Main Center provides information on the major genetic abilities of

certified sires (carcass weight, eye muscle area, backfat thickness, and intramuscular fat), as well as conformation traits and the genetic abilities of the top 10 primal cuts through its website and brochures.

Consumers' meat consumption patterns are continuously changing, and the Hanwoo industry must produce products that meet consumer demand. Recently, the consumption of preferred meat cuts has intensified, resulting in a wider price gap between different meat cuts (Jeong et

al., 2020). Cuts for grilling, such as tenderloins, loins, and strip loins, command high prices, whereas cuts not used for grilling have significantly lower prices. This wider price gap is closely related to consumer preferences (Kim, 2011).

Therefore, the Hanwoo industry must develop technologies to increase the production of preferred cuts to match changing consumer trends. Improvement technologies that consider both meat quality and yield, as well as cut-specific production, are required. Lee et al. (2013) analyzed the relationship between conformational traits measured in Hanwoo steers and primary cut yield and found significant differences. Developing technologies to increase the yield of preferred cuts is expected to play a crucial role in increasing farmers' incomes and enhancing the efficiency of the consumer-oriented Hanwoo industry. However, obtaining information on the yield of specific cuts during processing at a production site remains challenging, and collecting and distributing related information is difficult. Thus, this study aimed to estimate the genetic parameters for carcass traits (carcass weight, eye muscle area, back fat thickness, and intramuscular fat) and primal cut traits (tenderloin, loin, strip loin, neck, clod, top round, bottom round, brisket, shank, and rib) in a Hanwoo population to secure basic data for improving primal cut productivity.

MATERIALS AND METHODS

Materials

The materials used in this study were obtained from 1,905 Hanwoo steers slaughtered and processed at the Livestock Cooperative Federation (Jeonju, Gimje, and Wanju) Meat Processing Plant in the Jeollabuk-do region between 2018 and 2021. carcass traits (carcass weight, eye muscle area, back fat thickness, and intramuscular fat) of the analyzed group were collected from the Korea Institute for Animal Products Quality Evaluation website. Information on the yield of specific cuts of Hanwoo carcasses was provided by the Livestock Cooperative Federation (Jeonju, Gimje, and Wanju) Meat Processing Plant. Pedigree information and individual data were obtained from the Korea Animal Improvement Association.

Phenotype data collection

The cut-specific data used in the analysis were mea-

sured based on the following detailed standards of live-stock grading: carcass weight, eye muscle area, back fat thickness, and intramuscular fat. The carcasses were quartered, and the weight of each part was measured at the meat processing plant. The cuts were classified into 10 primary cuts, namely tenderloin, loin, strip loin, neck, clod, top round, bottom round, brisket, shank, and rib.

Estimation of genetic parameters

The relationship matrix of individuals was constructed using PreGSF90 and the genetic parameters were estimated using REMLF90, both from the BLUPF90 family program. Genetic parameters for carcass traits (carcass weight, eye muscle area, back fat thickness, and intramuscular fat) and 10 primal cuts (tenderloin, loin, strip loin, neck, clod, top round, bottom round, brisket, shank, and rib) were estimated by performing a multi-trait analysis using the relationship matrix. The additive genetic and environmental variances for each trait were estimated, and the matrix for the linear model used for the estimation was as follows:

$$Y_p = X\beta + Zu + e, \quad \text{Var} \begin{pmatrix} u \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & I\sigma_e^2 \end{pmatrix}$$

where:

Y_p : Observations of carcass traits (carcass traits, weights, and yields of 10 primary cuts).

X : Incidence matrix for fixed effects (birth year, birth month, slaughter year, slaughter month, and slaughter age).

β : Vector of fixed effects estimates.

Z : Incidence matrix for genetic effects.

u : Vector for additive genetic effects.

e : Vector of residual effects.

A : Relationship matrix among individuals.

I : Identity matrix with diagonal elements equal to 1.

