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Genetic Evaluation of Carcass Traits of Commercial Steers at Different Slaughter End-points

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Carcass records, including pedigree, for 10,441 steers born from 2003 to 2008 and 21,711 animals total, were made available by the Pyengchang Youngwal Jungsun Livestock Cooperative. Data for each trait were adjusted for each of 5 end-points: age (EPA), back fat (EPB), carcass weight (EPC), eye muscle area (EPE), and marbling score (EPM), and adjustments were made by fitting a linear. Genetic parameters were estimated using ASREML, which uses an average information algorithm. At different slaughter end-points, heritability estimates for CWT (range=0.25 to 0.37) and EMA (range=0.17 to 0.33) were more significantly different than heritability estimates for BF (range=0.41 to 0.42) and MS (range=0.40 to 0.45). Genetic correlations between BF and CWT, EMA and CWT, and EMA and MS were positive, and those between BF and EMA and BF and MS were negative. The genetic correlation between CWT and MS yielded conflicting results. Correlations of sire breeding value for BF, CWT, EMA, and MS were in the range of 0.91 to 0.99, 0.75 to 0.93, 0.72 to 0.95, and 0.90 to 0.99, respectively, and those of the dam were in the range of 0.90 to 0.97, 0.73 to 0.94, 0.71 to 0.94, and 0.91 to 0.99, respectively. Further study will be needed to determine whether these alternative end-points result in a more accurate estimate of BV than the traditional age end-point.

Key words: breeding value, genetic correlation, Hanwoo, heritability, slaughter end-points

INTRODUCTION

Hanwoo is a breed of cattle that is native to Korea and has been in use as draft animals for 5,000 years. Compared to Japanese Black cattle, the Hanwoo breed is known for their high marbling, having 15%–23% intramuscular fat (IMF) at final slaughter age (Kim *et al.*, 2005). With regard to carcass value, the marbling score (MS), carcass weight (CWT), eye muscle area (EMA) and back fat thickness (BF) have the greatest influence on profit in the Korean beef industry. The current Hanwoo breeding program has achieved significant rates of genetic gain. For example, an estimate of annual gain over the last 10 years was 8 kg for CWT (2.6% of the average phenotype) and 2.9 cm² (3.8%) for EMA (NIAS, 2009). The rate of improvement for CWT was 0.4 based on genetic standards of deviation per year, which is much higher than the gains in MS (0.04 of a genetic standard deviation). Several factors contribute toward the low rate of gain for MS (Lee, 2011, PhD. thesis). Firstly, MS is estimated using a subjective score rather than an objective measurement such as chemical fat percentage. Secondly, candidate bulls (n=400) are selected

based on live weight (LWT) and average daily gain (ADG) through performance tests. Both LWT and ADG traits are highly correlated with CWT and EMA, but not with MS. Finally, marbling is a late maturing trait in cattle (Pethick *et al.*, 2005). The premiums for high MS are prompting Korean farmers to extend the finishing period for Hanwoo beyond 30 months to further improve marbling scores. However, Korean proven (KPN) bulls are selected based on the breeding value estimated from carcass data slaughtered at 24 months of age from progeny tests. This may explain why genetic progress in CWT and EMA is much greater than in MS.

Currently, the progeny testing evaluation for the selection of KPN occurs every 6 months, and these bulls are distributed across the entire country. It is a well-structured Hanwoo beef production system such as large scale of farm based progeny test that could be re-evaluated breeding value for KPN bulls and cows at different age structure.

In the United States of America, most breed associations currently adjust carcass traits to a constant age when computing breeding value, but age is seldom the primary criterion determining slaughter date in the current production systems (Shanks *et al.*, 2001). It could be argued that the estimated carcass quality grade and external fat more closely represent the slaughter criteria. As for the genetic evaluation at different age structures, Cundiff *et al.* (1969) reported that carcass traits are known to be differently evaluated with different indirect genetic responses according to slaughter end-points, and Koch *et al.* (1995) reported that slaughter end-points can affect the expression of genetic and environmental differences. Because estimated breeding value is cur-

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rently adjusted to an end-point that does not closely match slaughter criteria, breeders need to know whether sires rank differently at alternative end-points (Shanks *et al.*, 2001).

The objective of this study was to estimate genetic parameters and breeding value for carcass traits at different slaughter end-points and to determine whether the ranks of sires and cows vary in EBV when computed at different slaughter end-points.

MATERIALS AND METHODS

Animals

Carcass records for 10,442 steers born from 2003 to 2008 were made available by the Pyengchang Youngwal Jungsun Livestock Cooperative. Summary statistics for the data are provided in Table 1. The completeness of pedigree information for up to 4 generations of Pyeongchang steers are provided in Figure 1. Going further back, the amount of ancestry information dramatically decreases.

