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Genetic Models for Carcass Traits with Different Slaughter Endpoints in Selected Hanwoo Herds

I. Linear Covariance Models

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ABSTRACT : Carcass characteristics data of Hanwoo (N = 1,084) were collected from two stations of the National Livestock Institute of Animal Science (NIAS), Korea and records from thirteen individual cow-calf operators were analyzed to estimate variance and covariance components and the effect of different slaughter endpoints. Carcass traits analyzed were cold carcass weight (CWT, kg), REA (rib eye area, cm^2), back fat thickness (mm) and marbling score (1-7). Four different models were examined. All models included sex and contemporary group as fixed effects and the animal's direct genetic potential and environment as random effects. The first model fitted a linear covariate of age at slaughter. The second model fitted both linear and quadratic covariates of age at slaughter. The third model fitted a linear covariate of body weight at slaughter. The fourth model fitted both linear covariates of age at slaughter and body weight at slaughter. Variance components were estimated using the REML procedure with Gibb's sampler. Heritability estimate of CWT was in the range of 0.08-0.11 depending on the model applied. Heritability estimates of BF, REA and MS were in the ranges of 0.23-0.28, 0.19-0.26, and 0.44-0.45, respectively. Genetic correlations between CWT and BF, between CWT and REA, and between CWT and MS were in the ranges of -0.33 - -0.14, 0.73-0.84, and -0.01- 0.11, respectively. Genetic correlations between REA and BF, between MS and BF and between REA and MS were in the ranges of -0.82 ~ -0.72, 0.04~0.28 and -0.08 ~ -0.02, respectively. Variance and covariance components estimated varied by model with different slaughter endpoints. Body weight endpoint was more effective for direct selection in favor of yield traits and body weight endpoints affected more of the correlated response to selection for the traits of yield and quality of edible portion of beef. (**Key Words :** Hanwoo, Carcass Trait, Slaughter Endpoint, Genetic Model)

INTRODUCTION

Hanwoo is one of the most favorite beef cattle breed also known as Korean Native cattle. Hanwoo population in South Korea had long been under selection process to increase meat production efficiency since 1960's. And Hanwoo breeders became to put more emphasis on beef quality targeting Korean consumers from late 2000's. Nation wide use of semen from proven bulls produced by a test station make Hanwoo breeders to inseminate as many as 30 sires every year. Performances of the bulls were tested and their progeny records of growth and carcass characteristics are collected for their genetic evaluation. Carcass traits are known to be differently evaluated with different genetic indirect responses according to their slaughter-end points (Cundiff et al., 1969). Current genetic evaluation models for Hanwoo carcass traits use age at slaughter in days as end point in linear covariate term in the model. However, Cundiff et al. (1969) and several other research works (Lee et al., 2000; Shanks et al., 2001) showed that co-variables of slaughter weight or carcass weight reflected differential growth for carcass traits. Since body weight comprises three major components, skeleton, muscle and fat with different development rates while growth (Choy, 2002), compositional changes by aging of animals would be considered for evaluation of carcass traits.

The objective of this study was to estimate genetic and phenotypic variation in carcass traits of Hanwoo population composed of all different sex categories and co-relationship between them when different biological slaughter end points were plugged into genetic evaluation models in place of age of animals at slaughter.

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Table 1. Number of observations for each carcass measurement collected from farms

Farm	SLWT[1]	CWT	REA	BF	MS
10	399	470	465	466	449
11	6	1	1	1	1
12	12	6	8	8	8
13	138	39	41	42	35
14	2	1	0	1	1
15	38	13	16	16	15
16	6	2	5	5	5
17	12	2	2	2	2
18	19	9	8	10	10
19	11	6	7	7	7
20	261	337	227	227	233
21	4	4	3	4	4
22	2	0	0	0	0
23	6	2	2	2	2
24	3	2	2	2	2
Total	919	894	787	793	774

[1] SLWT: body weight at slaughter (kg), CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

