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Genomic-based animal management in the early- and late-finishing system of Hanwoo cattle

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ABSTRACT

In the Korean cattle feedlot industry, profitability is largely dependent on the carcass value at slaughter, which is influenced by genetic and environmental factors, including finishing time and feeding strategies. This study evaluated the predictive potential of genomic information for four economic traits—carcass weight (**CWT**), eye muscle area (**EMA**), backfat thickness (**BFT**), and marbling score (**MS**)—and the final meat grades in 975 Hanwoo cattle. Animals were grouped according to slaughter timing (Early and Late Finishing), and the genomic estimated breeding values for each trait were calculated. The analysis confirmed that all traits, except for CWT, were unaffected by finishing time. However, CWT was found to be influenced by both environmental factors and paternal effects. Trends in the phenotypic values for CWT, EMA, and MS increased with higher selection indices, while BFT exhibited mixed patterns, which suggests environmental influences. A-grade proportions increased with higher indices, thereby demonstrating the potential of genomic data for the early selection of high-grade animals. These findings underscore the value of genomic information in Hanwoo cattle breeding strategies, although sample size expansion may improve prediction accuracy for certain grades.
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Implications

Accurate prediction of carcass traits is essential for improving efficiency in beef cattle production. This study assessed the utility of genomic selection in Hanwoo cattle under different finishing times. Genomic data showed high predictive accuracy (≥ 0.78) for most econoic traits and effectively identified animals likely to receive A-grade carcass scores. However, unlike other traits, carcass weight was strongly influenced by environmental and paternal effects. These results highlight the potential of combining genomic selection with management strategies to enhance breeding decisions, carcass quality, and profitability.

Introduction

In the Korean Hanwoo feedlot industry, several factors are associated with cattle profitability, with particular emphasis on the initial purchase price of calves, feed costs, and the carcass value at slaughter (Hine et al., 2021). Among these factors, carcass value at slaughter age and feeding play a crucial role in determining profitability (Chung et al., 2015). Conventional practices in the Hanwoo feedlot industry involve the purchase of bull semen that is distributed by seed stock distributors, which provides a known genetic background and breeding values for use in calf production for the feedlot (Gajaweera et al., 2023; Kim et al., 2018; Lee et al., 2014). Feedlot farmers establish measures to decrease the risk of animals underperforming in the feedlot by implementing high-concentration feeding strategies and adjusting the cattle finishing time to align with the Korean beef grading system (Gajaweera et al., 2023).

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However, this Hanwoo feeding and management system results in higher production costs and generates more waste, including animal manure and methane gas emissions (Lee et al., 2023b). Furthermore, in contrast to the beef grading system utilised in the United States (USDA, 1997) and Australia (Stewart et al., 2024), the Korean meat grading system is characterised by 15 distinct beef grading levels with different auction prices (Jo et al., 2012). As a consequence of the Korean beef grading system, feedlot farmers must achieve a certain level of meat grading to generate a profit. Therefore, feedlot farmers employ prolonged high-concentration feeding practices to meet the requirements for profitable meat grades (Kondreddy Eswar et al., 2018). In addition, given the consumer demand for highly marbled meat in Korea, farmers opt for extended periods of raising Hanwoo cattle with a high-concentration ration to attain better meat grades within the Korean grading system (Ahn et al., 2023; Ku et al., 2021).

Farm animal performance is predominantly influenced by a combination of genetic (heritable) and environmental (non-heritable) factors. Among the environmental factors, feeding plays a critical role as a determining variable (Asmelash et al., 2018). Regarding the nutritional aspects of feeding, feed efficiency is a key driver of farm profitability, given that feed costs constitute the greatest portion of the overall expenses in livestock production. Furthermore, the optimal age for slaughter, referred to as the proper finishing time, has considerable importance for beef producers aiming to maximise productivity. In Korea, many Hanwoo feedlot farmers aim to raise their animals until they reach 35 months of age (Lee et al., 2013). The range for the age at which the cattle are slaughtered spans from 24 to 35 months, with a mean slaughter age of 31 months (Ahn et al., 2023). In contrast, industry practices in the United States suggest that marketing cattle under 30 months, preferably between 18 and 24 months, provides the highest economic and environmental efficiency in most scenarios (Farmers Weekly, 2010; https://www.fwi.co.uk/livestock/beef/finishing-cattle-over-30-months-is-mostly-less-efficient).

Conversely, feed cost has increased by 70–80% over the past decade because of the high-concentration feed used and the extended fattening time for Hanwoo cattle (Chung et al., 2017; Kim et al., 2018). In recent decades, the enhanced feed efficiency in cattle has primarily been a byproduct of selective breeding for various quantitative production traits (VandeHaar et al., 2016). Nevertheless, further improvements in feed efficiency are expected to become increasingly challenging if the focus remains solely on the selection of production traits. Consequently, there has been a growing emphasis on the importance of dietary management, taking into account the animals' genetic background, with the primary goal of enhancing production, profitability, and environmental sustainability (Gajaweera et al., 2023; Hine et al., 2021; Kinghorn, 2012). In the livestock industry, there has been a recent development of genomic prediction methods aimed at accurately estimating the genomic breeding values (**GBVs**) (Meuwissen et al., 2001). These methods have been incorporated into animal breeding for the selection of bulls and have also been applied in feedlot management, where they are used for sorting steers based on their GBVs (Hine et al., 2021).

In this study, the genomic and phenotypic information of 975 Hanwoo steers was used to identify whether the genome affects the phenotype in four economic traits, namely carcass weight (**CWT**), eye muscle area (**EMA**), backfat thickness (**BFT**), and marbling score (**MS**). Furthermore, individuals were divided into two groups and subjected to statistical analysis to investigate the association between the phenotype and final grade according to finishing time.

