

## Original Article

# Genetic evaluation for economic traits of commercial Hanwoo population using single-step GBLUP

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### ABSTRACT

**Background:** Recently, the single-step genomic best linear unbiased prediction (ssGBLUP) method, which incorporates not only genomic information but also phenotypic information of pedigree, is under study. In this study, we performed a ssGBLUP analysis on a commercial Hanwoo population using phenotypic, genotypic, and pedigree data.

**Methods:** The test population comprised Hanwoo 1,740 heads raised in four regions of Korea, while the reference population used Hanwoo 18,499 heads raised across the country and two-generation pedigree data. Analysis was performed using genotype data generated by the Hanwoo 50 K SNP beadchip.

**Results:** The mean Genome estimated breeding values (GEBVs) estimated using the ssGBLUP methods for carcass weight (CWT), eye muscle area (EMA), back fat thickness (BFT), and marbling score (MS) were 7.348, 1.515, -0.355, and 0.040, respectively, while the accuracy of each trait was 0.749, 0.733, 0.769, and 0.768, respectively. When the correlation analysis between the GEBVs as a result of this study and the actual slaughter performance was confirmed, CWT, EMA, BFT, and MS were reported to be 0.519, 0.435, 0.444, and 0.543, respectively.

**Conclusions:** Our results suggest that the ssGBLUP method enables a more accurate evaluation because it conducts a genetic evaluation of an individual using not only genotype information but also phenotypic information of the pedigree. Individual evaluation using the ssGBLUP method is considered effective for enhancing the genetic ability of farms and enabling accurate and rapid improvements. It is considered that if more pedigree information of reference population is collected for analysis, genetic ability can be evaluated more accurately.

**Keywords:** accuracy, carcass traits, genetic evaluation, Hanwoo, ssGBLUP

## INTRODUCTION

Hanwoo (also known as Korean Native Cattle; *Bos taurus coronae*) is a native breed of beef cattle in South

Korea, well known (highly sought) for its excellent meat quality. Excessive marbling has emerged as a significant meat product quality determinant in commercial beef markets (Choy et al., 2012; Choi et al., 2015). Research

on Hanwoo breeds has been conducted for many years and has expanded in recent years. In breeding, selection is commonly based on the breeding value calculated using the best linear unbiased prediction (BLUP) approach, which utilizes an individual's phenotypic and pedigree data. BLUP is arguably the most frequently used selection technique for determining estimated breeding values (EBVs) (Henderson, 1984; Meuwissen et al., 2001). Genomic selection (GS) is a widely recognized tool for genetic improvement. GS implementation has evolved rapidly in various livestock and plant species (Meuwissen et al., 2001; VanRaden, 2012; Misztal et al., 2020). The statistical method for GS is the genomic best linear unbiased prediction (GBLUP) method, which is based on the infinitesimal model, and the breeding value is evaluated using the genomic relationship matrix (GRM) rather than the Numerator Relationship Matrix (Garrick, 2007; VanRaden, 2007; Zhang, 2007). The GBLUP method calculates single nucleotide polymorphism (SNP) effects based on individual SNP and phenotypic information using SNP data evenly distributed over the whole genome using SNP chips (Meuwissen et al., 2001). The breeding value of individuals lacking phenotypic data can be estimated using their SNP information and pre-calculated SNP effect values. Additionally, even with an identical pedigree, the breeding value of an individual can be estimated precisely because of the ability of the GBLUP method to create a GRM.

The single-step genomic best linear unbiased prediction (ssGBLUP) integrates all phenotypic, pedigree, and genomic information (genotypic data) in a single-step analysis, which is available simultaneously to predict genomic merit values for genotyped and non-genotyped animals through a combined matrix (Gao et al., 2019; Song et al., 2019). Furthermore, it enables more precise and effective estimates of genetic parameters. Numerous genomic selection studies in beef cattle (Gordo et al., 2016; Lee et al., 2017), dairy cattle (VanRaden, 2020), pigs (Forni et al., 2011; Xiang et al., 2016), and chickens (Chen et al., 2011) have demonstrated the advantages of ssGBLUP in various domesticated animals. Therefore, this study investigated the genomic estimated breeding value (GEBV) of a commercial Hanwoo population using the ssGBLUP method and phenotypic, genotypic, and pedigree information. Additionally, the accuracy of the estimated GEBV was determined by analyzing its accuracy.

