

ASSESSMENT OF GENOMIC PREDICTION ACCURACY FOR MEAT QUALITY TRAITS IN HANWOO CATTLE

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SUMMARY

In beef cattle, genomic selection has promising benefits for the improvement of carcass traits such as meat quality, because estimated breeding values can be obtained without sacrificing the selection candidates. The objective of this study was to assess genomic prediction accuracy for meat quality traits in Hanwoo beef cattle. Genomic and phenotypic data from 2,110 Hanwoo steers were used to predict genomic estimated breeding values for marbling score, meat texture and meat colour. The accuracy of the genomic breeding value was assessed by using cross-validation for two scenarios; 1) when the reference population of animals with phenotype and genotype included family members and 2) when family members were excluded. The mean cross-validation accuracy of genomic predictions for marbling score were 0.32 and 0.46 for the distantly and closely related validations set, respectively. These accuracies were 0.28 and 0.39 for meat texture and 0.19 to 0.31 for meat colour. The results indicated that the accuracy of prediction was affected by the heritability of the trait and the degree of relationship between reference and test population. These results were based on a small sample size and should be validated with a larger data set.

INTRODUCTION

Genomic prediction uses DNA information to produce genomically enhanced estimation of breeding values (GBV) and it is increasingly applied in breeding programs for livestock species. The Genome-wide SNP based genomic prediction has the most benefit for traits that are difficult to measure, expensive to record or that are measured late in an animal's life compared to pedigree-based estimates of breeding value (Meuwissen *et al.* 2001). Thus, genomic information can be applied to select young animals for meat quality traits without sacrificing the selection candidates, which is an important advantage of genomic selection in beef cattle. Prediction accuracy of GBV is an important parameter in designing breeding programs with genomic selection. The accuracy of genomic prediction mainly depends on the size and the diversity of the reference population, the heritability of the trait, the linkage disequilibrium (LD) between SNP and QTL, and the methods that will be used for prediction (Daetwyler *et al.* 2012). The accuracy also depends on the relationship between the reference population and the target animals to be predicted (Clark *et al.* 2012). The accuracy of GBVs should be validated before implementing a genomic selection-breeding program and the most common way to assess GBV accuracy is using cross-validation.

Several genomic prediction studies have been reported for meat quality and carcass traits on various beef cattle around the world (Chen *et al.* 2015; Magalhães *et al.* 2019). However, few have included indigenous Korean beef cattle (Hanwoo) and prediction accuracies may differ between breeds due to the effective population size (N_e) differences among breeds. As a result, there is no comprehensive study on assessment of genomic prediction accuracy for marbling score, meat texture and meat colour in Hanwoo cattle. Therefore, the objective of this study was to assess genomic prediction accuracy for meat quality traits in Hanwoo cattle.

MATERIALS AND METHODS

Data structure and quality control. Phenotypic data from 2110 Hanwoo steers were used and all individuals were slaughtered at the same age (24 months). Details of feeding, management practices and traits measurements are reported elsewhere (Bhuiyan *et al.* 2018). Marbling score (MS) was assessed and scored (1 to 9 scale). Similarly, meat colour (MC) was assessed and graded from very light red (grade 3) to dark red (grade 7), and meat texture (MT) was evaluated on a scale from very fine (grade 1) to coarse (grade 3). All animals with phenotypic data were genotyped with the 50k SNP Chip (Illumina Bovine SNP50 BeadChip; Illumina, San Diego, CA). SNPs that had a minor allele frequency (MAF) less than 1% were removed as well as those with p-values for Hardy-Weinberg equilibrium (HWE) less than 0.1%. Finally, 40197 SNPs passed the quality control thresholds and were used for the analysis.