Material and methods

Animals and management (n = 975)

All management and procedures involving live animals were performed in accordance with the guidelines outlined by the Research Council on Animal Care and Chungnam National University. The Hanwoo test population used in this study consisted of 975 Hanwoo steers collected from eight regions. These animals were born between April 2017 and November 2019 and were slaughtered between January 2020 and December 2021. The test population shared 70 sires and 898 dams. At the time of slaughter, their ages ranged from 26 to 35 months, with an average age of approximately 30.17 months. Carcass data for each individual were collected at slaughterhouses after processing (Supplementary Table S1).

Genomic information was generated using the bovine 50 K SNP bead chip from Illumina Inc. In addition, pedigree information was officially collected by the Korea Animal Improvement and Association (KAIA, https://www.aiak.or.kr/), while carcass data were recorded by the Korea Institute for Animal Products Quality Evaluation (KAPE, https://www.ekape.or.kr/). Quality control of the 50 K SNP data was performed during the process of estimating the genomic estimated breeding value (**gEBV**) for the 975 steers in the test population, which was based on the 16 971 commercial Hanwoo individuals in the reference population. Plink 1.9 software (Purcell et al., 2007) was used to filter and exclude SNP markers with missing call rates exceeding 0.1, minor allele frequencies less than 0.01, and *P*-values indicating deviation from Hardy-Weinberg equilibrium less than 0.0001. After quality filtering, a total of 40 635 SNP markers were retained and used in this study.

A Hanwoo reference population comprising 16 971 individuals was used to estimate the GBVs for a test population of 975 steers. The reference population shared 395 sires and 13 320 dams. The objective was to establish a functional relationship between the gEBV and their phenotypic traits and the final beef meat grade, as illustrated in Fig. 1. The data distribution of this reference population across the country has been previously described in the study performed by Lee et al. (2023a). The pedigree information for the reference population included three generations and a total of 44 145 animals (Lee et al., 2023a).

The 975 individuals were divided into two groups, the Early Finishing and Late Finishing groups. Hanwoo cattle slaughtered at 24–29 months of age were classified as the Early Finishing group, while those slaughtered at 30 months or older were classified as the Late Finishing group. The Test group consisted of 346 animals in the Early Finishing group and 629 animals in the Late Finishing group (Fig. 2). Data regarding the carcass traits, including CWT, EMA, BFT, and MS, for both groups were collected from various abattoirs. To determine the significance of phenotypic differences between the two groups, *t*-tests were performed using the R program.

To compare the early and late finishing groups while accounting for the effect of shared sires, a linear mixed model was used with the lme4 package in R and written with

$$y = \beta_0 + \beta_1 group + u_{sire} + \varepsilon$$

where y is a vector of phenotypic values for carcass traits. β_0 is the overall intercept, and β_1 is the fixed effect of the finishing group (early or late). u_{sire} is a vector of the random effect of sire, assumed to follow $u_{sire} \sim N(0, \sigma^2_{sire})$, and ε is a vector of the residuals, assumed to follow $\varepsilon \sim N(0, \sigma^2)$. The model was fitted using restricted maximum likelihood, and the significance of the fixed effect was evaluated using Wald t-tests, while the inclusion of the random sire effect was tested using a likelihood ratio test. Additionally,