## MATERIALS AND METHODS

### Test population

We performed a ssGBLUP analysis on a commercial Hanwoo population using phenotypic, genotypic, and pedigree data (Table 1). The analyzed population comprised a reference population and a test population. To determine the genotype of the test population, DNA was collected from 1,740 tail hair root samples from 1,221 Hanwoo cows and 519 steers raised in the Gyeonggi, Gangwon, Chungbuk, and Gyeongbuk provinces. The extracted DNA was analyzed by determining the genotype using a Hanwoo 50 K SNP BeadChip (Illumina, San Diego, CA, USA). For the test population, information on 1,740 heads was collected from three generations of pedigree.

### Reference population

The reference population for the analysis used genotype information from 18,499 cattle raised and transported across the country. Pedigree information was collected from the Korean Animal Improvement Association and used for analysis. For the reference population, information from two generations of pedigree on 18,499 heads was collected, and a total of 74,730 heads information were analyzed. The Livestock Product Quality Evaluation Institute provided phenotypic information on 62,567 of the 74,730 heads, including carcass weight (CWT), eye muscle area (EMA), back fat thickness (BFT), and marbling score (MS).

### Genomic information quality control (QC)

To increase the accuracy of the analysis, QC was performed on the SNP information, and unnecessary SNPs were removed. Genotype information was generated from raw data using the GenomeStudio 2.0 software (Illumina Inc., 2016). Plink version 1.9 (Purcell et al., 2007; Chang et al., 2015) was used for QC after the final report file was converted into an input file format. The QC criteria were

**Table 1.** Total number of references and test population

Sex	Test population	Reference population	
		Pedigree	Genotype
Cow	1,221	36,327	355
Steer	519	38,403	18,144
Total	1,740	74,730	18,499

minor allele frequency (MAF) < 1% (4,721), SNP call rate < 90% (730), and Hardy-Weinberg equilibrium  $p$ -value <  $1 \times 10^{-7}$  (1,898). After removing 6,647 SNPs that did not meet the QC criteria, The final dataset included 45,548 SNPs from 52,195 SNPs.

### Statistical analysis

The program used for object evaluation was the BLUPF90 family program (Miszta et al., 2014). Genetic parameters were estimated to assess GEBV. Genetic parameters were estimated using the AIREMLF90 program (Miszta et al., 2014), with year and month of birth, year and month of slaughter, and sex as fixed effects. The mixed linear model used to estimate the dielectric parameters of the additive genetic effect is as follows (Henderson, 1975):

$$Y_p = X\beta + Z\mu + e$$

where  $Y_p$  is the actual observed values of the four major economic traits (CWT, EMA, BFT, and MS), where  $Z$  is the random effect vector of individuals,  $\beta$  is a vector of estimates for unknown fixed effects (year and month of birth, year and month of slaughter, and sex),  $\mu$  is the additive genetic effect,  $e$  is the random environmental effect (Henderson and Quaas, 1976). The breeding value estimated using the ssGBLUP method was BLUPF90 (Miszta et al., 2014), and  $H^{-1}$  was generated using PREGSF90 (Miszta et al., 2014). The analysis was performed single trait analysis and the estimation of  $H^{-1}$  was performed using the following formula (Miszta et al., 2014):

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ \alpha G^{-1} & \beta A_{22}^{-1} \end{bmatrix}$$

$H$  is a relationship matrix constructed from the pedigree and genotype information.  $A$  is an NRM based on pedigree, whereas  $G$  is a GRM based on genotype.  $\alpha$  and  $\beta$  are the correction values for  $G$  and  $A$ , respectively.  $\alpha$  (0.95) and  $\beta$  (0.05) were analyzed using default parameter settings.

