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Genomic best linear unbiased prediction-based estimation and comparative analysis of carcass traits in Hanwoo (Korean Brown Cattle)

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Introduction

Hanwoo (Korean Brown Cattle) represents one of the most economically important beef cattle breeds in South Korea, valued for its distinctive marbling, tenderness, and juiciness characteristics. Genomic selection (GS) has emerged as a powerful tool to accelerate genetic improvement in livestock breeding programs by integrating high-density molecular markers with phenotypic data. The adoption of GS techniques has significantly improved the accuracy and efficiency of genetic evaluations in beef cattle populations. Genomic estimated breeding values (GEBVs) computed using genome-wide single–nucleotide polymorphisms (SNPs), enable more reliable and earlier prediction of animal breeding potential compared to traditional pedigree-based methods (Meuwissen *et al*., 2001). Genomic best linear unbiased prediction (GBLUP) is a widely implemented methodology for GEBV estimation due to its computational efficiency and robust predictive accuracy. In Hanwoo cattle breeding, while genomic selection has been predominantly focused on steers for carcass trait improvement, limited information exists regarding the comparative relationship between dam (cow) genomic evaluations and their progeny (steer) carcass performance. Understanding the genetic relationship between dams and their offspring is crucial for optimizing dam selection within integrated breeding systems–a principle whose relative importance shifts markedly when one considers the operational differences between Korea's small-scale, space-constrained feedlot farming and the expansive grazing ranches of the United States and Europe, thereby elevating the significance of dam genetic merit in the Korean system. To address this gap, this study aimed to estimate and compare GEBVs for carcass traits between dams and their progeny steers using the GBLUP method, and to evaluate the predictive accuracy and genetic correlations across maternal and progeny populations.

Materials & Methods

Population structure and genotyping. The test population comprised 962 Hanwoo cattle: 464 dams (cows at the end of their productive life) and 498 of their progeny steers. The dams and steers in the test population represented parent–offspring relationships, with the steers being the progeny of the dams in the test set. All animals were genotyped using a SNP50K chip. Carcass measurements for both dams and steers were obtained at slaughter, and four carcass traits were measured: carcass weight (CWT), eye muscle area (EMA), backfat thickness (BFT), and marbling score (MS). In this test population, dams were slaughtered at an average age of 102.3 months, whereas their progeny steers were slaughtered at an average age of 29.0 months. To examine the genetic merit of dams based on their progeny's performance, the carcass phenotypes of the steers were analyzed as a representation of maternal genetic contribution rather than considering the dams own phenotypes. The reference population consisted of 9,170 steers with both genotypic and phenotypic records

for the same four carcass traits, including sires of the test population steers. No overlap was observed between the test population steers and the reference population.

Genetic variance estimation and GBLUP model. Variance components were estimated using AIREMLF90 (Misztal *et al.*, 2024). The GBLUP model was structured as follows:

$$\mathbf{y}=\mathbf{Xb}+\mathbf{Z}u+\mathbf{e} \quad (1)$$

where y represents the vector of phenotypic observations, X and Z denote the incidence matrices for fixed and genomic random effects respectively, b is the vector of fixed effect estimates, u is the vector of genomic breeding values following $u \sim N(0, G\sigma^2_a)$ where G is the realized genomic relationship matrix, and e is the random error vector following $e \sim N(0, I\sigma^2_e)$. Fixed effects included sex, birth month–year, and slaughter month–year. GEBVs and prediction accuracies were estimated using BLUPF90 (Misztal *et al.*, 2024).

Heritability and accuracy calculation. Heritability was estimated as

$$\mathbf{h^2} = \boldsymbol{\sigma^2_a}/(\boldsymbol{\sigma^2_a} + \boldsymbol{\sigma^2_e}) \quad (2)$$

where σ^2_a is the additive genetic variance, σ^2_e is the residual environmental variance, and $\sigma^2_a + \sigma^2_e$ represents the total phenotypic variance. Prediction accuracy was calculated as

$$\mathbf{Acc} = \sqrt{[1 - (\mathbf{PEV}/\boldsymbol{\sigma^2_a})]} \quad (3)$$

where Acc represents the accuracy of genomic prediction for individual i, PEV is the prediction error variance, and σ^2_a denotes the additive genetic variance. Phenotypic and genomic correlations between dams and steers were estimated for all carcass traits.

Results

Genetic parameters and GEBV prediction. Heritability estimates were moderate to high: 0.464 for CWT, 0.388 for EMA, 0.377 for BFT, and 0.454 for MS. On the phenotypic scale, dams had lower carcass performance than steers, with mean CWT, EMA, BFT, and MS of 356.1 ± 56.1 kg, 85.4 ± 14.3 cm², 14.5 ± 6.9 mm, and 3.70 ± 1.98 points, respectively, compared with 462.2 ± 59.4 kg, 97.5 ± 12.7 cm², 13.3 ± 5.1 mm, and 6.29 ± 1.92 points in steers. Mean GEBVs for dams were −5.18 ± 23.25 kg (CWT), −0.81 ± 4.93 cm² (EMA), 0.03 ± 2.07 mm (BFT), and −0.11 ± 0.75 points (MS). For steers, mean GEBVs were 4.80 ± 29.40 kg (CWT), 0.76 ± 5.69 cm² (EMA), −0.02 ± 1.98 mm (BFT), and 0.10 ± 0.95 points (MS). The observation that dams often showed higher standard deviations (SD) in their GEBVs compared to steers was primarily a result of their representation in the study's test population versus the reference population.