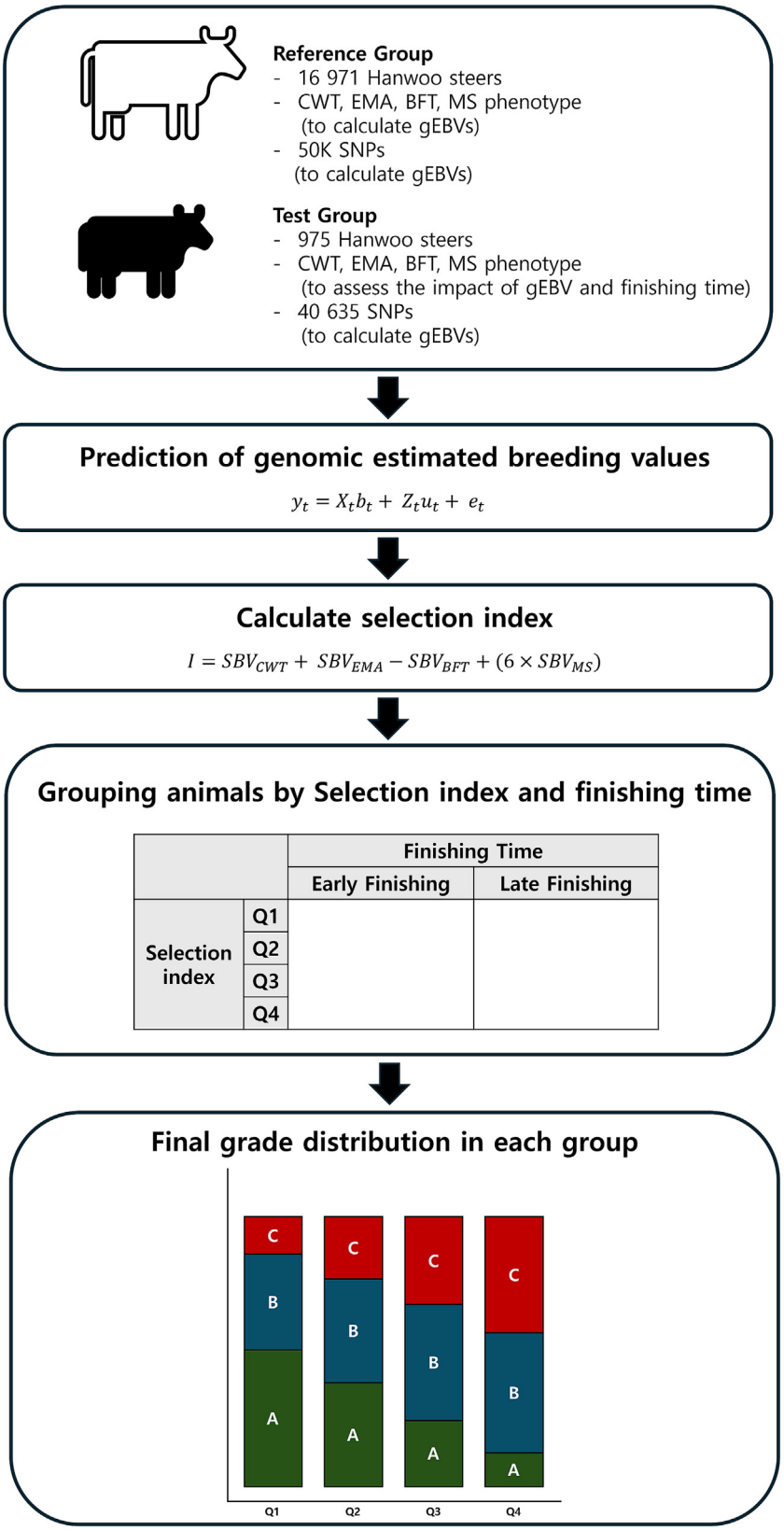

Fig. 1. The study aimed to evaluate the genetic impact of genomic selection on final carcass grades in 975 Hanwoo cattle by calculating estimated breeding values for carcass weight (CWT), eye muscle area (EMA), backfat thickness (BFT), and marbling score (MS). Cattle were grouped according to genomic estimated breeding values and finishing time to examine how these factors influenced the traits. By examining the final grade distribution within each group, the study assessed whether genomic factors significantly affect final carcass grades. Abbreviations: gEBV = genomic estimated breeding values; SNP = Single Nucleotide Polymorphism; SBV = Selected breeding value; A = group with an actual final grade of A; B = group with an actual final grade of B; C = group with an actual final grade of C.

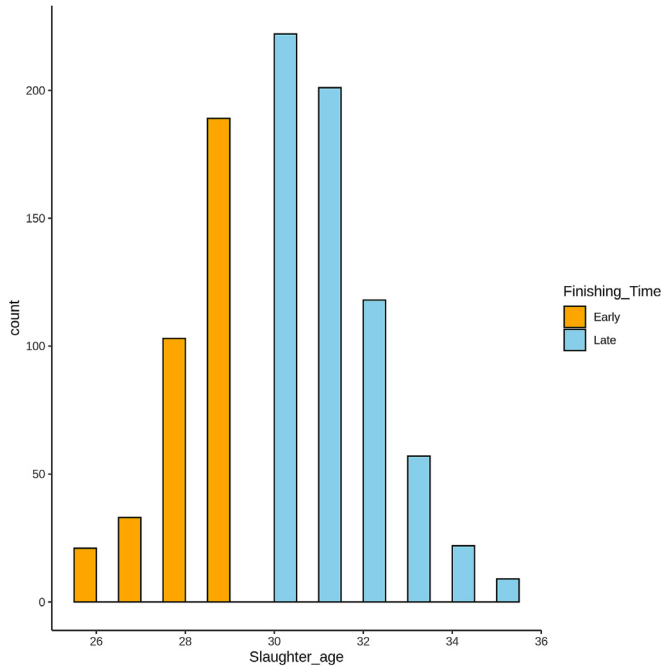

Fig. 2. Distribution of slaughter age for Hanwoo steers in this study (n = 97), classified into early and late finishing groups. The x-axis represents slaughter age, while the y-axis indicates the number of animals within each age interval. The early finishing group is shown in orange, and the late finishing group in light blue.

K-means clustering analysis was performed to visually assess whether the offspring of specific sires were predominantly distributed in a particular finishing group.

Prediction of genomic estimated breeding values

Data on a total of 17 946 Hanwoo steers (16 971 reference animals and 975 test animals) with recorded carcass traits were included in this study. For genomic evaluations, the following multiple-trait animal model was used:

$$y_t = X_t b_t + Z_t u_t + e_t$$

where y is a vector of phenotype for *t*th trait (CWT, EMA, BFT, and MS). b, u, and e are vectors of the fixed effects of birth year-month, slaughter year-month, and a covariate of age at slaughter, random additive direct genetic effects, and random residuals, respectively; X and Z are incidence matrices for b and u, respectively (Supplementary Table S2).

Genomic evaluations were performed using the Genomic Best Linear Unbiased Prediction (**GBLUP**). In this method, the inverse of the genomic relationship matrix (G^{-1}) in the mixed model equations was fitted as a random effect. GBLUP uses the genomic relationship matrix (G) based on the SNP markers. The G matrix is expressed as:

$$G = \frac{MM\prime}{\sum_{i=1}^{m} 2p_i(1-p_i)}$$

and

$$Var(u) = G\sigma_u^2$$

where M is the matrix for genes of individuals, m is the total number of SNP markers, and p_i is the frequency at the i^{th} position of the SNP.

The general linear mixed model equation for GBLUP was:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z+\lambda G^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

where Z is the incidence matrix for the animal effect, X is the incidence matrix for the fixed effect, σ_e^2 is residual variance, and $a \sim N(0, G\,\sigma_a^2)$. $\lambda = \sigma_e^2/\sigma_a^2$. Therefore, GBLUP is a best linear unbiased prediction (BLUP) that replaces A (numeric relationship matrix) with G (genomic relationship matrix). The accuracy of EBV for steer cows was calculated using the prediction error variance (SE^2) and the additive genetic variance (σ_g^2) of the trait calculated using the airemlf90 program (Misztal et al., 2010). The equation using prediction error variance for the theoretical accuracy was:

$$Acc_{gEBV} = \sqrt{1 - \frac{SE^2}{\sigma_g^2}}$$

To evaluate the significance of the differences in the gEBV between the Early Finishing and Late Finishing groups, *t*-tests were performed using the R program.