Statistical model and data analysis. Genomic best linear unbiased prediction (GBLUP) was used to predict the breeding value for each trait. The genomic relationship matrix (G) (Yang *et al.* 2010) was used in a univariate linear mixed model to estimate the GBV and heritability. The model was: $y = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$, with \mathbf{b} being a fixed effect of kill group and \mathbf{u} was a random additive genetic effect of the animal with $\text{var}(\mathbf{u}) = \mathbf{G}$. ASReml version 4.1 (Gilmour *et al.* 2015) was used for the data analysis.

Cross-validation. Two 10-fold cross-validation (CV) scenarios were used. In the first scenario, 2110 steers were divided into 10 folds using random sampling of individuals (RCV). Each of the folds ($n=211$, 10%) was used as validation whereas the other folds ($n=1,899$, 90%) were used as the reference population. In the RCV scenario, there was a relatively close relationship between validation and the reference population, because half-sibs of animals in the validation set could be present in the reference population. In the second CV scenario, the 2110 steers were divided into ten folds based on family-based sampling techniques (FCV). Steers in every ten subsets came from 25 sires and the number of steers in each validation data set was varied from 179 to 238. Thus, in the FCV scenario, the validation steers did not have any siblings in the corresponding reference population, indicating that there was a relatively distant relationship between validation and reference population. Finally, the accuracy of GBV was assessed using the Pearson product-moment correlation between GBV and corrected phenotypic value (y_c) divided by the square root of heritability, where y_c was the phenotypic value corrected for the kill batch effect. The bias in the variance of the estimated breeding values was measured through the regression coefficient (slope) of the corrected phenotypes on the estimated

predicted breeding values. $Prediction\ accuracy = \frac{R_{corr}(GBV, y_c)}{\sqrt{h^2}}$ $Prediction\ accuracy = \frac{R_{corr}(GBV, y_c)}{\sqrt{h^2}}$

Summary statistics for meat quality traits Mean, minimum (Min), maximum (Max), standard deviation (SD) and coefficient of variation (CV%) are shown in Table 1.

Table 1. Summary statistics for the three meat quality traits in the 2110 Hanwoo steers

Traits	Sample size	Min	Mean	SD	Max	CV%
Marbling score	2110	1	3.23	1.50	9	46.4
Meat texture	2110	1	1.65	0.50	3	30.3
Meat colour	2110	3	4.8	0.55	7	11.5

RESULTS AND DISCUSSION

Assessment of genomic prediction accuracy. The estimated heritabilities for MS, MT and MC are shown in Table 2, with traits with higher heritability having higher prediction accuracy (Figure 1). In the RCV scenario, MS had the highest (0.46) prediction accuracy, with accuracies being 0.39 for MT and 0.31 for MC. In the FCV scenario, the accuracy of genomic prediction for MC was lower (0.19) compared with 0.32 for MS and 0.28 for MT. As shown in Table 2, the RCV scenario was more accurate and less biased than the FCV scenario for all studied traits.

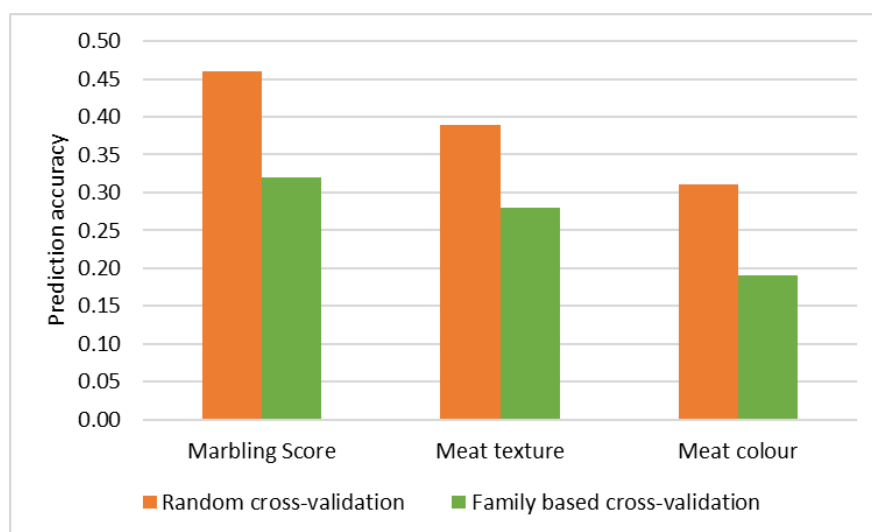


Figure 1. Accuracies of genomic prediction for the three studied traits with random and family-based cross-validations