Carcass traits analyzed were back fat thickness (BF), cold weight (CWT), ear muscle area (EMA) and marbling score (MS). CWT was measured after overnight chilling. EMA (cm²) and BF (mm) were measured between the 12th–13th ribs. MS (graded on a scale from 1 to 9 where 1 is no intramuscular fat particles found, and 9 is abundant fat particles found) was subjectively evaluated by skilled practitioners at each of the slaughter houses.

Statistical Models

Genetic parameters were estimated for BF, CWT, EMA and MS using an animal model. Before variance component analyses, the GLM procedure of SAS (SAS Inst. Inc., Cary, NC) was used to test the significance of the fixed effects of year of slaughter, month of slaughter, owner, and the linear and quadratic effect of age (covariate). Data for each trait were adjusted to each of the 5 end-points: age (EPA), back fat (EPB), carcass weight (EPC), eye muscle area (EPE), and marbling score (EPM). Adjustments were made by fitting a linear covariate for the chosen end-point. For BF, CWT, EMA and MS were not undertaken when the adjustment was the trait itself.

The data were analyzed using an animal model. For calculation of genetic parameters, the model used was:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{e},$$

where \mathbf{y} is the vector of the observed phenotypes; $\boldsymbol{\beta}$ is the vector of fixed effects, which included the contemporary group (year of slaughter, month of slaughter, owner); \mathbf{a} is the vector of additive genetic effects; \mathbf{e} is the vector of random error effects; \mathbf{X} is the known incidence matrix associating fixed effects in $\boldsymbol{\beta}$ with phenotypes in \mathbf{y} ; and \mathbf{Z} is the known incidence matrix associating random effects with phenotypes in \mathbf{y} .

Furthermore,

Table 1. Simple statistics for carcass traits

	n	Mean	S.D.	Min	Max
AGE ¹	10,442	929.65	56.13	701.00	1263.00
BF ²	10,442	13.66	5.31	1.00	49.00
CWT ³	10,442	424.47	43.81	172.00	614.00
EMA ⁴	10,442	92.01	10.01	9.00	141.00
MS ⁵	10,442	5.71	1.83	1.00	9.00

¹Age=slaughter day; ²BF=back fat thickness; ³CWT=carcass weight; ⁴EMA=eye muscle area;

⁵MS=marbling score

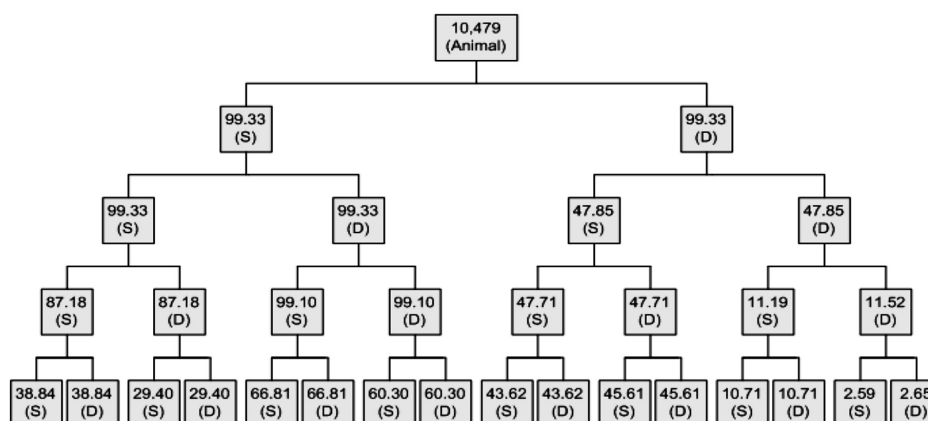


Fig. 1. Completeness of pedigree information for up to 4 generations of Pyeong Chang steer. S stands for sire and D for Dam.

$E[y]=X\beta$; and

$$Var \begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 \\ 0 & I\sigma_e^2 \end{bmatrix}$$

where A is the numerator relationship matrix of the 21,711 animals included in the pedigree, I is the identity matrix of proper order σ_a^2 is the variance due to additive genetic effects, and σ_e^2 is the variance due to random error.

Genetic parameters were estimated using ASREML (Gilmour *et al.*, 2006), which uses an average information algorithm. The program routinely reports log-likelihood statistics, which were used for model comparison, whereas variance components were used to estimate phenotypic and genetic parameters. The animal variance component represented an estimate of the additive genetic variance (σ_a^2), whereas the phenotypic variance (σ_p^2) was obtained from the sum of all variance components. Heritability (h^2) was computed as the ratio between the additive genetic and phenotypic variances.