Assessing the influence of genomic estimated breeding values and finishing time on carcass traits

The selection index values for the 975 steers were calculated using the gEBV values for four traits. The selection index formula is as follows:

$$I = SBV_{CWT} + SBV_{EMA} - SBV_{BFT} + (6 \times SBV_{MS})$$

where SBV_{CWT} is the standardised breeding value for CWT, SBV_{EMA} is the standardised breeding value for EMA, SBV_{BFT} is the standardised breeding value for BFT, and SBV_{MS} is the standardised breeding value for MS.

The yield grade in Hanwoo beef represents the quantity of meat obtained from the carcass and is determined by combining the CWT, BFT, and EMA. It is classified into three grades: A, B, and C. In addition, the quality grade assesses the meat quality based on MS, meat colour, fat colour, texture, and maturity, and is categorised into five grades: 1++, 1+, 1, 2, and 3. In this study, the final grade represents a composite score combining both the yield and quality grades, ranging from C3 to A1++. The selection index was used to divide the Early and Late Finishing groups into four subgroups based on quartiles. The final grade distribution for animals within each subgroup was then visualised using the "ggplot2" package in R.

Results

To compare the phenotypic differences between the two groups, summary statistics were calculated (Table 1). Also, both groups share 41 sires and 27 dams. The mean and SD of the phenotypes in the Early Finishing group were 458.10 ± 47.18 kg, 97.84 ± 12.53 cm^2, 13.33 ± 5.26 mm, and 6.27 ± 1.92 for the CWT, EMA, BFT, and MS, while those in the Late Finishing group were 472.20 ± 54.97 kg, 98.77 ± 12.82 cm^2, 13.42 ± 5.06 mm, and 6.36 ± 1.91, respectively. In all of the traits, the Late Finishing group exhibited higher values of 14.1 kg, 0.9 cm^2, 0.1 mm, and 0.1 for CWT, EMA, BFT, and MS, respectively. However, only the CWT trait showed a significant difference between both groups (P = 2.84×10^{-5}, 2.76×10^{-1}, 7.92×10^{-1}, and 4.57×10^{-1} for CWT, EMA, BFT, and MS, respectively).

Given that the individuals in both groups share 41 sires and 27 dams, they exhibited a common genetic background. To evaluate the potential influence of genetic effects on the observed phenotypic differences, a comparative analysis was conducted by examining sire-related variates. After adjusting for sire effects, the

Table 1
Phenotype statistics of four economic traits of Hanwoo cattle in early (24 ~ 29 months) and late (30 ~ 35 months) finishing groups.

	Early Finishing (24 ~ 29 Months; n = 346)			Late Finishing (30 ~ 35 Months; n = 629)			T-test *P*-value[1]	LMM *P*-value[2]
Traits	Mean ± SD	Max	Min	Mean ± SD	Max	Min		
CWT (kg)	458.1 ± 47.18[a]	618	330	472.2 ± 54.97[b]	637	240	2.80×10^{-5}**	2.15×10^{-1}
EMA (cm^2)	97.84 ± 12.53	138	68	98.77 ± 12.82	145	57	2.76×10^{-1}	3.36×10^{-1}
BFT (mm)	13.33 ± 5.26	55	3	13.42 ± 5.06	36	3	7.92×10^{-1}	9.31×10^{-2}
MS (1 ~ 9)	6.27 ± 1.92	9	2	6.36 ± 1.91	9	1	4.57×10^{-1}	9.75×10^{-1}

Abbreviations: Max = Maximum phenotype value; Min = Minimum phenotype value, LMM *P*-value = Linear mixed model *P*-value; CWT = Carcass weight, EMA = Eye muscle area; BFT = Backfat thickness; MS = Marbling score.
[1] *P*-values for the differences in four traits between the early and late finishing Hanwoo groups using a simple *t*-test.
[2] The statistical significance of phenotypic differences in carcass traits between early- and late-finishing Hanwoo groups using a linear mixed model after accounting for sire effects.
[a,b] Values with different superscript letters significantly differ ($P < 0.05$).

Table 2
Comparison of Genomic Estimated Breeding Values for Each Trait Between Early- and Late-Finishing Hanwoo cattle.

Traits	Early Finishing (24 ~ 29 Months; n = 346)			Late Finishing (30 ~ 35 Months; n = 629)			T-test *P*-value[1]	Average of Prediction Accuracy[2]
	Mean ± SD	Max	Min	Mean ± SD	Max	Min		
CWT	19.723 ± 36.208	120.334	−71.400	16.836 ± 36.817	144.945	−82.399	2.37×10^{-1}	0.79 ± 0.03
EMA	4.5487 ± 8.351	27.528	−20.619	3.689 ± 8.7549	30.723	−25.167	1.31×10^{-1}	0.78 ± 0.03
BFT	−0.4005 ± 2.682	9.677	−11.223	−0.3102 ± 2.530	7.720	−7.702	6.08×10^{-1}	0.78 ± 0.03
MS	0.5966 ± 1.149	4.166	−2.922	0.4793 ± 1.189	3.687	−2.766	1.32×10^{-1}	0.81 ± 0.03

Abbreviations: Max = Maximum; Min = Minimum; CWT = Carcass weight; EMA = Eye muscle area; BFT = Backfat thickness; MS = Marbling score.
[1] The significance *P*-value of differences in estimated genomic breeding values for each trait between the early and late finishing Hanwoo groups using *t*-test.
[2] Prediction accuracy was defined as the correlation between the adjusted phenotype and the estimated breeding values on carcass traits.

differences between the two groups were no longer statistically significant (*P*-value = 2.15×10^{-1}, 3.36×10^{-1}, 9.31×10^{-2}, and 9.75×10^{-1} for CWT, EMA, BFT, and MS, respectively in Table 2).