The heritability was calculated using the following formula using the estimated genetic parameters.

$$h^2 = \frac{\sigma_\alpha^2}{\sigma_p^2} \quad \sigma_p^2 = \sigma_\alpha^2 + \sigma_e^2$$

Where  $h^2$  is heritability for each trait,  $\sigma_\alpha^2$  is the represents genetic variance,  $\sigma_e^2$  is the represents residual variance and  $\sigma_p^2$  is phenotypic variance. Heritability can be calculated as the percentage of genetic variance to phenotypic variance, which is the sum of genetic and residual variances.

### Accuracy analysis

The accuracy of the GEBV estimated using the ssGBLUP method was estimated. Accuracy was calculated using the standard error of the breeding value estimated for each individual among the solution values generated using the BLUPF90 program (Miszta et al., 2014) and the additive genetic variance estimated using the AIREMLF90 program (Miszta et al., 2014) analysis. Accuracy was calculated as follows:

$$\text{Accuracy} = \sqrt{1 - \left(\frac{PEV}{\sigma_\alpha^2}\right)}$$

where accuracy is the estimated breeding value accuracy,  $PEV$  is the standard error of the estimated breeding value for each individual, and  $\sigma_\alpha^2$  is the estimated genetic variance. Accuracy was analyzed by determining the correlation coefficient between the observed phenotype of the test population and GEBV using the ssGBLUP method, and the proximity between carcass characteristics and GEBV was confirmed.

## RESULTS

### Basic statistical analysis of the reference population

To estimate the GEBV using the ssGBLUP method, phenotypic data from 62,567 heads of the Hanwoo population slaughtered throughout the country were used for analysis, and genotype data from 18,499 heads of the Hanwoo population slaughtered throughout the country served as reference population genotype data. Table 2 presents the basic statistics. The basic statistics for the entire pedigree information were  $349.37 \pm 54.13$  kg,  $83.86 \pm 12.67$  cm<sup>2</sup>,  $13.80 \pm 6.09$  mm, and  $4.01 \pm 1.93$  score for Hanwoo cows CWT, EMA, BFT, and MS, respectively. However, for steers, the statistics were  $442.02 \pm 55.20$  kg,  $95.15 \pm 12.33$  cm<sup>2</sup>,  $13.80 \pm 5.10$  mm, and  $5.82 \pm 1.95$  score, respectively. Kim et al. (2022) compiled the genomic and phenotypic information of Hanwoo cows and steers shipped across the country as the reference population for ssGBLUP analysis after researching the basic statistics of the reference population analyzed in previous studies. The basic statistics including cows without genomic information  $352.92 \pm 46.77$  kg,  $83.73 \pm 11.49$  cm<sup>2</sup>,  $13.32 \pm 5.37$  mm, and  $4.36 \pm 1.9$  score, respectively. Furthermore, for steers without genomic information, the basic statistics were  $443.51 \pm 49.80$  kg,  $93.72 \pm 11.53$  cm<sup>2</sup>,  $13.62 \pm 5.05$  mm, and  $5.94 \pm 1.84$  score, respec-