To measure agreement between the carcass trait BV computed at different slaughter end-points, Spearman rank correlations (SAS Inst. Inc., Cary, NC) were computed among BV values estimated for the same trait at different slaughter end-points. This was done two ways using BV of the sire and dam.

RESULTS AND DISCUSSION

Fixed Effect

The source of the variation, degree of freedom, mean square and test of significance for each trait are shown in Table 2. The year of birth, month of birth and owner of farm were significant ($P<0.05$) for all traits. The linear and quadratic covariate for slaughter age was only non-significant for MS. Because the fixed effect and covariate were significant except for place of EMA and SD1 and SD2 of MS, the year of birth, month of birth, place, owner, linear covariate for slaughter age and quadratic covariate for slaughter age were included in the model.

Heritability

Heritability estimates for carcass traits at different slaughter end-points are shown in Table 3. At different slaughter end-points, heritability estimates for BF, CWT, EMA and MS ranged from 0.41 to 0.42, from 0.25 to 0.37, from 0.17 to 0.33 and from 0.40 to 0.45, respectively. Differences between heritabilities for carcass traits based on age and weight covariates were smaller than other end-points. Heritability estimates for BF and MS differed slightly; however, those for CW and EMA differed greatly. This difference may be due to the effect of slaughter day, which ranged from 701 to 1,263 days. Heritability of BF and MS may have a smaller effect than CWT and EMA on day of slaughter. Our heritability estimates of

Table 2. Source of variation, degrees of freedom, mean square and test of significance for each trait

Source	d.f	BF	CW	EMA	MS
Year ¹	6	890.81**	86,761.89**	3,189.48**	23.65**
Month ²	11	268.13**	2,952.50*	264.68**	6.27*
Place ³	2	148.21**	6,192.12*	45.27	31.73**
Owner ⁴	66	161.11**	15,956.18**	396.93**	17.78**
SD ⁵	1	735.09**	366,412.06**	5,402.79**	1.12
SD2 ⁶	1	616.79**	299,234.90**	4,721.84**	0.21
Error	10,354	26.24	1542.37	93.19	3.19

¹AYear=year of birth; ²Month=month of birth; ³Place=Pyengchang, Youngwal, Jungsun; ⁴SD=slaughter day (linear);

⁵SD2=slaughter day (quadratic); *= $p<0.05$; **= $p<0.01$

Table 3. Heritability estimates for carcass traits at different slaughter end-points

End point	Trait			
	BF	CWT	EMA	MS
EPA ¹	0.42	0.32	0.26	0.44
EPB ²	–	0.25	0.20	0.42
EPC ³	0.42	–	0.33	0.45
EPE ⁴	0.41	0.37	–	0.40
EPM ⁵	0.41	0.28	0.17	–

¹EPA=end point adjusted to age; ²EPB=end point adjusted to backfat; ³EPC=end point adjusted to carcass weight; ⁴EPE=end point adjusted to ear muscle area; ⁵EPM=end point adjusted to marbling score

MS were higher than in other studies of Hanwoo cattle (Lee *et al.*, 2000; Choy *et al.*, 2005; Choy *et al.*, 2008). This might have been due to scalar differences in MS; previous studies used a 1–5 or 1–7 scoring system, while we used a 1–9 scoring system.

When heritability estimates were computed at a constant age, heritability of CWT (0.32) was similar to those (0.32 and 0.33, respectively) reported by Shanks *et al.* (2001) and Rumph *et al.* (2007), and heritability of EMA (0.26) was similar to those reported by Shanks *et al.* (2001), Ríos-utrera *et al.* (2005) and Rumph *et al.* (2007) (0.26, 0.24 and 0.26, respectively). Choi *et al.* (2005), Choi *et al.* (2005) and Ríos-utrera *et al.* (2005) reported a heritability of 0.42, 0.45 and 0.40, respectively, which was similar to the heritability found in the present study (0.44). However, heritability estimates computed at a constant age in this study were generally higher than those reported by other researchers (the difference was greater than 0.05).

When adjusted to a constant BF, heritability estimates for CW and EMA were lower than estimates previously reported (Choy *et al.*, 2005; Shanks *et al.*, 2001; Ríos-utrera *et al.*, 2005; Rumph *et al.*, 2007). However, heritability for MS was higher than previously reported. There was no reported heritability adjusted to a constant

EMA. Heritability estimates computed at a constant weight were higher than those reported by Shanks *et al.* (2001), Ríos-utrera *et al.* (2005) and Rumph *et al.* (2007). There were few reported carcass trait heritabilities adjusted to a constant marbling.