The prediction accuracy for carcass traits was high, with values of 0.79 ± 0.03, 0.78 ± 0.03, 0.78 ± 0.03, and 0.81 ± 0.03 for CWT, BFT, EMA and MS, respectively. In addition, to determine whether there were differences in genetic potential between the two groups, their breeding values were compared. The average gEBV in the Late Finishing group was 0.0903 higher than in the Early Finishing group for the BFT trait, while it was lower by 2.887, 0.8597, and 0.1173 for the CWT, EMA, and MS traits, respectively (Table 2). However, there were no significant differences in the gEBV between the groups (*P* = 0.2368, 0.1309, 0.6081, and 0.1324 for CWT, EMA, BFT, and MS, respectively).

The selection index for test group individuals was calculated using the selection index formula. Based on the quantile values of the selection index, the Early Finishing and Late Finishing groups were further divided into four subgroups. The Early Finishing group was divided as follows: animals with a selection index of ≤ −3.8514 were classified as Q1, between −3.8514 and 0.6136 as Q2, between 0.6136 and 5.1527 as Q3, and between 5.1527 and 21.8666 as Q4. This resulted in group sizes of 87, 86, 86, and 87 animals for Q1–Q4, respectively. Similarly, the Late Finishing group was divided based on selection index values of ≤ −5.1 as Q1, between −5.1 and −0.651 as Q2, between −0.651 and 4.747 as Q3, and between 4.747 and 20.424 as Q4. This grouping resulted in 158 animals in Q1 and 157 animals each in Q2, Q3, and Q4 (Table 3).

Table 3
Quartile values of the selection index for each group of early and late finishing Hanwoo cattle according to the selection index formula using genomic estimated breeding values.

Quartile	Early Finishing (24 ~ 29 Months; n = 346)		Late Finishing (30 ~ 35 Months; n = 629)	
	Quartile value	N	Quartile value	N
Q1	−3.851	87	−5.074	158
Q2	0.614	86	−0.651	157
Q3	5.153	86	4.747	157
Q4	21.867	87	20.424	157

Abbreviations: Q1 = Quartile 1; Q2 = Quartile 2; Q3 = Quartile 3; Q4 = Quartile 4; N = Number of animals.

In the Early Finishing group, the average selection index for groups Q1 to Q4 increased sequentially from −8.314 to −1.51, 2.43, and 9.75. Correspondingly, the average CWT increased from 446.5 kg in Q1 to 467.9 kg in Q4 (Table 4). The average EMA also exhibited an upward trend from 92.92 cm^2 in Q1 to 102.1 cm^2 in Q4, while the average MS increased from 5.103 in Q1 to 7.287 in Q4. In contrast, the average BFT values ranked in the order of Q1, Q3, Q2, and Q4. In the Late Finishing group, the average selection index for Q1 to Q4 was −9.547, −2.851, 2.0806, and 9.497, respectively (Table 4). The average CWT increased from 452.3 kg to 492.9 kg, the average EMA from 92.32 cm^2 to 106.8 cm^2, and the average MS from 5.158 to 7.631, revealing a progressive increase from Q1 to Q4. However, the average values for BFT ranked in the order of Q2, Q1, Q3, and Q4.

The final grade ranged from C2 to A1++, and the proportions of grades within the Q1 to Q4 groups in both the Early and Late Finishing groups are presented in Fig. 3. In the Early Finishing group, the percentage of animals that achieved an A grade (A1, A1+, A1++, A2, and A3) progressively increased from 25.29% in Q1 to 33.33% in Q4. Similarly, in the Late Finishing group, the A grade percentage increased from 20.25% in Q1 to 35.67% in Q4. In contrast, the C grade (C1, C1+, C1++, C2) did not present a consistent decreasing trend from Q1 to Q4 in the Early Finishing group. Q1 had a significantly higher proportion at 31.03% compared to the other groups, while Q4 had a notably lower proportion at 11.49%. In the Late Finishing group, Q1 and Q2 revealed a minimal difference of 0.79%, and Q4 had a considerably lower C grade proportion of 14.65% compared to the other groups (Table 5).

Table 4
Phenotypic statistics for Q1 to Q4 pools within groups of early and late finishing Hanwoo cattle.

Group	N	Selection Index (Mean ± SD)	Phenotype (Mean ± SD)			
			CWT (kg)	EMA (cm2)	BFT (mm)	MS (1 ~ 9)
Early Finishing (24 ~ 29 Months; n = 346)						
Q1[1]	87	−8.314 ± 3.734	446.5 ± 40.553	92.92 ± 11.580	14.52 ± 7.253	5.103 ± 1.880
Q2[2]	86	−1.511 ± 1.382	458.3 ± 42.746	96.85 ± 11.927	12.76 ± 4.336	5.965 ± 1.863
Q3[3]	86	2.43 ± 1.379	459.6 ± 51.848	99.51 ± 12.985	13.24 ± 4.604	6.721 ± 1.524
Q4[4]	87	9.748 ± 3.834	467.9 ± 50.863	102.1 ± 11.914	12.79 ± 4.095	7.287 ± 1.656
Late Finishing (30 ~ 35 Months; n = 629)						
Q1[1]	158	−9.547 ± 3.379	452.3 ± 46.731	92.32 ± 8.837	13.53 ± 5.477	5.158 ± 1.725
Q2[2]	157	−2.851 ± 1.298	466.4 ± 47.815	96.97 ± 11.055	13.71 ± 5.225	6.07 ± 1.773
Q3[3]	157	2.081 ± 1.487	477.2 ± 65.387	99.05 ± 12.876	13.39 ± 4.786	6.605 ± 1.742
Q4[4]	157	9.497 ± 3.737	492.9 ± 50.098	106.8 ± 13.601	13.05 ± 4.728	7.631 ± 1.495

Abbreviations: N = Number of animals; CWT = Carcass weight; EMA = Eye muscle area; BFT = Backfat thickness; MS = Marbling score.
[1] A group with selection index values in the bottom 25% (Q1).
[2] A group with selection index values in the bottom 25–50% range.
[3] A group with selection index values in the bottom 50–75% range.
[4] A group with selection index values within the top 25%.