MATERIALS AND METHODS

Animals

A total of 1,084 records of carcass measures were analyzed. Data were collected from two test stations of the National Institute of Animal Science (NIAS), Korea and thirteen individual Hanwoo cow-calf operators that participate in Hanwoo nucleus herd program directed by the NIAS. Hanwoo's slaughtered with records were of three different sexes, bulls, steers and cows. Table 1 summarizes distribution of data from 15 farms. Most carcass data were from a few farms and the other individual farms produced only around ten animals' carcass data. Farm number 10 which is the Hanwoo Experiment Station of NIAS produced most of bull carcass data while steer data are broadly distributed from all the farms. Cow carcass data came mostly from farm number 20 which is the Livestock Genetic Resources Station of NIAS.

Carcass traits analyzed were cold carcass weight (CWT), longissimus muscle area (REA), back fat thickness (BF) and marbling score (MS). Cold carcass weight was measured after overnight chilling. REA (cm^2), and BF (mm) were measured at between 12th-13th ribs. Marbling scores (1-7: 1 is no intramuscular fat particle found, and 7 is abundant) were subjectively evaluated by skilled practitioners at each slaughter houses.

Two test stations of NIAS make cows and heifers graze from spring to fall with some grain supplements. In winter they feed cows and heifers in the housed feedlot with hays and grain diets. Fattening cows are housed in the feedlot for about three months before slaughter and are fed rice straw and grain diets. Bulls or steers are grown and fattened in the housed feedlot from birth to slaughter. They are fed on similar formulae to private farms. Bulls or steers from NIAS stations are slaughtered around 24 months of age while those at private farms are slaughtered around 27 months of age. Private farms feed cows and heifers in the housed feedlot all year around feeding mostly rice straw and grain diets but feeding formulation is different from fattening animals.

Statistical models

Four different statistical models were examined. Bi-variable animal models were applied to all four models with animal's breeding value and environment effect as random. Fixed effects fit in all four models were contemporary group effect and sex as class variables and slaughter-end-points as linear co-variables. Contemporary group effect was defined as the group of animals within the same herd, year and season at birth. The only differences between models were the co-variables.

$$Y = X_1B+X_2b+ZU+E$$

Where, B is the fixed effect matrix of overall mean, contemporary group and sex, b is the vector of co-variables for two observed variables in Y matrix, U is the random animal effect matrix and E is the random environmental effect matrix.

And, X_1, X_2 and Z are incidence matrices that relate Y to B, b and U, respectively.

Model 1 included age at slaughter in days as a linear co-variable. Model 2 included age at slaughter in days as linear and quadratic co-variables. Model 3 included body weight at slaughter (SLWT) as a linear co-variable and model 4 included both age at slaughter and SLWT as linear co-variables. Park et al. (2003) reported significant quadratic effect of SLWT on both carcass quality and yield grades of Hanwoo. However, this study focus on estimation of genetic relationship between component traits of those carcass grades, only linear function of SLWT only was applied.

Estimation of genetic and environmental variances (and co-variances) of (and between) carcass traits were performed with multiple trait Gibb's sampling to animal models variance component estimation procedure (MTGSAM version 1.11) developed by Van Tassell and Van Vleck (1995 http://aipl.arsusda.gov/curtvt/mtgsam.html). To find globally maximal values, 100 different independent sets of variance-covariance matrix values were given as initial priors. Each independent sampling procedure was kept through until converged using posterior estimates from previous runs as priors for successive runs. And those estimates converged only were collected and averaged.