Where, Y_p represents the observed values for carcass traits, X is the incidence matrix for fixed effects, and Z is the incidence matrix for genetic effects. u represents the additive genetic effects, e represents the random residual effects, I is the relationship matrix among individuals, and I is the identity matrix with diagonal elements equal to one. σ_a^2 and σ_e^2 are the genetic variance and residual variance, respectively. The genetic correlation between carcass traits was estimated based on the variance and covariance estimates obtained during the analysis pro-

cess. The phenotypic correlation between carcass traits was analyzed using the Pearson correlation method.

$$r_G(i,j) = \frac{Cov_{\alpha(i,j)}}{\sqrt{\sigma_{\alpha(i)}^2 \times \sigma_{\alpha(j)}^2}} \quad (i \neq j), \quad r_P(i,j) = \frac{Cov_{p(i,j)}}{\sqrt{\sigma_{p(i)}^2 \times \sigma_{p(j)}^2}} \quad (i \neq j)$$

where, σ_{α}^2 and σ_p^2 are the genetic variance and phenotypic variance, respectively. Cov_{α} and Cov_p represent the genetic covariance and phenotypic covariance between carcass traits, respectively. r_G is the genetic correlation, and r_P is the phenotypic correlation.

Estimation of heritability

Heritability was estimated using REMLF90, and the calculated heritability was derived from the genetic and residual variance using the following formula:

$$Heritability(h^2) = \frac{\sigma_{\alpha}^2}{\sigma_p^2}, \quad \sigma_p^2 = \sigma_{\alpha}^2 + \sigma_e^2$$

where,

h^2 is the heritability,

σ_p^2 is the phenotypic variance,

σ_{α}^2 is the genetic variance,

σ_e^2 is the residual variance.

RESULTS

Basic statistics of phenotypic traits

Table 1 presents the basic statistics for the phenotypic traits. We analyzed 1,905 Hanwoo steers raised in Jeollabuk-do. The mean and standard deviation of carcass traits—carcass weight, eye muscle area, backfat thickness, and marbling score—were 446.43 ± 44.38 kg, 93.39 ± 10.20 cm², 12.95 ± 5.11 mm, and 6.10 ± 1.94 , respectively.

For the weights of the 10 primal cuts, the mean and standard deviation were as follows: tenderloin (6.02 ± 0.71 kg), loin (36.63 ± 4.42 kg), strip loin (9.12 ± 1.15 kg), neck (15.30 ± 2.22 kg), clod (24.54 ± 3.45 kg), top round (21.51 ± 4.99 kg), bottom round (35.45 ± 3.94 kg), brisket (29.81 ± 3.96 kg), shank (16.18 ± 1.73 kg), and rib (54.09 ± 6.09 kg).

Table 1. Basic statistics for reference population in four major traits, primal cut weight, and percentage

	Trait	Min	Max	Mean	S.D.
Carcass traits	CWT (kg)	314.0	597.0	446.43	44.38
	EMA (cm ²)	53.0	135.0	93.39	10.20
	BFT (mm)	2.0	39.0	12.95	5.11
	MSC (score)	1.0	9.0	6.10	1.94
Weight of primal cut	TDL (kg)	3.9	8.8	6.02	0.71
	LN (kg)	21.1	54.6	36.63	4.42
	STL (kg)	5.8	14.0	9.12	1.15
	NK (kg)	8.4	26.4	15.30	2.22
	CL (kg)	13.2	36.0	24.54	3.45
	TR (kg)	12.3	39.7	21.51	4.99
	BR (kg)	20.6	52.8	35.45	3.94
	BK (kg)	16.2	46.6	29.81	3.96
	SK (kg)	10.1	23.7	16.18	1.73
	RIB (kg)	34.9	79.6	54.09	6.09
Percentage of primal cut	TDL (%)	1.0	1.9	1.35	0.13
	LN (%)	5.7	11.1	8.22	0.73
	STL (%)	1.4	2.8	2.05	0.18
	NK (%)	2.3	5.4	3.43	0.39
	CL (%)	2.9	7.9	5.51	0.64
	TR (%)	2.7	8.3	4.85	1.16
	BR (%)	6.0	11.4	7.95	0.60
	BK (%)	4.4	8.8	6.67	0.56
	SK (%)	2.8	5.0	3.63	0.28
	RIB (%)	10.0	18.5	12.11	0.62

CWT, carcass weight; EMA, eye muscle area; BFT, back fat thickness; MS, marbling score; TDL, tender loin; LN, loin; STL, strip loin; NK, neck; CL, clod; TR, top round; BR, bottom round; BK, brisket; SK, shank; RIB, rib; S.D., standard deviation.