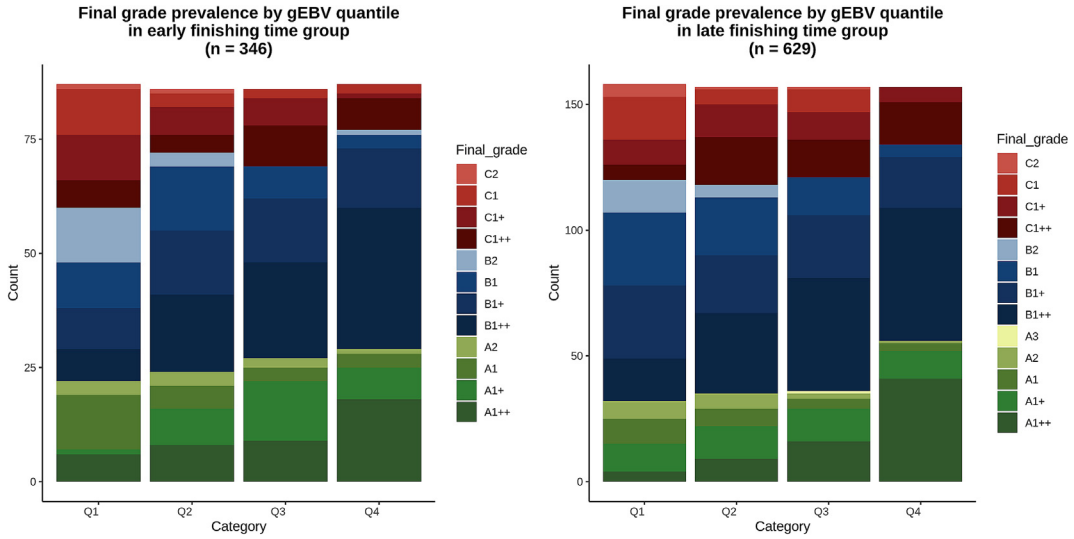

Fig. 3. Distribution of final grades of Hanwoo steers among Q1–Q4 groups in both the early- and late-finishing groups. This figure illustrates the proportion of final grades within each Q1–Q4 group for Hanwoo in early and late finishing. Actual final grades A, B, and C are represented in green, blue, and red, respectively, with a gradient effect that lightens from grade 1++ to grade 3. Abbreviations: gEBV = genomic estimated breeding values; A = group with an actual final grade of A; B = group with an actual final grade of B; C = group with an actual final grade of C.

Table 5
The final grade ratios for Q1 to Q4 pools within groups of early and late finishing Hanwoo cattle.

Group	Quartile pools	Final grade		
		A[1]	B[2]	C[3]
Early Finishing (24 ~ 29 Months; n = 346)	Q1	25.29%	43.68%	31.03%
	Q2	27.91%	55.81%	16.28%
	Q3	31.40%	48.84%	19.77%
	Q4	33.33%	55.17%	11.49%
Late Finishing (30 ~ 35 Months; n = 629)	Q1	20.25%	55.70%	24.05%
	Q2	22.29%	52.87%	24.84%
	Q3	22.93%	54.14%	22.93%
	Q4	35.67%	49.68%	14.65%

[1] Group with an actual final grade of A.
[2] Group with an actual final grade of B.
[3] Group with an actual final grade of C.

Discussion

This study aimed to assess the predictive potential of genomic information for the phenotypes and final meat grades in Hanwoo cattle. A total of 975 cattle were divided into Early and Late Finishing groups based on the time of slaughter, and the EBVs for four traits—CWT, EMA, BFT, and MS—were calculated. Subsequently, a selection index was constructed based on these EBVs, and the groups were then further subdivided into quartiles (Q1, Q2, Q3, and Q4) to analyse the phenotypic differences and grade distributions between the subgroups.

When the groups were divided by finishing time, the *t*-test results for EMA, BFT, and MS traits indicated that there were no significant differences between the Early and Late Finishing groups, with *P*-values greater than 0.05 (Table 1). In contrast, the average CWT was significantly higher in the Late Finishing group than in the Early Finishing group. At 30 months of age, the growth rate decreases compared to that at 24 months, which leads to a shift in energy allocation from muscle development and skeletal growth to overall weight gain. Consequently, cattle at 30 months exhibit a greater BW than those at 24 months (Bang et al., 2016; Berry et al., 2005; Domínguez et al., 2015; Marlowe et al., 1962). Thus, unlike EMA, BFT, and MS, CWT appears to be significantly influenced by slaughter age and appears to be a trait that is more susceptible to environmental factors. Building upon these findings, we further investigated whether the differences in carcass weight between finishing groups were attributable to genetic differences. While the *t*-test results indicated a significant increase in CWT in the Late Finishing group ($P = 2.84 \times 10^{-5}$), gEBV analysis indicated no significant genetic differences. However, the assumption of independence among individuals in the *t*-test does not account for the potential genetic influence of shared sire lineage, which may have confounded the results. This presents a critical limitation, as it remains unclear whether the observed differences between two groups from inherent genetic differences among individuals or from the overrepresentation of offspring from particular sires within specific groups. To address this, we applied a linear mixed model to account for sire effects. The results indicated that the differences in carcass traits between the two groups were not statistically significant after adjusting for these genetic factors (*P*-values = 2.15×10^{-1}, 3.36×10^{-1}, 9.31×10^{-2}, and 9.75×10^{-1} for CWT, EMA, BF, and MS, respectively). Furthermore, the offspring of specific sires were disproportionately concentrated within particular finishing groups (Supplementary Fig. S1). This finding suggests that the observed differences in carcass weight between finishing groups are likely not due to genetic differences among individual animals but rather a consequence of the structuring of finishing groups based on shared sire lineage.