Table 2. Genetic variances (covariances) of (between) carcass traits and their standard errors

Trait[1]	Model 1[2]		Model 2		Model 3		Model 4	
	N	Ave±SE	N	Ave±SE	N	Ave±SE	N	Ave±SE
CWT	81	281.55±267.67	69	235.46±130.49	102	161.08±77.73	82	216.24±113.17
BF	38	5.50±2.84	68	5.01±1.08	106	5.46±1.53	82	4.83±1.03
REA	52	27.76±13.69	101	35.88±12.56	101	27.93±11.94	101	35.02±12.25
MS	9	1.43±1.52	10	1.35±1.42	7	1.57±1.71	9	1.38±1.50
CWT×BF	29	0.34±20.05	14	-7.43±5.54	50	-6.97±5.80	28	-5.95±7.02
CWT×REA	50	68.18±37.76	50	82.00±34.51	50	54.54±32.02	50	80.89±33.96
CWT×MS	2	0.02±0.29	5	1.06±1.21	2	0.31±0.59	4	0.98±0.86
REA×BF	1	-0.58±0.00	50	-9.71±2.28	50	-11.20±2.29	50	-9.98±2.21
MS×BF	7	0.62±0.33	4	0.09±0.22	5	0.54±0.33	4	0.07±0.21
REA×MS	1	-0.38±0.00	1	-0.12±0.00	1	-0.43±0.00	1	-0.19±0.00

[1] CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

[2] Co-variables in each model. Model 1: age at slaughter (days) in linear term, Model 2: age at slaughter (days) in linear and quadratic terms, Model 3: body weight at slaughter (kg) in linear term, Model 4: age at slaughter (days) and body weight at slaughter (kg) both in linear terms.

Table 3. Environmental variances (covariances) of (between) carcass traits and their standard errors

Trait[1]	Model 1[2]		Model 2		Model 3		Model 4	
	N	Ave±SE	N	Ave±SE	N	Ave±SE	N	Ave±SE
CWT	82	1,782.91±202.95	69	1,811.21±99.09	102	1,843.54±60.42	82	1,729.86±86.50
BF	38	15.71±1.98	68	15.91±0.86	105	14.35±2.30	82	16.03±0.85
REA	52	113.71±11.49	101	104.28±10.43	101	103.98±12.70	101	99.51±9.92
MS	10	2.26±3.76	10	2.26±3.75	8	2.60±4.13	9	2.40±3.93
CWT×BF	30	71.65±17.01	14	78.63±4.38	50	77.93±4.66	28	74.56±5.63
CWT×REA	50	276.30±31.94	50	263.55±27.63	50	274.70±26.98	50	242.28±27.00
CWT×MS	2	9.82±0.17	5	9.26±0.87	2	7.83±0.40	4	6.84±0.56
REA×BF	1	4.49±0.00	50	12.10±1.78	50	7.48±1.76	50	11.37±1.71
MS×BF	7	0.33±0.27	4	0.72±0.16	5	0.34±0.28	4	0.68±0.16
REA×MS	1	1.35±0.00	1	1.33±0.00	1	0.95±0.00	1	0.93±0.00

[1] CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

[2] Co-variables in each model. Model 1: age at slaughter (days) in linear term, Model 2: age at slaughter (days) in linear and quadratic terms, Model 3: body weight at slaughter (kg) in linear term, Model 4: age at slaughter (days) and body weight at slaughter (kg) both in linear terms.

RESULTS AND DISCUSSION

Variances

Genetic, environmental and phenotypic variances (co-variances) of (between) the four carcass traits from Gibb's sampler are summarized in Table 2, 3, and 4. Significant amount of genetic variation in carcass weight was lost by regressing on. SLWT (model 3) compared to models 1 and 2 where CWT's were regressed on ages at slaughter. Phenotypic variances of carcass weight (CWT, Table 4) were reduced in models 3 and 4 by regressing on body weight at slaughter. But the proportion of genetic variances in model 4 for carcass weight was unchanged by regressing on age at slaughter in addition to body weight at slaughter. Genetic variance from model 2 or that from model 4 was less than those from models 1 or 3 while environmental variance and phenotypic variance from model 3 was less than those from the other three models. Genetic variances of back fat thickness (BF) were estimated to be higher in models 2 and 4 than those from models 1 or 3. Environmental variance of BF from model 3 was lower than those estimated from the other three models, which was consistent with phenotypic variances. Phenotypic variances of rib eye area (REA) were smaller when body weight at slaughter was involved in the covariance models (Models 3 and 4) than when only age at slaughter was considered (Models 1 and 2). However, genetic variance of REA from Model 4 was greater than that from Model 3. And it was similar to the one from Model 2. Marbling score seemed not to be greatly affected by the regression of age at slaughter or body weight at slaughter except that all phenotypic, genetic and environmental variance tended to be high from Model 3 than the others. These marginal posterior means of variances were reflected in their heritability estimates shown in Table 5. Heritability estimate of CWT was the greatest from Model 1 when only linear effect of age at slaughter was involved and was the smallest from Model 3 when body weight at slaughter was involved. Heritability estimates for BF were somewhat higher from Models 1 and 3 than those from Models 2 and 4. And this trend was reversed for REA. Heritability estimates for MS were similar from all four models.

