

PREDICTION OF GENOMIC BREEDING VALUES OF PRIMAL CUT WEIGHTS IN KOREAN HANWOO CATTLE FROM DIFFERENT GROWTH AND CARCASS TRAITS

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SUMMARY

In Korean beef industry, selection indices are currently limited to carcass weight (CWT), marbling score (MS), eye muscle area (EMA) and back fat thickness (BFT), which are the four traits used to determine the grade of a carcass. However, other important traits have received less attention; for example, yearling weight which influences both meat quality and the yields of the primal cuts that command premium prices. In this paper, we evaluate how well genomic prediction based on routinely measured phenotypes (body weight at different ages 6, 12, 18 and 24 months, CWT and EMA) can predict other commercially important traits (MS, BFT, various primal cuts and total percentage of meat yield) which are not usually recorded. We also compare the prediction accuracy of the primal cuts and yield derived from body weight and carcass weight predictors with the prediction accuracy using the trait itself. Our results suggest that, direct genomic prediction of primal cuts and yield had a higher accuracy, and in the future some consideration should be given to better account for primal cuts and yield in the breeding program.

INTRODUCTION

Hanwoo is the most important cattle in Korea and its history traces back 5,000 years (Jo *et al.* 2012). Hanwoo beef has unique marbling characteristics which makes it highly sought after by consumers at premium prices (Han and Lee 2010; Kim *et al.* 2010; Jo *et al.* 2012). Korean cattle breeding policies are primarily focused on increasing marbling and body weight. These two traits, particularly marbling score, are the key determinants of the carcass' grade and, consequently, its price (Park *et al.* 2002; Kim *et al.* 2010; Alam *et al.* 2013). Since marbling drives most of the profit in the Korean beef industry, producers often prolong feeding periods to achieve better marbling, even if at the expense of increased backfat thickness (BFT) which incurs a grading penalty.

Considerable effort to select superior Hanwoo bulls based on the genetic parameter estimates of carcass traits has already been made (Lee *et al.* 2000; Baik *et al.* 2003; Choy *et al.* 2008). However, selection indices are currently limited to carcass weight (CWT), marbling score (MS), eye muscle area (EMA) and backfat (BFT), which are the four traits used to determine the grade of a carcass. However, other important traits have received less attention; for example, yearling weight which influences both meat quality and quantity (Lopez-Campos *et al.* 2012), and the yields of the primal cuts that command premium prices. Differences in price exist between different primal cuts (Morris *et al.* 2010) 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 out in the payment system. Thus, the current grading scheme based on CWT, MS, EMA and BFT may not accurately reflect the differences within the carcass primal cuts and the actual *realized* sales price in the retail market.

The broad adoption of molecular technologies for genomic selection in livestock species (Hayes *et al.* 2009; Goddard *et al.* 2010) has significantly increased the rate of genetic progress. Genomic selection can provide more accurate estimates of breeding values earlier in the life of breeding animals, higher selection accuracy and shortening of generation intervals. Additionally, hard or expensive to measure traits can be improved more effectively by predicting EBVs of un-phenotyped animals directly from their genotypes (Gondro *et al.* 2013). Thus, genomic selection allows new

traits to be selected on and provides the information needed for better indexes and payment/reward systems. The ability to better align the grading system with the actual retail value of the carcass can provide significant benefits to the Korean beef industry.

In this paper, we evaluate how well genomic prediction based on routinely measured phenotypes (body weight at different ages 6, 12, 18 and 24 months, carcass weight and eye muscle area) can predict other commercially important traits (MS, BFT, various primal cuts and total percentage of meat yield) which are not usually recorded. We also compare the prediction accuracy of the primal cuts derived from body weight and carcass weight predictors with the prediction accuracy using the trait itself.

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. 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), and total primal cut (TPC, sum of all primal cuts) and percentage of meat yield (Meat %). Summary data on different weights, carcass traits and primal-cut yields 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 was 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 was 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 linear model in R.

Prediction of genomic breeding values were obtained from the genomic best linear unbiased prediction (GBLUP) method in MTG2. Prediction accuracy was calculated as the Pearson correlation between the adjusted phenotypes (residuals of the phenotypes after accounting for the fixed effects) divided by the square root of the heritability of the trait. The average of 10-fold cross validation with 10 replicates is reported herein.

RESULTS AND DISCUSSION

Heritabilities for the traits were all moderate to high, ranging from 0.24 for WT6m to 0.71 for RND. Comparing the rest of the traits, top round and round have very high heritability. Standard errors for the heritabilities ranged between 0.07 and 0.08.

Genetic correlations between body weight, carcass weight and EMA with different primal cuts

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

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

are shown in Table 2. Genetic correlations between weights and different primal cuts increase as the cattle become older. Although all primal cuts and the total primal cuts have medium to very high genetic correlations with body weight, carcass weight and EMA, Meat % has very low or negative correlations with these traits except for EMA. EMA has moderate generic correlations with Meat % (0.47±0.12) and selection for EMA can increase percentage of meat yield. WT12m had a relatively higher correlation with TLN and CWT had a higher correlation with STLN compared to other loin cuts.