Lee (2016) reported the mean and standard deviation of the weights of the same primal cuts in Hanwoo steers as 5.86 ± 0.71 kg, 35.16 ± 3.98 kg, 7.15 ± 0.90 kg, 12.47 ± 2.68 kg, 22.74 ± 2.48 kg, 19.55 ± 2.10 kg, 31.81 ± 3.35 kg, 28.26 ± 4.20 kg, 14.09 ± 1.50 kg, and 56.09 ± 7.04 kg, respectively. Compared to these results, the weights of all primal cuts in this study were higher. This discrepancy is attributed to the age differences at the time of slaughter. In the study by Lee (2016), the steers were slaughtered at 24 months for progeny testing, whereas the steers in this study were slaughtered at an older age, which is typical of commercial farms.

Genetic parameters of carcass traits and primal cuts

The estimated genetic parameters (genetic variance, residual variance, and heritability) for carcass traits (carcass weight, eye muscle area, backfat thickness, and marbling score) and primal cut weights (tenderloin, loin, strip loin, neck, clod, top round, bottom round, brisket, shank, and rib) are summarized in Table 2. The genetic variances

of carcass weight, eye muscle area, back fat thickness, and marbling score were 970.20, 43.90, 6.52, and 1.64, respectively. The corresponding residual variances were 906.70, 55.75, 18.93, and 2.16, and the heritability values were 0.52, 0.44, 0.26, and 0.43, respectively.

For the weights of primal cuts (tenderloin, loin, strip loin, neck, clod, top round, bottom round, brisket, shank, and rib) the genetic variances were 0.23, 0.23, 7.25, 0.81, 1.67, 3.58, 0.99, 8.18, 6.73, and 1.48, respectively. The residual variances were 0.24, 10.41, 0.45, 2.73, 7.02, 15.50, 7.10, 7.17, 1.48, and 14.51, respectively. The heritability ranged from 0.06 to 0.64, with strip loin exhibiting the highest heritability. Lee et al. (2014) reported heritability of 0.53, 0.50, 0.57, 0.17, 0.78, 0.69, 0.75, 0.18, 0.49, and 0.14 for these cuts in Hanwoo steers slaughtered at 24 months. This study found a notably lower heritability for the top round, unlike the low heritability reported for the neck, brisket, and ribs in previous studies.

The estimated genetic variances for primal cut yields (tenderloin, loin, strip loin, neck, clod, top round, bottom

Table 2. Estimated genetic parameters for the four major traits, primal cut weight, and percentage

	Trait	Genetic variance(s)	Residual variance(s)	Heritability
Carcass traits	CWT	970.20	906.70	0.52
	EMA	43.90	55.75	0.44
	BFT	6.52	18.93	0.26
	MSC	1.64	2.16	0.43
Weight of primal cut	TDL	0.23	0.24	0.49
	LN	7.25	10.41	0.41
	STL	0.81	0.45	0.64
	NK	1.67	2.73	0.38
	CL	3.58	7.02	0.34
	TR	0.99	15.50	0.06
	BR	8.18	7.10	0.54
	BK	6.73	7.17	0.48
	SK	1.48	1.48	0.50
	RIB	19.92	14.51	0.58
Percentage of primal cut	TDL	0.005	0.009	0.34
	LN	0.100	0.310	0.24
	STL	0.020	0.012	0.63
	NK	0.023	0.098	0.19
	CL	0.061	0.258	0.19
	TR	0.121	0.727	0.14
	BR	0.144	0.193	0.43
	BK	0.107	0.146	0.42
	SK	0.021	0.052	0.28
	RIB	0.166	0.164	0.50

CWT, carcass weight; EMA, eye muscle area; BFT, back fat thickness; MS, marbling score; TDL, tender loin; LN, loin; STL, strip loin; NK, neck; CL, clod; TR, top round; BR, bottom round; BK, brisket; SK, shank; RIB: rib.