Table 4. Phenotypic variances (covariances) of (between) carcass traits and their standard errors

Trait[1]	Model 1[2]		Model 2		Model 3		Model 4	
	N	Ave±SE	N	Ave±SE	N	Ave±SE	N	Ave±SE
CWT	81	2,044.42±29.30	70	2,046.17±33.93	102	2,004.43±23.79	82	1,945.78±29.80
BF	37	21.05±0.33	68	20.92±0.26	105	19.86±1.31	82	20.86±0.25
REA	52	141.43±3.03	102	140.18±3.92	101	131.90±6.27	101	134.54±4.37
MS	10	3.61±5.23	10	3.60±5.14	8	4.05±5.76	9	3.77±5.39
CWT×BF	29	70.17±1.29	14	71.22±1.62	50	70.96±1.32	28	68.66±1.70
CWT×REA	50	344.36±6.53	51	345.41±7.25	50	329.11±5.78	50	323.09±7.41
CWT×MS	2	9.86±0.08	5	10.37±0.39	2	8.15±0.15	4	7.85±0.36
REA×BF	1	3.76±0.00	50	2.40±0.55	50	-3.70±0.56	50	1.41±0.53
MS×BF	7	0.94±0.07	4	0.80±0.06	5	0.88±0.08	4	0.75±0.06
REA×MS	1	0.97±0.00	1	1.22±0.00	1	0.52±0.00	1	0.75±0.00

[1] CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

[2] Co-variables in each model. Model 1: age at slaughter (days) in linear term, Model 2: age at slaughter (days) in linear and quadratic terms, Model 3: body weight at slaughter (kg) in linear term, Model 4: age at slaughter (days) and body weight at slaughter (kg) both in linear terms.

Table 5. Heritability estimates of carcass traits and their standard errors

Trait[1]	Model 1[2]		Model 2		Model 3		Model 4	
	N	Ave±SE	N	Ave±SE	N	Ave±SE	N	Ave±SE
CWT	81	0.14±0.13	69	0.11±0.06	102	0.08±0.04	82	0.11±0.06
BF	37	0.27±0.13	68	0.24±0.05	105	0.28±0.08	82	0.23±0.05
REA	52	0.19±0.10	101	0.25±0.09	101	0.21±0.09	101	0.26±0.09
MS	10	0.45±0.09	10	0.45±0.12	8	0.43±0.12	9	0.44±0.12

[1] CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

[2] Co-variables in each model. Model 1: age at slaughter (days) in linear term, Model 2: age at slaughter (days) in linear and quadratic terms, Model 3: body weight at slaughter (kg) in linear term, Model 4: age at slaughter (days) and body weight at slaughter (kg) both in linear terms.