**Table 2.** Basic statistics of reference population according to the ssGBLUP method

Subset	Sex	No.	Traits	Mean	S.D.	Max	Min
Pedigree + genotype	Cow	27,264	CWT (kg)	349.37	54.13	667	110
			EMA (cm <sup>2</sup> )	83.86	12.67	147	22
			BFT (mm)	13.80	6.09	77	1
			MS (score)	4.01	1.93	9	1
	Steer	35,303	CWT (kg)	442.02	55.20	745	148
			EMA (cm <sup>2</sup> )	95.15	12.33	171	20
			BFT (mm)	13.80	5.10	51	1
			MS (score)	5.82	1.95	9	1
Genotype	Cow	355	CWT (kg)	356.16	47.94	498	159
			EMA (cm <sup>2</sup> )	87.87	12.17	119	38
			BFT (mm)	13.89	5.03	37	4
			MS (score)	4.95	1.99	9	1
	Steer	18,144	CWT (kg)	444.01	49.57	692	160
			EMA (cm <sup>2</sup> )	96.70	12.25	160	20
			BFT (mm)	14.27	4.93	47	1
			MS (score)	5.98	1.87	9	1

CWT, carcass weight; EMA, eye muscle area; BFT, back fat thickness; MS, marbling score; SD, standard deviation.

tively.

Park et al. (2020) conducted a genetic evaluation on Korean Hanwoo steer information raised by the National Institute of Animal Science. They included Hanwoo steers without genomic information and computed basic statistics for CWT, EMA, BFT, and MS. The reported scores were  $371.63 \pm 42.07$  kg,  $81.65 \pm 8.82$  cm<sup>2</sup>,  $9.71 \pm 3.82$  mm, and  $3.58 \pm 1.62$  score, respectively. When compared with the results of this study, the reference livestock basic statistics value of Kim et al. (2022) showed similar values to the study's results, although it was higher than the findings of Park et al. (2020). Park et al. (2020) used nationally managed steering data from 1997 to 2018, which was thought to be the result of including relatively young individuals.

To test the normality of the complete reference population, the findings of quantile-quantile plots (Q-Q plots) for each trait (CWT, EMA, BFT, and MS) are shown in Fig. 1. As a result of the Q-Q plots, outlier values that strayed from the line were identified, but they were included in the analysis because they represented the diversity of the individual.

### Estimation of genetic parameter

Genetic parameters were estimated by the ssGBLUP method. Table 3 presents the estimation results of the genetic parameters for genetic variance, residual variance, and heritability. The genetic variance was estimated

to be 980.84, 50.594, 15.072, and 1.609 for CWT, EMA, BFT, and MS, respectively. The residual variances were estimated to be 1530.4, 97.642, 17.660, and 1.894, and the heritability values using genetic and residual variances were estimated to be 0.391, 0.341, 0.460, and 0.459, respectively. After reviewing previous studies, Kim et al. (2022) estimated the ssGBLUP accuracy based on the amount of genomic information available in the pedigree. They reported heritability values of 0.429, 0.372, 0.357, and 0.471 for the CWT, EMA, BFT, and MS treatments, respectively. Lopez et al. (2020) found heritability values of 0.38, 0.34, 0.38, and 0.48 in an imputation accuracy study using the Bovine HD BeadChip (777 k) and Hanwoo 50 K SNP beadchip. Compared to the results of this study, the analysis included the phenotype of cows, which is thought to be the reason why the BFT heritability was estimated to be low. According to Park et al. (2020), heritability estimates for CWT, EMA, BFT, and MS were 0.35, 0.44, 0.46, and 0.56, respectively. In contrast to the results of this study, the heritability of BFT and CWT was low because the population used in the previous study differed from the population used in this study by using nationally managed individuals.

### Accuracy analysis of breeding value

Table 4 lists the GEBV, GEBV accuracy, and realized accuracy of the subjects, estimated using the ssGBLUP method. The mean GEBV estimated using the ssGBLUP