When dividing both groups by selection index quartiles (Q1–Q4), an increasing trend was observed in the average phenotypic values for CWT, EMA, and MS from Q1 to Q4 in both groups (Table 4). However, in terms of BFT, the Early Finishing group showed a decreasing trend in the average values from Q1 to Q4. Given that lower BFT is associated with higher meat quality, this suggests an overall improvement in meat quality across all the tested phenotypic traits from Q1 to Q4 (Yokoo et al., 2008). However, in the Late Finishing group, no clear pattern was observed for BFT, which may indicate that environmental factors or management practices during the finishing period also influence BFT other than genomic factors. Yokoo et al. (2008) further demonstrated that subcutaneous fat deposition, including BFT, is significantly affected by animal age and environmental variables, such as seasonal variations.

On average, in the Late Finishing group, a selection index difference of 18.062 corresponded to differences of 21.4 kg in CWT, 9.18 cm^2 in EMA, −1.73 mm in BFT, and 2.184 in MS. In the Early Finishing group, a selection index difference of 19.044 corresponded to differences of 40.6 kg in CWT, 14.48 cm^2 in EMA, −0.48 mm in BFT, and 2.473 in MS. Although the selection index differences between Q4 and Q1 were similar between the groups, the phenotypic differences were greater in the Late Finishing group, likely because of the more substantial influence of the prolonged feeding period on weight and body development. These results highlight the influence of genomic information on the four economic traits of Hanwoo, with interactions of feeding duration that affect phenotypic development (Haque et al., 2024).

The analysis of final grade distribution in each group revealed an increasing trend in the proportion of A-grade animals (A1++, A1+, A1, A2, and A3) from Q1 to Q4 in both the Early and Late Finishing groups (Fig. 3). In the Early Finishing group, the proportion of A-grade animals in Q4 was 8.05% higher than in Q1, while in the Late Finishing group, this difference was 15.42%. Conversely, the proportion of C-grade animals (C1++, C1+, C1, and C2) from Q1 to Q4 decreased by 19.54 and 9.40% in the Early and Late Finishing groups, respectively. However, the proportion of C-grade animals in Q2 was lower than in Q3 in the Early Finishing group. Moreover, in the Late Finishing group, there was little difference in the proportion of C-grade animals between Q1 and Q2, but Q4 had a notably lower proportion at 14.65%. Overall, these results suggest that genomic data can be valuable for the early selection of animals likely to achieve high final grades. Furthermore, increasing the size of the Test group is expected to improve the accuracy of C-grade predictions.

In conclusion, this study yielded notable results for assessing the predictive potential of genomic information for key economic traits (CWT, EMA, BFT, MS) and the final meat grade (A, B, and C grades) in Hanwoo cattle. The analysis by finishing time indicated that CWT was significantly higher in the Late Finishing group, which was influenced by age and feeding period, thus supporting the relationship between age and BW. However, further investigation revealed that this difference was not solely due to genetic variation among individuals but was also affected by the structuring of groups based on shared sire lineage, suggesting that CWT is relatively more influenced by environmental factors and paternal effects than other carcass traits. Additionally, while higher selection index values were generally associated with improved trait quality and an increase in A-grade proportion, inconsistencies in BFT and C-grade proportions indicate limitations in predicting all grading outcomes solely with genomic data. Despite these challenges, genomic information remains a valuable tool for the early selection of high-grade animals, and it is expected to substantially contribute to breeding strategies aimed at improving the economic value and quality of Hanwoo cattle.

Conclusion

In this study, we evaluated the importance of genomic information and finishing time in beef cattle production by classifying 972 Hanwoo steers into early and late finishing groups. The results showed that BFT, EMA, and MS were not significantly affected by finishing time, whereas CWT was influenced by environmental and paternal effects. Genomic prediction for all four traits showed high accuracy (≥ 0.78). Furthermore, a selection index based on gEBVs effectively predicted final carcass grades, particularly identifying animals that achieved A grade. These findings demonstrate that genomic information provides valuable insights for developing effective breeding strategies, not only in Hanwoo but also in other beef cattle populations.

Supplementary material

Supplementary Material for this article (https://doi.org/10.1016/j.animal.2025.101526) can be found at the foot of the online page, in the Appendix section.

Ethics approval

Approval from Animal Care and Use Committee was not necessary as the data set was accumulated from the existing repository of Animal Genomic and Breeding Lab, Chungnam National University (CNU) and National Institute of Animal Science (NIAS), Republic of Korea, and no animals were handled to generate data for this study.

Data and model availability statement

Data were not deposited in any official repository. However, data would be available upon reasonable request to the corresponding author.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used ChatGPT 4.0 for translation. After using this tool, the authors reviewed and edited the content as needed and took full responsibility for the content of the publication.

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Declaration of interest

None.

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References

Ahn, J.S., Kwon, E.G., Lee, H.J., Kim, U.H., Won, J.I., Jang, S.S., Park, B.K., 2023. Effect of short-term fattening period and castration method on productivity, serum testosterone, and economic efficacy in Hanwoo cattle. Journal of Animal Science and Technology 65, 149–159. https://doi.org/10.5187/jast.2022.e88.

Asmelash, B., Mahlet, D., Brhane, H., 2018. Livestock nutrigenomics applications and prospects. Journal of Veterinary Science and Technology 9, 1–4.

Bang, N.N., Hiep, T., Dang, P.K., Huyen, N.T.D., Trach, N.X., 2016. Physiological characteristics, nutrition requirements and some considerations when feeding beef cows. Journal of Science and Development 14, 130–142.

Berry, D., Horan, B., Dillon, P., 2005. Comparison of growth curves of three strains of female dairy cattle. Animal Science 80, 151–160.

Chung, K.Y., Chang, S.S., Lee, E.M., Kim, H.J., Park, B.H., Kwon, E.G., 2015. Effects of high energy diet on growth performance, carcass characteristics, and blood constituents of final fattening Hanwoo steers. Korean Journal of Agricultural Science 42, 261–268.