Table 2. Slope of genomic predictions and heritability for the studied traits

Traits	MS	MT	MC
Slope RCV	0.92±0.11	0.90±0.07	0.77±0.16
Slope FCV	0.88±0.11	0.88±0.15	0.70±0.24
Heritability	0.46±0.05	0.30±0.05	0.15±0.04

In the current study, the empirical accuracy based on FCV were 14, 11 and 12% lower than those based on RCV for MS, MT and MC traits, respectively. A similar study in chicken for the traits associated with growth showed that FCV yielded lower genomic prediction accuracy than RCV (Liu *et al.* 2017). In our study, the accuracy of genomic prediction increased with increasing the relationship between validation and reference population. Similarly, (Clark *et al.* 2012) found that the prediction accuracy was improved as the degree of relationship between the validation and reference population increased. The way of a data splitting strategy for cross-validation affects prediction accuracy. For instance, the RCV does not consider the data structure such as age, family and relatedness, while FCV increases relationships within a group but decreases between groups. Thus, the genetic distance of the reference population from the group of selection candidates determines the accuracy of GBV.

Reports on the accuracy of genomic prediction for beef cattle are limited and are usually based on small data sets. A previous study in Hanwoo cattle showed that the genomic prediction accuracy for IMF varied from 0.37 to 0.45 based on different GRMs (Choi *et al.* 2017) using 778 genotyped Hanwoo steers. The study used 5-fold family-based cross-validation techniques and sampled 706 and 72 steers into reference and validation data sets, respectively. The genomic prediction accuracies for meat quality traits have also been studied in other beef cattle breeds. Chen *et al.* (2015) reported an accuracy of 0.37 for genomic prediction of marbling score in Angus cattle using 543 genotyped steers. A recent study (Magalhães *et al.* 2019) reported a prediction accuracy of 0.40 for a trait associated with meat colour in Nellore cattle using 5000 genotyped animals. In that study, the animals were divided into two groups for reference and validation sets based on year of birth and animals born in

the last year were used as a validation population.

In general, it is difficult to compare the accuracies from different studies because of differences in trait heritabilities, training and validation set sizes, data splitting strategies to reference and validation, and statistical methods to estimate marker effects. Likewise (Luan *et al.* 2009; Daetwyler *et al.* 2012) established that the data splitting strategies to reference and validation affected prediction accuracy.

Furthermore, different breeds have different population structure and vary in diversity. In a less diverse population with small effective population size (N_e), animals share large chromosome segments, which lead to relatively high prediction accuracy. In the current study, moderate (0.31 to 0.46) prediction accuracies were found in the RCV scenario for the studied meat quality traits. The small sample size could affect the prediction accuracy in our study. Therefore, the obtained prediction accuracy in the current study should be confirmed with a large sample size prior to starting the intended breeding program in Hanwoo cattle.

CONCLUSIONS

Genomic predictions for meat quality traits in beef cattle are potentially valuable because it can be applied early in life and do not require potential selection candidates to be sacrificed. Our study shows that marbling score and meat texture traits had higher genomic prediction accuracy, suggesting that selection for these traits may improve meat quality in Hanwoo cattle. The accuracy of genomic prediction was affected by the heritability of the studied traits and the method of sampling the training and validation sets, which affected the degree of relationship between validation and reference populations. Overall, the current estimated genomic prediction accuracy could be affected by the small sample size used in the study and should be confirmed with large sample sizes.

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