

GENETIC AND PHENOTYPIC CORRELATIONS BETWEEN VARIOUS GROWTH AND CARCASS TRAITS WITH PRIMAL CUT MEAT YIELD TRAITS IN HANWOO CATTLE

H.A. Al-Mamun¹, B. H. Park², M. N. Park², S. Kim² and C. Gondro¹

¹ School of Environmental and Rural Science, University of New England, Australia

² Animal Breeding & Genetics Division, National Institute of Animal Science, Republic of Korea

SUMMARY

Genetic parameters associated with growth, carcass traits and primal cut yields of 1,098 Korean Hanwoo cattle were investigated using medium density (50k) SNP data. The growth and carcass traits considered in the present study included body weights at different ages (6, 12, 18 and 24 months), cold carcass weight (CWT), eye muscle area (EMA), back fat thickness (BFT) and marbling score (MS). Primal-cut yield (percent of carcass weight; composed of both unique and composite meat cuts from the forequarters and hindquarters) included the yields of chuck (CHK), shoulder (SLD), brisket and flank (BAF), ribs (RIB), tenderloin (TLN), striploin (STLN), sirloin (SLN), top round (TRND), round (RND), fore- and hind-shins (FHS), total primal cut (TPC) and Meat %. Heritabilities for traits were all moderate to high, ranging from 0.24 for WT6m to 0.71 for RND. All of the genetic correlations were positive to varying degrees except those between EMA and BFT, and MS and BFT. Genetic correlations among the primal cuts ranged from 0.46±13 (CHK and RIB) to 0.98±13 (TRND and FHS). Except for RIB (-0.29±13), all the other primal cuts had moderate positive genetic correlations with meat yield percentage.

INTRODUCTION

Hanwoo is the most important cattle in Korea and its history traces back 5,000 years. In Korea, it is highly sought after by consumers at premium prices. Both quality and yield determine the carcass' grade and, consequently, its price. Marbling is the major qualitative factor that determines the carcass' grade and drives most of the profit in the Korean beef industry. However, other important traits have received less attention such as yearling weight which influences both meat quality and quantity, and the yields of the primal cuts that command premium prices. Differences in price exist between different primal cuts and large variation in yield of the primals within each grade has been reported (Moon *et al.* 2003). This variation affects the accuracy of the estimates of grading and consequently there is significant averaging in the payment system. Thus, grading based on carcass weights may not reflect the differences within the carcass primal cuts.

Selection for weight of primal cuts requires genetic parameters for these traits as well as other traits that may be used as selection criteria. Few studies have reported genetic parameters for Hanwoo carcass traits and no report to date has used genomic data to estimate these parameters. In this study, we summarize estimates of genetic parameters for several traits including weight at different ages (6, 12, 18 and 24 months), back fat thickness, eye muscle area, marbling score, carcass weight and different primal-cut weights of Korean Hanwoo cattle using medium density SNP data.

MATERIALS AND METHODS

Animals and Traits. The present study analysed the records of 1,092 Hanwoo males raised under the Korean National Hanwoo Cattle Improvement System from 1997 to 2013. Summary data of different traits are shown in Table 1.

Statistical Analysis. Heritability of each trait was estimated using a univariate model in MTG2 software (Lee and van der Werf 2016). As multi-trait (3 x 3 and more) analyses failed to converge, a series of bivariate analyses using MTG2 were used to calculate the genetic correlations between

the traits. Relationship among the animals were accounted for using a genomic relationship matrix (GRM) obtained from SNP data and fitted as a random effect in the model. Phenotypic correlations were calculated as the Pearson correlations between the residuals of the phenotypes after removing the fixed effects using a liner model in R.