Table 3. Phenotypic correlations (above the diagonal) and genetic correlations (below the diagonal) between the four major traits and primal cut weight

Trait	Weight of primal cut													
	CWT	EMA	BFT	MSC	TDL	LN	STL	NK	CL	TR	BR	BK	SK	RIB
CWT		0.48	0.30	0.17	0.63	0.69	0.70	0.62	0.56	0.16	0.75	0.78	0.72	0.89
EMA	0.61		-0.02	0.35	0.45	0.50	0.67	0.45	0.33	0.08	0.52	0.50	0.48	0.43
BFT	0.30	-0.11		0.03	0.01	0.08	0.08	0.01	0.01	0.01	-0.02	0.10	-0.01	0.19
MSC	0.34	0.55	-0.07		0.08	0.23	0.33	0.08	0.12	-0.01	0.07	0.19	0.01	0.23
TDL	0.78	0.70	0.15	0.35		0.65	0.64	0.54	0.62	0.34	0.80	0.70	0.76	0.61
LN	0.88	0.83	0.06	0.56	0.79		0.67	0.47	0.60	0.37	0.69	0.67	0.65	0.70
STL	0.72	0.88	0.10	0.54	0.70	0.86		0.55	0.53	0.19	0.70	0.72	0.63	0.66
NK	0.87	0.82	0.01	0.32	0.84	0.92	0.79		0.43	0.10	0.61	0.54	0.60	0.51
CL	0.84	0.72	0.01	0.41	0.89	0.87	0.72	0.92		0.35	0.67	0.59	0.67	0.51
TR	0.52	0.54	-0.14	0.35	0.76	0.61	0.47	0.67	0.82		0.29	0.23	0.29	0.18
BR	0.82	0.67	0.05	0.33	0.89	0.82	0.74	0.86	0.91	0.83		0.75	0.87	0.68
BK	0.84	0.75	0.00	0.35	0.81	0.92	0.82	0.93	0.87	0.65	0.86		0.71	0.76
SK	0.87	0.68	0.07	0.21	0.89	0.83	0.72	0.87	0.88	0.67	0.94	0.84		0.65
RIB	0.93	0.65	0.18	0.48	0.68	0.88	0.71	0.82	0.82	0.52	0.75	0.77	0.79	

CWT, carcass weight; EMA, eye muscle area; BFT, back fat thickness; MS, marbling score; TDL, tender loin; LN, loin; STL, strip loin; NK, neck; CL, clod; TR, top round; BR, bottom round; BK, brisket; SK, shank; RIB, rib.

Table 4. Phenotypic correlations (above the diagonal) and genetic correlations (below the diagonal) between the four major traits and primal cut percentage

Trait	Percentage of primal cut													
	CWT	EMA	BFT	MSC	TDL	LN	STL	NK	CL	TR	BR	BK	SK	RIB
CWT		0.48	0.30	0.17	-0.27	-0.18	-0.12	-0.08	-0.18	-0.26	-0.22	0.05	-0.30	0.02
EMA	0.61		-0.02	0.35	0.06	0.15	0.42	0.16	-0.01	-0.13	0.13	0.24	0.05	0.01
BFT	0.29	-0.09		0.03	-0.30	-0.22	-0.21	-0.24	-0.23	-0.11	-0.42	-0.19	-0.39	-0.15
MSC	0.35	0.56	-0.05		-0.08	0.13	0.27	-0.05	0.00	-0.08	-0.12	0.11	-0.21	0.17
TDL	-0.19	0.21	-0.18	0.05		0.40	0.37	0.26	0.44	0.37	0.66	0.39	0.60	0.10
LN	-0.14	0.50	-0.44	0.47	0.31		0.38	0.09	0.37	0.39	0.38	0.28	0.34	0.27
STL	0.03	0.66	-0.15	0.44	0.30	0.67		0.22	0.25	0.14	0.39	0.38	0.29	0.10
NK	0.10	0.57	-0.42	0.08	0.41	0.54	0.43		0.15	0.02	0.29	0.10	0.29	-0.12
CL	-0.13	0.28	-0.42	0.17	0.66	0.46	0.32	0.54		0.35	0.49	0.27	0.49	0.02
TR	-0.67	-0.23	-0.38	-0.12	0.52	0.36	0.12	0.18	0.58		0.31	0.15	0.31	0.08
BR	-0.10	0.22	-0.34	0.03	0.70	0.30	0.36	0.39	0.69	0.55		0.38	0.74	0.03
BK	0.05	0.48	-0.40	0.13	0.43	0.61	0.56	0.66	0.50	0.28	0.53		0.30	0.25
SK	-0.14	0.18	-0.36	-0.22	0.68	0.20	0.25	0.36	0.58	0.41	0.80	0.40		0.01
RIB	0.23	0.34	-0.21	0.50	-0.24	0.33	0.16	0.08	0.08	-0.10	-0.11	-0.02	-0.15	