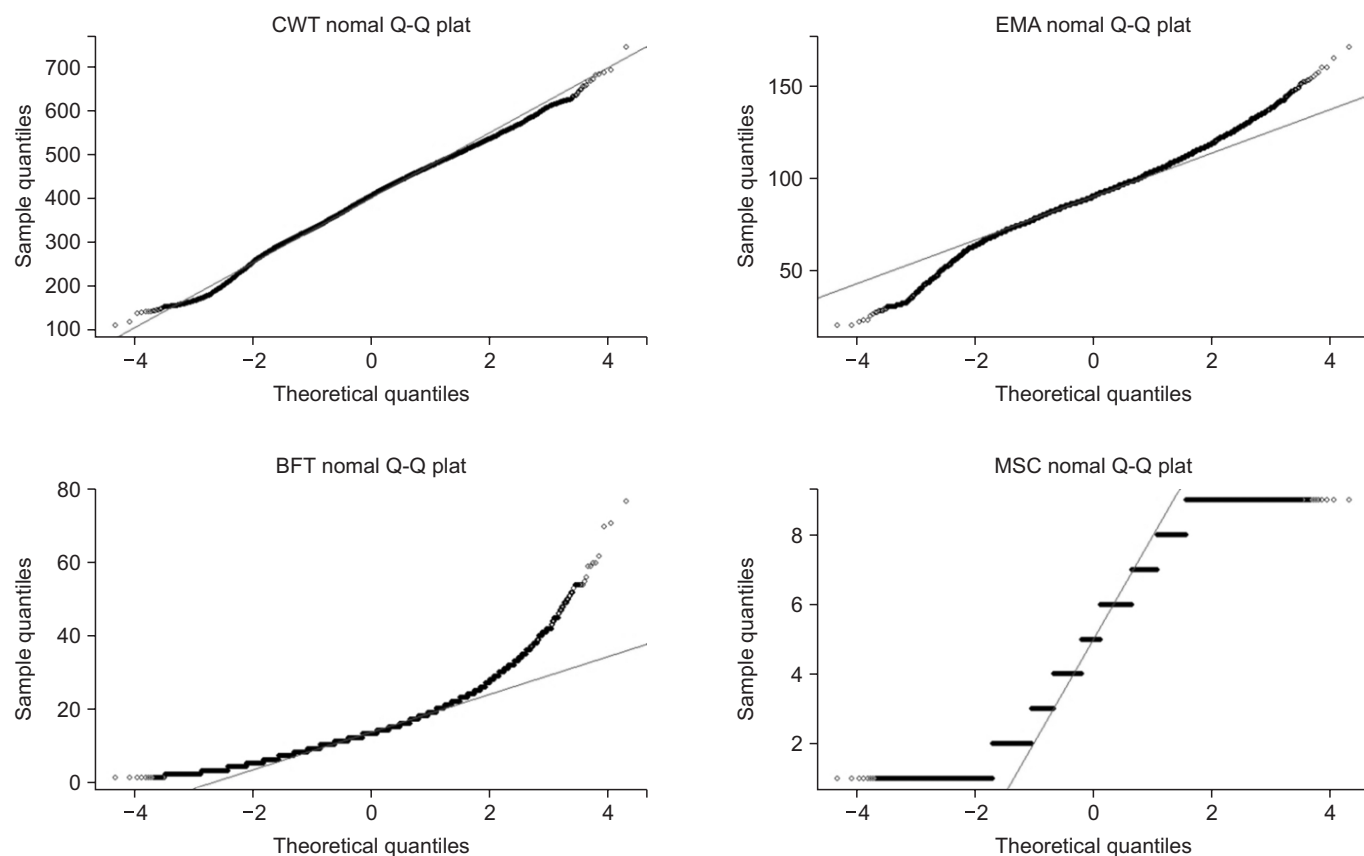


Fig. 1. Quantile-quantile plot (Q-Q plot) for the four carcass traits in the ssGBLUP reference population.