RESULTS AND DISCUSSION

Summary statistics for the traits are presented in Table 1. Heritabilities for traits were all moderate to high, ranging from 0.24 for WT6m to 0.71 for RND. Standard errors for the heritabilities ranged between 0.07 and 0.08. Our estimates of heritability differ from the estimates reported by (Choi *et al.* 2015). This may be due to differences in the models used for analysis and sample size. In our analysis, heritabilities were estimated using genomic data (GRM as random effect) whereas Choi *et al.* used pedigree information to estimate the heritabilities. Our heritability estimate for WT12m (0.29±0.07) was slightly lower than literature values ranging from 0.33 to 0.55 (Koots *et al.* 1994; Kemp *et al.* 2002). Our calculated CWT and EMA heritabilities were higher than reported in other literature (Kemp *et al.* 2002; Choi *et al.* 2015). The BFT heritability (0.48±0.08) of the present study was moderate and consistent with the reported BFT by (Reverter *et al.* 2000; Choi *et al.* 2015). In American Shorthorn cattle, (Pariacote *et al.* 1998) reported a similar value (0.46) for carcass fat thickness. Our estimate of MS heritability (0.56±0.08) was slightly higher than those reported in earlier studies ranging from 0.48 to 0.54.

Table 1. Phenotypic mean, standard deviation and heritability with SE

Trait	Mean	SD	h^2 (\pm SE)
WT6m	169.07	31.08	0.24±0.07
WT12m	320.91	41.27	0.29±0.07
WT18m	483.93	52.08	0.39±0.08
WT24m	634.86	67.66	0.48±0.08
CWT	362.33	41.14	0.56±0.08
EMA	81.28	8.72	0.49±0.07
BFT	8.48	3.3	0.48±0.08
MS	3.38	1.56	0.56±0.08
CHK	12.94	3.71	0.34±0.07
SLD	22.84	2.84	0.62±0.07
BAF	27.92	4.95	0.38±0.08
RIB	55.68	7.59	0.41±0.08
TLN	5.8	0.79	0.49±0.08
STLN	34.8	4.55	0.51±0.08
SLN	7.46	1.08	0.50±0.08
TRND	19.52	2.31	0.70±0.07
RND	31.87	3.75	0.71±0.07
FHS	14.46	2.61	0.32±0.08
TPC	233.28	26.15	0.58±0.08
Meat %	64.46	2.72	0.43±0.07

Significant variation in heritabilities were observed for the different primal cuts. For example, CHK and FHS had low heritability (0.34 and 0.32), whereas TRND and RND had higher heritability (0.70 and 0.71). However, all three loin weights had very similar heritabilities ranging from 0.49 (TLN) to 0.51 (STLN). It is difficult to directly compare these heritability estimates with literature values since the definition of primal cuts differ between studies. Nevertheless, in Irish cattle, (Pabiou *et al.* 2009) reported higher heritability for CHK, BAF and SLN, and lower heritability for STLN and RND, and similar heritability for RIB. In terms of meat percentage yield in the present study, our result was in line with the figure (0.42 to 0.47) reported by (Koots *et al.* 1994; Gregory *et al.* 1995). The estimates of heritability for the primal cuts indicate that direct selection may exert a notable influence on traits and that such selection may be accurate because the h^2 estimates of primal cuts are favourable. Table 2 presents the genetic and phenotypic (residuals) correlation between different weight and carcass traits. All of the genetic correlations are positive to varying degrees except those between EMA and BFT; and MS and BFT, which were statistically not different from zero. This may indicate that the traits are independent and genetically distinct. The genetic correlation between weight at different ages and CWT are very high ranging between 0.6 and 0.97, indicating that these traits are probably controlled by similar genes and selection for increased weight is very likely to increase carcass weight. However, selection for carcass traits does not necessarily translate into high meat yield percentage as indicated by the nearly zero correlation (-0.08±0.13) between CWT and Meat % traits. Genetic correlation between EMA and the weight traits are medium and with each of BFT and MS are low to medium.