Table 2. Genetic correlations with SE between weight at different ages, carcass traits and primal-cut yields

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

Prediction accuracy of growth traits and carcass traits using weights at different ages, CWT and EMA are given in Table 3. Weight traits, not surprisingly, are good predictors of each other but poor predictors of BFT and marginally better for MS. EMA could be predicted with reasonable and increasing accuracy from the body weights as the animal ages and from CWT.

| Prediction accuracies of primal cuts and meat yield percentage using weights at different | WT6m | WT12m | WT18m | WT24m | CWT | EMA | BFT | MS |
|---|------|-------|-------|-------|------|------|-------|------|
| | WT6m | 0.34 | 0.31 | 0.25 | 0.22 | 0.23 | 0.18 | 0.03 |
| WT12m | - | 0.38 | 0.34 | 0.29 | 0.30 | 0.22 | 0.06 | 0.10 |
| WT18m | - | - | 0.39 | 0.37 | 0.36 | 0.26 | 0.09 | 0.11 |
| WT24m | - | - | - | 0.41 | 0.41 | 0.29 | 0.08 | 0.12 |
| CWT | - | - | - | - | 0.45 | 0.33 | 0.09 | 0.13 |
| EMA | - | - | - | - | 0.30 | 0.46 | -0.08 | 0.13 |

ages, CWT and EMA are summarized in Table 4. On average, accuracies of primal predictions increase as age increases (0.205 WT6m; 0.279 WT12m, 0.322 WT18m, 0.365 WT24m, 0.405 CWT) but always lower than the accuracies derived from the primal traits themselves (average 0.456). Interestingly all body weights at different ages and CWT failed completely to predict the percentage of meat yield. This could be explained with the fact that, we observed very low or negative genetic and phenotypic (data not shown) correlations between these traits and Meat% trait. However, in comparison to the other traits, EMA performed quite well to predict the percentage of meat yield (accuracy was 28%).

The last row of Table 4 shows the prediction accuracies for the primal cuts when the trait itself was used in the prediction model. On average, prediction of primal cuts from the primal cuts phenotypes themselves increased prediction accuracies in 122.8% in relation to WT6m, 63.27%

WT12m, 41.29% WT18m, 24.87% WT24m, 12.78% CWT and 34.42% EMA. Prediction accuracy of percentage of meat yield from itself had a 46% accuracy.

CONCLUSIONS

Genomic predictions from weights measured later in life and CWT are useful correlated traits to select on primals but come at an increase in generation interval (and CWT is essentially nonsensical in practice). The highest accuracies of selection were obtained directly from the primal cuts themselves but adoption requires investment in phenotyping and genotyping. There is good potential to make better use of genomics to improve selection for high valued cuts and redesign the selection indexes as well as the grading system to better reflect the true value of a carcass.

EMA was somewhat useful to predict yield but weights were very poor predictors; here again, direct genomic prediction of yield had a high accuracy, in the future some consideration should be given to better account for yield in the breeding program.

Table 4. Prediction accuracy of primal cuts weights from weights at different ages, CWT and EMA

| | CHK | SLD | BAF | RIB | TLN | STLN |
|-------|------|------|------|------|------|--------|
| WT6m | 0.18 | 0.23 | 0.18 | 0.18 | 0.23 | 0.22 |
| WT12m | 0.26 | 0.31 | 0.23 | 0.25 | 0.31 | 0.28 |
| WT18m | 0.28 | 0.34 | 0.29 | 0.32 | 0.32 | 0.33 |
| WT24m | 0.29 | 0.39 | 0.35 | 0.39 | 0.35 | 0.38 |
| CWT | 0.34 | 0.43 | 0.38 | 0.42 | 0.36 | 0.42 |
| EMA | 0.32 | 0.37 | 0.27 | 0.26 | 0.30 | 0.38 |
| ^ | 0.41 | 0.52 | 0.38 | 0.42 | 0.45 | 0.47 |
| | SLN | TRND | RND | FHS | TPC | Meat % |
| WT6m | 0.20 | 0.21 | 0.22 | 0.18 | 0.22 | 0.00 |
| WT12m | 0.29 | 0.28 | 0.29 | 0.27 | 0.30 | 0.03 |
| WT18m | 0.32 | 0.34 | 0.34 | 0.30 | 0.36 | 0.01 |
| WT24m | 0.35 | 0.39 | 0.38 | 0.34 | 0.41 | 0.03 |
| CWT | 0.38 | 0.43 | 0.43 | 0.40 | 0.46 | 0.05 |
| EMA | 0.38 | 0.39 | 0.36 | 0.36 | 0.37 | 0.28 |
| ^ | 0.46 | 0.52 | 0.51 | 0.38 | 0.49 | 0.46 |

^ Prediction of the trait from itself

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