Table 6. Genetic correlation coefficients between carcass traits and their standard errors

Trait[1]	Model 1[2]		Model 2		Model 3		Model 4	
	N	Ave±SE	N	Ave±SE	N	Ave±SE	N	Ave±SE
CWT×BF	29	-0.14±0.24	14	-0.33±0.22	50	-0.32±0.23	28	-0.27±0.28
CWT×REA	50	0.73±0.23	50	0.82±0.11	50	0.73±0.25	50	0.84±0.11
CWT×MS	2	-0.01±0.07	5	0.10±0.13	2	0.02±0.07	4	0.11±0.10
REA×BF	1	-0.06±0.00	50	-0.72±0.15	50	-0.82±0.14	50	-0.78±0.13
MS×BF	7	0.28±0.14	4	0.05±0.12	5	0.24±0.14	4	0.04±0.12
REA×MS	1	-0.08±0.00	1	-0.02±0.00	1	-0.09±0.00	1	-0.04±0.00

[1] CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

[2] Co-variables in each model. Model 1: age at slaughter (days) in linear term, Model 2: age at slaughter (days) in linear and quadratic terms, Model 3: body weight at slaughter (kg) in linear term, Model 4: age at slaughter (days) and body weight at slaughter (kg) both in linear terms.

Covariances

Phenotypic co-variances between CWT and BF were similar from all four models (Table 4). Environmental co-variances between these two traits were also similar except that environmental co-variance from Model 1 was somewhat less than those from the other three models. Genetic covariance between CWT and BF was estimated to be negative but the correlation coefficient of which was almost zero when linear function of age at slaughter was engaged (Model 1 and 4 in Table 6). Phenotypic and environmental co-variances and their correlation coefficients between CWT and REA were also similar between models. And the genetic co-variances (Table 2) and their correlation coefficients (Table 6) from Models 2 and 4 were higher than those from Models 1 and 3. Phenotypic co-variances between CWT and MS were small and their correlation coefficients were low and positive. And their environmental co-variances and correlation coefficients became somewhat lower when they were regressed on body weight at slaughter in Models 3 and 4 than when only ages were involved in Models 1 and 2 (Table 7). Genetic correlations between CWT and MS were estimated to be low but slightly positive correlations were found in Models 2 and 4. Covariance estimates between REA and BF were all small resulting in near zero phenotypic correlation coefficient estimates in Table 8. However, their variance components were positive environmentally (Table 7) and highly negative genetically (Table 6). And its magnitude was the highest genetically and negatively from Model 3 (Table 2) and was the highest environmentally and

Table 7. Environmental correlation coefficients between carcass traits and their standard errors

Trait[1]	Model 1[2]		Model 2		Model 3		Model 4	
	N	Ave±SE	N	Ave±SE	N	Ave±SE	N	Ave±SE
CWT×BF	30	0.40±0.19	14	0.45±0.02	50	0.45±0.03	28	0.44±0.03
CWT×REA	50	0.61±0.03	50	0.60±0.03	50	0.60±0.03	50	0.58±0.03
CWT×MS	2	0.22±0.01	5	0.23±0.03	2	0.17±0.02	4	0.17±0.02
REA×BF	1	0.10±0.00	50	0.31±0.06	50	0.23±0.06	50	0.30±0.05
MS×BF	7	0.06±0.05	4	0.14±0.07	5	0.06±0.05	4	0.14±0.07
REA×MS	1	0.11±0.00	1	0.11±0.00	1	0.08±0.00	1	0.08±0.00

[1] CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

[2] Co-variables in each model. Model 1: age at slaughter (days) in linear term, Model 2: age at slaughter (days) in linear and quadratic terms, Model 3: body weight at slaughter (kg) in linear term, Model 4: age at slaughter (days) and body weight at slaughter (kg) both in linear terms.

Table 8. Phenotypic correlation coefficients between carcass traits and their standard errors

Trait[1]	Model 1[2]		Model 2		Model 3		Model 4	
	N	Ave±SE	N	Ave±SE	N	Ave±SE	N	Ave±SE
CWT×BF	29	0.34±0.01	14	0.35±0.01	50	0.35±0.01	28	0.34±0.01
CWT×REA	50	0.64±0.01	51	0.64±0.01	50	0.62±0.01	50	0.62±0.01
CWT×MS	2	0.16±0.00	5	0.17±0.01	2	0.13±0.00	4	0.13±0.01
REA×BF	1	0.07±0.00	50	0.04±0.01	50	-0.08±0.01	50	0.03±0.01
MS×BF	7	0.14±0.04	4	0.11±0.04	5	0.12±0.04	4	0.10±0.04
REA×MS	1	0.06±0.00	1	0.07±0.00	1	0.03±0.00	1	0.04±0.00

[1] CWT: cold carcass weight (kg), REA: longissimus muscle area (cm^2), BF: back fat thickness (mm), MS: marbling score (1-7).