Table 2. Genetic correlation (above diagonal) and phenotypic correlation (below diagonal) with SE between weight and carcass traits

Trait	WT6m	WT12m	WT18m	WT24m	CWT	EMA	BFT	MS
WT6m	-	0.86±0.05	0.72±0.09	0.63±0.11	0.6±0.11	0.4±0.15	0.15±0.16	0.27±0.15
WT12m	0.86	-	0.94±0.03	0.86±0.04	0.81±0.05	0.51±0.12	0.17±0.15	0.27±0.14
WT18m	0.7	0.89	-	0.97±0.02	0.92±0.02	0.58±0.1	0.28±0.13	0.28±0.13
WT24m	0.61	0.81	0.91	-	0.96±0.01	0.6±0.09	0.23±0.12	0.31±0.12
CWT	0.57	0.77	0.88	0.95	-	0.64±0.08	0.27±0.11	0.26±0.11
EMA	0.28	0.4	0.49	0.54	0.6	-	-0.09±0.13	0.33±0.11
BFT	0.3	0.3	0.28	0.28	0.31	0.05	-	-0.11±0.13
MS	0.14	0.13	0.09	0.08	0.12	0.18	0.1	-

Table 3. Genetic correlations with SE between weight at different ages, carcass traits and primal-cut yields

Trait	WT6m	WT12m	WT18m	WT24m	CWT	EMA	BFT	MS
CHK	0.37±0.18	0.61±0.14	0.61±0.12	0.59±0.11	0.67±0.09	0.58±0.11	-0.16±0.15	0.05±0.14
SLD	0.45±0.13	0.68±0.09	0.73±0.06	0.76±0.05	0.82±0.04	0.70±0.07	-0.04±0.12	0.10±0.11
BAF	0.44±0.16	0.61±0.12	0.73±0.09	0.85±0.06	0.86±0.06	0.60±0.10	0.00±0.15	0.15±0.14
RIB	0.5±0.13	0.71±0.08	0.85±0.05	0.94±0.03	0.96±0.02	0.57±0.10	0.22±0.13	0.44±0.12
TLN	0.59±0.13	0.8±0.08	0.76±0.07	0.76±0.06	0.76±0.06	0.60±0.09	-0.04±0.13	0.18±0.12
STLN	0.52±0.13	0.68±0.08	0.76±0.06	0.83±0.04	0.87±0.03	0.81±0.05	0.03±0.13	0.43±0.11
SLN	0.45±0.14	0.73±0.09	0.77±0.07	0.77±0.06	0.80±0.05	0.85±0.05	0.07±0.13	0.33±0.11
TRND	0.4±0.13	0.62±0.09	0.75±0.06	0.81±0.05	0.86±0.04	0.77±0.06	-0.01±0.11	0.11±0.11
RND	0.45±0.12	0.67±0.08	0.76±0.06	0.8±0.05	0.85±0.03	0.70±0.06	-0.05±0.11	0.20±0.11
FHS	0.4±0.18	0.7±0.12	0.74±0.1	0.78±0.08	0.89±0.06	0.83±0.10	0.16±0.15	0.29±0.14
TPC	0.51±0.12	0.75±0.07	0.85±0.04	0.91±0.02	0.96±0.01	0.76±0.06	0.05±0.12	0.28±0.11
Meat%	-0.21±0.16	-0.12±0.16	-0.15±0.14	-0.1±0.13	-0.08±0.13	0.47±0.12	-0.72±0.08	0.07±0.13

Table 4. Phenotypic correlations between weight at different ages, carcass traits and primal-cut yields

Trait	CHK	SLD	BAF	RIB	TLN	STLN	SLN	TRND	RND	FHS	TPC	Meat %
WT6m	0.23	0.35	0.34	0.52	0.39	0.47	0.41	0.36	0.4	0.26	0.49	-0.22
WT12m	0.35	0.57	0.49	0.68	0.55	0.65	0.57	0.55	0.6	0.44	0.7	-0.19
WT18m	0.44	0.68	0.56	0.75	0.61	0.76	0.65	0.65	0.7	0.54	0.81	-0.17
WT24m	0.47	0.74	0.63	0.82	0.65	0.82	0.69	0.71	0.76	0.58	0.89	-0.16
CWT	0.53	0.8	0.65	0.86	0.69	0.88	0.74	0.76	0.81	0.61	0.94	-0.15
EMA	0.47	0.58	0.43	0.46	0.54	0.69	0.68	0.61	0.6	0.42	0.66	0.2
BFT	-0.02	0.01	0.06	0.36	0.05	0.11	0.1	0.01	0.04	0.06	0.15	-0.48
MS	-0.05	-0.04	-0.12	0.23	0.09	0.2	0.13	-0.05	0.01	0	0.07	-0.13