Table 3. Genetic parameters estimated using the ssGBLUP method based on genotype and pedigree information

Analysis method	Type	Trait			
		CWT	EMA	BFT	MS
ssGBLUP method	Genetic Variance	980.84	50.594	15.072	1.609
	Residual Variance	1,530.4	97.642	17.660	1.894
	Heritability	0.391	0.341	0.460	0.459

ssGBLUP, single-step genomic best linear unbiased prediction; CWT, carcass weight; EMA, eye muscle area; BFT, back fat thickness; MS, marbling score.

methods for CWT, EMA, BFT, and MS were 7.348, 1.515, -0.355, and 0.040, respectively and the accuracy of each trait was 0.749, 0.733, 0.769, and 0.768, respectively. The accuracy of GEBV was highest for BFT and lowest for EMA. Because the breeding value accuracy was affected by the estimated heritability, it showed the same pattern as that of the previous heritability. Kim et al. (2022) conducted a comparative study of the accuracy of ssGBLUP based on the amount of genomic information in the pedigree. They observed that the highest accuracies among the GEBV were 0.736, 0.718, 0.713, and 0.747 for CWT,

EMA, BFT, and MS, respectively. Park et al. (2020) reported that for CWT, EMA, BFT, and MS, the accuracies of the estimated breeding values using the ssGBLUP method were 0.68, 0.69, 0.69, and 0.73, respectively. Lopez et al. (2020) reported that the breeding value accuracy estimated using the ssGBLUP method through single-trait analysis was 0.47, 0.42, 0.33, and 0.37 for CWT, EMA, BFT, and MS, respectively. Previous studies have reported a lower accuracy of the mean GEBV than the results obtained in this study. This difference is attributed to the larger size of the reference population used in this study compared to



**Table 4.** Breeding value, accuracy, and realized accuracy were estimated using the ssGBLUP method

Analysis method	Reference population size	Type	Trait			
			CWT (kg)	EMA (cm <sup>2</sup> )	BFT (mm)	MS (score)
ssGBLUP method	18,499 + 74,730	GEBV	7.348	1.515	-0.355	0.040
		Standard Error	20.689	4.824	2.475	0.809
		Accuracy	0.749	0.733	0.769	0.768
		Realized accuracy	0.519	0.435	0.444	0.543

ssGBLUP, single-step genomic best linear unbiased prediction; CWT, carcass weight; EMA, eye muscle area; BFT, back fat thickness; MS, marbling score; GEBV, genomic estimated breeding value.

previous studies. Because the ssGBLUP method estimates GEBV using individual genotype information and pedigree phenotypic information, the larger the reference population, the more diverse the information can be explained.

After confirming the correlation analysis (realized accuracy) between the GEBV and the actual slaughter performance, CWT, EMA, BFT, and MS were reported to be 0.519, 0.435, 0.444, and 0.543, respectively. The realized accuracy was the highest for MS and the lowest for EMA. In a previous study, Lee et al. (2023) demonstrated that the realized accuracy values in the genetic ability evaluation of a commercial Hanwoo population using the GBLUP method were 0.522, 0.404, 0.444, and 0.539 for CWT, EMA, BFT, and MS. Kim (2021) reported the realized accuracy of GEBV as 0.509, 0.446, 0.415, and 0.555, respectively, when using the ssGBLUP method based on the phenotypic information of 202,808 heads and the genotype information of 14,000 heads. When comparing the results of this study, the realized accuracy values demonstrated an increase compared with the GBLUP method. Collecting more phenotypic data related to pedigree will enable more accurate genetic evaluation.

## DISCUSSION

The results of this study show that the ssGBLUP method allows for a more accurate evaluation of individuals because it incorporates into its analysis not only the genotype and phenotype information used in the current GBLUP method but also the pedigree and phenotype information of the reference population. Currently, the Korean Hanwoo industry is experiencing difficulties, such as rising feed prices and inflation, owing to changes in the international situation. To ensure a stable income, it is necessary to enhance the average genetic ability of

Hanwoo cattle raised on farms to produce stable, high-grade Hanwoo cattle. Individual evaluation using the ssGBLUP method is considered effective for enhancing the genetic ability of farms and enabling accurate and rapid improvements. This study used the two generations of pedigree information on the reference population for analysis. Based on the results of this study, it is considered that obtaining further pedigree information of the reference population will enable high-accuracy individual selection.

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