[2] Co-variables in each model. Model 1: age at slaughter (days) in linear term, Model 2: age at slaughter (days) in linear and quadratic terms, Model 3: body weight at slaughter (kg) in linear term, Model 4: age at slaughter (days) and body weight at slaughter (kg) both in linear terms.

positively from Models 2 or 4 (Table 3). Phenotypic co-variances between MS and BF or between REA and MS were estimated to be small with low phenotypic correlations (Table 8). However, genetic correlation coefficients between MS and BF were observed from Models 1 and 3, which were positive.

Heritability estimates of carcass weight were smaller than those by Choy et al. (2005) estimated from Hanwoo population of steers on progeny tests or than those by Kim et al. (2006) for Japanese Black cattle. They (Choy et al., 2005) reported that regressing CWT or REA on body weight at slaughter significantly reduces genetic variances relevant to these traits, which was not the case in this study. This little change might be due to inclusion of data from old cows. The only observable reduction was in the genetic variance of CWT from Model 3. And this difference may be due to very high contribution of environmental variances unidentified by sex and ages at slaughter of females. Heritability estimates of REA, BF and MS were similar to their estimates or to the estimates of REA and MS by Lee et al. (2000). Rios-Utera et al. (2005) analyzed heritability estimates of purebred and composite breeds and showed similar values to Hanwoo population about REA, MS and BF.

Genetic correlation coefficients between CWT and REA estimated in this study (0.73-0.84) were higher than those estimated by Rios-Utera et al. (2005, 0.32-0.52) or by Devitt and Wilton (2001) for crossbred steers in Canada. And these were even higher than those estimated for Hanwoo steers (0.28-0.69) by Choy et al. (2005). Genetic correlation coefficients between CWT and MS in this study (-0.01-0.11) were lower than those estimated by Shanks et al. (2001; 0.20-0.30). Rios-Utera et al. (2005) estimated genetic correlation between hot carcass weight and MS as negative: -0.32 at age-constant endpoint and -0.03 at fat-constant endpoint. Genetic correlation coefficients between REA and BF estimated (-0.82 - -0.72 from Models 2 through 4) were higher in magnitude than those estimated by Rios-Utera et al. (2005). They estimated these to be -0.42 at age-constant basis and -0.55 at weight constant basis. Choy et al. (2005) estimated these in Hanwoo steer population to be -0.09 at age-constant basis and -0.23 at weight constant basis. Very low genetic correlation coefficients between REA and MS estimated in this study (-0.09 - -0.02) were well agreed with those estimated by Rios-Utera et al. (2001) or by Lee et al. (2000). Choy et al. (2005), however, estimated those to be also low but somewhat positive in Hanwoo steer population. Body weight endpoint was more effective for direct selection in favor of yield traits and body weight endpoints affected more of correlated response to selection for the traits of yield and quality of edible portion of beef.

IMPLICATIONS

Genetic variances and co-variances reflect how selection can be applied in the farms. Different slaughter endpoints would be importantly considered when designing mating. Direct and correlated selection responses of and between economically important traits especially carcass characteristics would have considerable amount of directional changes. Most researches in this area dealt with only steer populations. But if carcass measures from different sexes, bulls, heifers or cows were to be analyzed together with steers, slaughter endpoints should be carefully chosen. From the results of this study, body weight at slaughter was favored for faster selection response of carcass yields than age at slaughter endpoint. But if correlated response of fat deposition were to be of interest, body weight at slaughter endpoint would be favored.

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