Genetic, Phenotypic and Breeding Value Correlations

Genetic and phenotypic correlations among carcass traits at different slaughter end-points are shown in Table 4. Genetic correlations between BF and CWT, EMA and CWT, and EMA and MS were positive, and genetic correlations between BF and EMA and BF and MS were negative. The genetic correlation between CWT and MS yielded conflicting results. The results of this study were similar to a genetic evaluation report of Hanwoo (NIAS, 2011) but low to high in magnitude. In comparison to several previous studies (Choy *et al.*, 2005; Choy *et al.*, 2008; Lee *et al.*, 2000; Ríos-utrera *et al.*, 2005; Rumph *et al.*, 2007, and Shanks *et al.*, 2001), the genetic correlation between EMA and BF were equally negative, but other genetic correlations were conflicting. These differences may be due to in breed groups, effects of the model, method of estimation, number of observations, measurement errors, and so on.

Table 4. Genetic and phenotypic correlations among carcass traits at different slaughter end-points

Trait and end-point	BF	CWT	EMA	MS
BF				
EPA	–	0.3506	0.0714	0.0810
EPB	–	–	–	–
EPC	–	–	–0.1380	0.0510
EPE	–	0.3671	–	0.0585
EPM	–	0.3259	0.0366	–
CWT				
EPA	0.3053	–	0.5370	0.1077
EPB	–	–	0.5932	0.1215
EPC	–	–	–	–
EPE	0.5012	–	–	0.0037
EPM	0.4331	–	0.5614	–
EMA				
EPA	–0.2892	0.3150	–	0.2156
EPB	–	0.2473	–	0.2407
EPC	–0.4345	–	–	0.1858
EPE	–	–	–	–
EPM	–0.1689	0.1704	–	–
MS				
EPA	–0.2307	0.0671	0.6201	–
EPB	–	0.0511	0.6057	–
EPC	–0.2690	–	0.6128	–
EPE	–0.1984	–0.2871	–	–
EPM	–	–	–	–

phenotypic correlations=above the diagonal; genetic correlations=below the diagonal

Correlations of breeding value for carcass traits at different slaughter end-points are shown in Table 5. At different slaughter end-points, correlations of sire breeding value for BF, CWT, EMA, and MS were in the range of 0.91 to 0.99, 0.75 to 0.93, 0.72 to 0.95, and 0.90 to 0.99, respectively, and correlations of dam breeding value for BF, CWT, EMA, and MS were in the range of 0.90 to 0.97, 0.73 to 0.94, 0.71 to 0.94, and 0.91 to 0.99, respectively. Correlations of BV for the same trait adjusted to different end-points from the sire and dam were small in this study. However, the correlation of CWT and EMA differed greatly with BF and MS. This may be due to heritability estimations for CWT and EMA.

Few studies (Lee *et al.*, 2000; Choy *et al.*, 2005; Choy *et al.*, 2008) have compared estimates of heritability and genetic correlations for carcass traits adjusted to different slaughter end-points in Hanwoo cattle. Therefore, further study will be needed to determine whether these alternative end-points result in a better estimate of BV than the traditional age end-point.

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Table 5. Correlations of breeding value for carcass traits at different slaughter end-points

Trait and end-point	EPA	EPB	EPC	EPE	EPM
BF					
EPA	–	–	0.9378	0.9751	0.9785
EPB	–	–	–	–	–
EPC	0.9495	–	–	0.9063	0.9240
EPE	0.9718	–	0.8984	–	0.9857
EPM	0.9688	–	0.9046	0.9719	–
CWT					
EPA	–	0.8592	–	0.7524	0.8738
EPB	0.8622	–	–	0.7889	0.8867
EPC	–	–	–	–	–
EPE	0.8038	0.7291	–	–	0.9332
EPM	0.9118	0.8431	–	0.9352	–
EMA					
EPA	–	0.9479	0.8493	–	0.7624
EPB	0.9429	–	0.8348	–	0.7810
EPC	0.9213	0.8852	–	–	0.7248
EPE	–	–	–	–	–
EPM	0.7252	0.7064	0.7114	–	–
MS					
EPA	–	0.9902	0.9931	0.8980	–
EPB	0.9792	–	0.9861	0.8990	–
EPC	0.9974	0.9778	–	0.9160	–
EPE	0.9079	0.9169	0.9166	–	–
EPM	–	–	–	–	–

Correlations from sires above diagonal, and correlations from dams below diagonal. All correlations significantly different from zero ($P < 0.0001$)

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