CWT, carcass weight; EMA, eye muscle area; BFT, back fat thickness; MS, marbling score; TDL, tender loin; LN, loin; STL, strip loin; NK, neck; CL, clod; TR, top round; BR, bottom round; BK, brisket; SK, shank; RIB, rib.

round, brisket, shank, and rib) were 0.005, 0.100, 0.020, 0.023, 0.061, 0.121, 0.144, 0.107, 0.021, and 0.166, and the residual variances were 0.009, 0.310, 0.012, 0.098, 0.258, 0.727, 0.193, 0.146, 0.052, and 0.164, respectively. Heritability values were 0.34, 0.24, 0.63, 0.19, 0.19, 0.14, 0.43, 0.42, 0.28, and 0.50, respectively, with strip loin yield showing the highest heritability. Lee (2016) reported

heritability values for primal cut yields as 0.53, 0.58, 0.65, 0.28, 0.78, 0.60, 0.66, 0.22, 0.57, and 0.43, respectively. This study showed notable differences, particularly in the heritability of clod and top round yields.

Phenotypic and genetic correlations

Table 3 and 4 present the results of the phenotypic and

genetic correlation analyses. The genetic correlations between carcass weight and primal cut weights ranged from 0.52 to 0.93, with the highest correlation observed for the rib (0.93). The genetic correlations between eye muscle area and primal cut weights were high for the loin, strip loin, and neck (0.83, 0.88, and 0.82, respectively), likely because these cuts were derived from the same muscle group. The genetic correlations between backfat thickness and primal cut weights were low (0.00–0.18), with neck, clod, and brisket showing nearly zero correlation (0.01, 0.01, and 0.00, respectively). Marbling score had genetic correlations of 0.21–0.56 with primal cut weights, with the highest correlation observed for the loin (0.56).

Phenotypic and genetic correlations among primary cut weights were generally positive. The genetic correlations for tenderloin weight with other primal cut weights ranged from 0.68 to 0.89, with high correlations for neck, clod, bottom round, brisket, and shank (0.84, 0.89, 0.89, 0.81, and 0.89, respectively). The loin weight had genetic correlations of 0.61–0.92 with other primal cuts, with relatively lower correlations for loin (0.79) and top round (0.61). The genetic correlations for strip loin weight with other cuts ranged from 0.47 to 0.86, with higher correlations for loin and brisket (0.86 and 0.82, respectively). The genetic correlations for top round weight with strip loin and rib were lower (0.47 and 0.52), while loin weight had high genetic correlations with neck and brisket (0.92 and 0.92), and neck weight had high correlations with clod and brisket (0.92 and 0.93). The bottom-round weight had high genetic correlations with clod and shank (0.93 and 0.94, respectively).

Genetic correlations among primary cut yields showed a range of values. The genetic correlations with other yields ranged from -0.24 to 0.70 for tenderloin yield, with high correlations observed for clod, top round, bottom round, and shank yields (0.66, 0.52, 0.70, and 0.68, respectively). Loin yield had genetic correlations of 0.20–0.67 with other yields, with high correlations noted for strip loin, neck, and brisket yields (0.67, 0.54, and 0.61, respectively). Strip loin yield had genetic correlations of 0.12–0.67 with other yields, with a relatively high correlation with loin yield (0.67). The genetic correlations of clod yield with top-round, bottom-round, brisket, and shank yields were 0.58, 0.69, 0.50, and 0.58, respectively. In contrast, the bottom-round yield had genetic correlations of 0.55 and 0.80 with top-round and shank yields, respectively.