Table 1. Genetic parameters and prediction accuracy for carcass traits.

Trait	Heritability	Accuracy				R^2	
		Dam		Steer			
		Mean	SD	Mean	SD	Dam	Steer
CWT	0.464	0.650	0.075	0.730	0.034	0.515	0.680
EMA	0.388	0.625	0.073	0.705	0.035	0.478	0.590
BFT	0.377	0.605	0.072	0.685	0.036	0.505	0.682
MS	0.454	0.643	0.075	0.723	0.034	0.483	0.717

[1] CWT: carcass weight; EMA: eye muscle area; BFT: backfat thickness; MS: marbling score; R^2: coefficient of determination between GEBV and phenotype.

Prediction accuracy and genetic relationships. Mean prediction accuracies for dams ranged from 0.605 to 0.650 across traits, with CWT achieving the highest value (0.650) and BFT the lowest (0.605). For steers, prediction accuracies were substantially higher, ranging from 0.685 to 0.730, with MS showing the highest value (0.723). These accuracies in steers were highly dependent on the reference population (n=9,170) and close genomic relationships to reference animals. Specifically, coefficients of determination between

GEBVs and phenotypic values were 0.59–0.72 in steers and 0.48–0.52 in dams across all traits. For instance, GEBV explained 68% of CWT variation in steers compared with only 51.5% in dams, and 71.7% and 48.3% for MS, respectively. These differences reflect both prediction accuracy variations and closer genomic relationship strength between steers and reference population animals. Pairwise correlation analysis revealed positive genetic correlations (r>0.50) between dam and steer GEBVs for all carcass traits, indicating substantial genetic similarity in breeding values for carcass performance between maternal and progeny groups. These findings confirm the availability of using maternal genomic information to predict progeny carcass performance and demonstrate that both dam and progeny genomic data provide complementary information for integrated breeding programs.

Discussion

This study demonstrates that GBLUP-based genomic prediction provides reliable estimates of breeding values for carcass traits in Hanwoo cattle, with prediction accuracy and reliability varying between dams and steers. The heritability estimates (0.38–0.46) align with previous findings in Hanwoo and other beef cattle populations, indicating substantial genetic variation and significant potential for improvement through selection. The prediction accuracies of 0.61–0.65 for dams and 0.69–0.73 for steers represent meaningful improvements over pedigree-based methods and are comparable to previously reported genomic studies in Hanwoo (Mehrban *et al*., 2021; Haque *et al*., 2023). The enhanced accuracy in steers compared to dams is primarily attributable to the reference population of steers (n=9,170), which provides substantial genetic information for effect estimation and closer genomic relationships between test and reference animals. Although these model-based accuracies derived from prediction error variances are informative, they are conditional on the genomic relationship structure between the test and reference populations, and thus partly reflect the closer relationships of steers to the reference animals. A more direct assessment of predictive ability would be obtained from cross-validation schemes based on the correlation between GEBV and adjusted phenotypes within the reference population; however, such cross-validation analyses were beyond the scope of this four-page contribution and are therefore identified as an important direction for future studies. Additionally, SNP effects were captured more efficiently in steers, likely due to more uniform environmental conditions in performance testing facilities. The positive genetic correlations (r>0.50) between dam and steer GEBVs for all traits indicate that dam genomic information effectively predicts progeny carcass performance, supporting the integration of dam genomic data into breeding programs (Lee *et al*., 2022). This finding has important implications for integrated breeding systems, suggesting that incorporating dam genomic selection can improve accuracy of offspring phenotypic prediction, even before progeny reach slaughter age. The moderate R^2 values in dams (0.48–0.52), while lower than in steers, confirm that GEBVs capture approximately half of phenotypic variation, providing substantial value for selection despite dams' absence from the reference population. These findings support implementing comprehensive genomic evaluation of both sexes to optimize genetic gain and manage inbreeding more effectively in Hanwoo breeding programs. The fact that reliable GEBVs can be estimated for dams when the reference population comprises only steers suggests that genomic selection should be implemented for dam’s genetic improvement. Future advancement in Hanwoo breeding programs requires constructing reference populations that include both sexes and expanding their size to achieve higher accuracy and more reliable GEBV estimates.

Conclusions

GBLUP-based genomic prediction provides accurate and reliable estimates of breeding values for carcass traits in both Hanwoo dams and progeny steers. Moderate heritability

(0.38–0.46) and positive genetic correlations (r>0.50) between populations confirm substantial genetic variation and similarity in carcass trait expression across generations. Prediction accuracies of 0.61–0.65 in dams and 0.69–0.73 in steers demonstrate the utility of genomic information for selection of breeding candidates. The significant genetic correlations between maternal and offspring GEBVs establish the feasibility of using dam genomic data to predict progeny performance. These findings indicate that incorporating genomic information from both dams and steers into current Hanwoo breeding programs can enhance selection accuracy and accelerate genetic improvement for economically important carcass traits. Future research should explore multi-trait genomic selection approaches to simultaneously improve multiple carcass traits while maintaining genetic diversity, and investigate long-term response to selection and inbreeding rates under genomic selection schemes to ensure sustainable genetic improvement.

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