Poster presentations

In fact, BFT has very low correlation with the rest of the traits. The low correlations between CWT and each of BFT and MS were also reported in (Choi *et al.* 2015) 0.12 and 0.25 respectively, and in (Kemp *et al.* 2002) 0.17 and 0.27 respectively. Phenotypic correlations are also following very similar trend of genetic correlations but generally lower compared to the genetic correlations.

Genetic and phenotypic correlations between weight and carcass traits with different primal cuts are given in Table 3 and Table 4 respectively. There is a clear trend of increase in genetic and phenotypic correlations between weights and different primal cuts as the cattle became older. The WT12m exhibited relatively stronger correlation with TLN and the CWT exhibited stronger correlation with STLN compared to other loin cuts. Choi *et al.* (2015) reported that CWT was more associated with the forequarters and WT12m was more associated with the hindquarters. However, in the present study we did not find any significant differences in association between forequarter and hindquarter cuts with either of the CWT and WT12m traits. BFT has very little or no genetic and phenotypic correlations with the primal cuts. EMA has moderate to high genetic and phenotypic correlations with the primal cuts. MS has low to moderate genetic correlations despite showing very low or no phenotypic correlations.

The correlations among the primal cuts are positive to varying degree (data not shown). Genetic correlations among the primal cuts ranged from 0.46 ± 13 (CHK and RIB) to 0.98 ± 13 (TRND and FHS). Except RIB (-0.29 ± 13), all other primal cuts had moderate positive genetic correlation with Meat %. This indicates that, selection for RIB yield may have a small decreasing effect on total meat yield. Phenotypic correlations ranged from 0.19 (CHK and BAF) to 0.91 (TRND and FHS).

The objective of this study was to estimate genetic parameters for different weight, carcass and primal cut weights in Korean Hanwoo cattle and to determine their correlations using medium-density SNP data. Our present study was limited by the small amount of available carcass data. Together with the recently obtained estimates, further analysis of a larger carcass data set should allow better prediction of outcomes and enhance ongoing genomic evaluation of Korean Hanwoo cattle. We believe that our results will aid in decision making when carcass traits are to be selected to optimize primal-cut yields.

ACKNOWLEDGEMENT

This project was supported by a grant from the Next-Generation BioGreen 21 Program PJ01134906, Rural Development Administration, Republic of Korea and Australian Research Council (DP130100542).

REFERENCES

- Choi T.J., Alam M., Cho C.I., Lee J.G., Park B., et al. (2015) *J. Anim. Sci.* **93**, 1511 - 21.
Gregory K.E., Cundiff L.V. and Koch R.M. (1995) *J. Anim. Sci.* **73**, 1920-6.
Kemp D.J., Herring W.O. and Kaiser C.J. (2002) *J Anim Sci* **80**, 1489-96.
Koots K.R., J.P.Gibson, Smith C. and Wilton J.W. (1994) *Anim Breed* **62**, 308-9.
Lee S.H. and van der Werf J.H. (2016) *Bioinformatics* **32**, 1420-2.
Moon S., Hwang H., Jin K., Lee G., Joo T. et al. (2003) *Asian-Aust J. Anim Sci* **16**, 1049-54.
Pabiou T., Fikse F., Nasholm A., Cromie R., Drennan M.J., et al. (2009) *J Anim Sci* **87**, 3865-76.
Pariacote F., Vleck L.D.V. and Hunsley R.E. (1998) *J. Anim. Sci.* **76**, 2584–8.
Reverter A., Johnston J., Graser U., Wolcott L. and Upton H. (2000) *J. Anim. Sci.* **78**, 1786–95.