DISCUSSION

In the present study, the heritability estimates for carcass weight, eye muscle area, back-fat thickness, and marbling score were 0.52, 0.44, 0.26, and 0.43, respectively. Different studies have reported varying heritability for these traits. Lee and Yoon (2021) reported heritability values of 0.52, 0.39, 0.39, and 0.47 for carcass weight, eye muscle area, backfat thickness, and marbling score, respectively, in Hanwoo steers slaughtered at 30 months in the Jeongeup region of Jeollabuk-do. Sun (2021) reported heritability values of 0.34, 0.26, 0.32, and 0.57 in steers raised in Gyeongnam. Dang et al. (2013) reported heritability values of 0.30, 0.21, 0.42, and 0.42 in Hanwoo steers slaughtered in Pyeongchang, Gangwon-do. These differences in heritability values highlight the influence of region, environment, and herd size on heritability estimates. This study's focus on primal cut traits is particularly relevant given the changing consumer preferences and the economic implications of producing high-value cuts. The high heritability observed for strip loin (0.63) and other primal cuts suggests that these traits should be effectively targeted in breeding programs to enhance the overall value of Hanwoo carcasses.

However, this study also highlighted the challenges of collecting and distributing information on the yield of specific cuts during processing. Improving data collection methods and enhancing the accuracy of genetic evaluations at production sites could further optimize breeding programs. Additionally, integrating advanced technologies such as genomic selection and precision livestock farming could enhance the efficiency and effectiveness of genetic improvement.

CONCLUSION

This study provides a comprehensive framework for understanding the genetic parameters of economically important Hanwoo cattle traits. The Hanwoo industry can implement more targeted and effective breeding programs by leveraging the identified high heritability and genetic correlations. These efforts are crucial for adapting to consumer trends, increasing profitability, and ensuring the sustainable development of the Hanwoo industry.

Author Contributions: Conceptualization, H.S.K.; meth-

odology, J.D.O., G.H.L., H.S.K.; investigation, J.D.O., G.H.L.; writing - original draft preparation, J.D.O., G.H.L.; writing - review and editing, J.D.O., G.H.L., H.S.K.; supervision, H.S.K.; project administration, H.S.K.; funding acquisition, H.S.K.

Funding: None.

Ethical Approval: The study was approved by the Han-kyong National University Animal Ethics Committee (No. 2021-3).

Consent to Participate: Not applicable.

Consent to Publish: Not applicable.

Availability of Data and Materials: Not applicable.

Acknowledgements: None.

Conflicts of Interest: No potential conflict of interest relevant to this article was reported.

REFERENCES

- Dang CG, Kim HC, Jang SS, Lee JM, Hong YH, Jeon GJ, Yeon SH, Kang HS, Yang BS, Hong SK, Lee JH, Lee SH. 2013. Estimation of genetic parameter for carcass traits of commercial steers in Pyeongchang. *Korean J. Agric. Sci.* 40:339-345.
- Jeong MK, Kim HJ, Lee HW. 2020. Consumer behavior for meat consumption and tasks to respond to its changes. *Korea Rural Economic Institute.* no.R913. 1-240.
- Kim HS, Hwang JM, Choi TJ, Park BH, Cho KH, Park CJ, Cho KH, Park CJ, Kim SD. 2010. Research on the reformation of the selection index for Hanwoo proven bull. *J. Anim. Sci. Technol.* 52:83-90.
- Kim SD. 2011. A study on consumer preferences for Hanwoo meat. *Doctors degree thesis.* Konkuk University, Korea.
- Lee DJ and Yoon D. 2021. Estimation of genetic parameters and analysis of environmental effects on carcass traits of the Hanwoo brand steer. *J. Anim. Breed. Genom.* 5:113-123.
- Lee JG. 2016. Research for the improvement of primal cut traits in Hanwoo. *Doctors degree thesis,* Chungnam National University, Korea.
- Lee JG, Lee SS, Cho KH, Cho C, Choy YH, Choi JG, Park B, Na CS, Roh SH, Do C, Choi T. 2013. Estimation of primal cuts yields by using body size traits in Hanwoo steer. *J. Anim. Sci. Technol.* 55:373-380.
- Lee JG, Park SB, Lee SS, Cho KH, Cho C, Choy YH, Choi JG, Alam M, Roh SH, Choi TJ. 2014. A study on genetic parameters of primal cuts and body size traits in Hanwoo steers. *J. Agric. Life Sci.* 48:151-160.
- Sun DW. 2021. A study on the estimation of genetic parameters on carcass traits in Gyeongnam Hanwoo. *J. Anim. Breed. Genom.* 5:85-90.