Chung, C.S., Cho, W.K., Jang, I.S., Lee, S.S., Moon, Y.H., 2017. Effects of feeding system on growth performance, plasma biochemical components and hormones, and carcass characteristics in Hanwoo steers. Asian-Australasian Journal of Animal Sciences 30, 1117.

Domínguez, R., Crecente, S., Borrajo, P., Agregán, R., Lorenzo, J., 2015. Effect of slaughter age on foal carcass traits and meat quality. Animal 9, 1713–1720.

Gajaweera, C., Kang, D.H., Lee, D.H., Kim, Y.-K., Park, B.H., Chang, S.S., Kim, U.H., Lee, S.H., Chung, K.Y., 2023. Development of nutrigenomic based precision management model for Hanwoo steers. Journal of Animal Science and Technology 65, 596.

Haque, M.A., Lee, Y.-M., Ha, J.-J., Jin, S., Park, B., Kim, N.-Y., Won, J.-I., Kim, J.-J., 2024. Genome-wide association study identifies genomic regions associated with key reproductive traits in Korean Hanwoo cows. BMC Genomics 25, 496. https://doi.org/10.1186/s12864-024-10401-3.

Hine, B.C., Duff, C.J., Byrne, A., Parnell, P., Porto-Neto, L., Li, Y., Ingham, A.B., Reverter, A., 2021. Development of Angus SteerSELECT: a genomic-based tool to identify performance differences of Australian Angus steers during feedlot finishing: Phase 1 validation. Animal Production Science 61, 1884–1892. https://doi.org/10.1071/AN21051.

Jo, C., Cho, S., Chang, J., Nam, K., 2012. Keys to production and processing of Hanwoo beef: a perspective of tradition and science. Animal Frontiers 2, 32–38.

Kim, T.-I., Mayakrishnan, V., Lim, D.-H., Yeon, J.-H., Baek, K.-S., 2018. Effect of fermented total mixed rations on the growth performance, carcass and meat quality characteristics of Hanwoo steers. Animal Science Journal 89, 606–615. https://doi.org/10.1111/asj.12958.

Kinghorn, B., 2012. The use of genomics in the management of livestock. Animal Production Science 52, 78–91.

Kondreddy Eswar, R., Jin Young, J., Sang Yun, J., Youl-Chang, B., Seul, L., Minseok, K., Young Kyun, O., Hyun-Jeong, L., 2018. Effects of high levels of nutrients on growth performance and carcass characteristics of Hanwoo cattle. Journal of the Korean Society of Grassland and Forage Science 38, 180–189.

Ku, M.J., Mamuad, L., Nam, K.C., Cho, Y.I., Kim, S.H., Choi, Y.S., Lee, S.S., 2021. The effects of total mixed ration feeding with high roughage content on growth performance, carcass characteristics, and meat quality of Hanwoo steers. Food Science of Animal Resources 41, 45–58. https://doi.org/10.5851/kosfa.2020.e73.

Lee, S.-C., Choi, H.-H., Shin, J.-S., Kim, K.-H., Oh, Y.-K., Cheon, D.-W., 2013. Carcass characteristics and profitability analysis based on slaughter age of Hanwoo steers. Journal of Animal Science and Technology 55, 315–323.

Lee, H.S., Kim, Y., Lee, D.H., Seo, D., Lee, D.J., Do, C.H., Dinh, P.T.N., Ekanayake, W., Lee, K.H., Yoon, D., 2023a. Comparison of accuracy of breeding value for cow from three methods in Hanwoo (Korean cattle) population. Journal of Animal Science and Technology 65, 720.

Lee, S., Kim, J., Baek, Y., Seong, P., Song, J., Kim, M., Kang, S., 2023b. Effects of different feeding systems on ruminal fermentation, digestibility, methane emissions, and microbiota of Hanwoo steers. Journal of Animal Science and Technology 65, 1270.

Lee, S.H., Park, B.H., Sharma, A., Dang, C.G., Lee, S.S., Choi, T.J., Choy, Y.H., Kim, H.C., Jeon, K.J., Kim, S.D., Yeon, S.H., Park, S.B., Kang, H.S., 2014. Hanwoo cattle: origin, domestication, breeding strategies and genomic selection. Journal of Animal Science and Technology 56, 1–8.

Marlowe, T., Freund, R., Graham, J., 1962. Influence of age, breed, flesh condition, nursing, and season on weight and grade of beef cattle. Journal of Animal Science 21, 346–354.

Meuwissen, T.H., Hayes, B.J., Goddard, M., 2001. Prediction of total genetic value using genome-wide dense marker maps. Genetics 157, 1819–1829.

Misztal, I., Tsuruta, S., Lourenco, D., Masuda, Y., Aguilar, I., Legarra, A., Vitezica, Z., & ENSAT, F. (2010). Manual for BLUPF90 family of programs. University of Georgia, Athens, GA, USA.

Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M.A., Bender, D., Maller, J., Sklar, P., de Bakker, P.I., Daly, M.J., Sham, P.C., 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. The American Journal of Human Genetics 81, 559–575. https://doi.org/10.1086/519795.

Stewart, S.M., Polkinghorne, R., Pethick, D.W., Pannier, L., 2024. Carcass assessment and value in the Australian beef and sheepmeat industry. Animal Frontiers 14, 5–14.

USDA. (1997). Official United States standards for grades of carcass beef. USDA, Washington, DC, USA.

VandeHaar, M.J., Armentano, L.E., Weigel, K., Spurlock, D.M., Tempelman, R.J., Veerkamp, R., 2016. Harnessing the genetics of the modern dairy cow to continue improvements in feed efficiency. Journal of Dairy Science 99, 4941–4954.

Yokoo, M.J., Albuquerque, L.G., Lôbo, R.B., Bezerra, L.A.F., Araujo, F.R.C., Silva, J.A.V., Sainz, R.D., 2008. Genetic and environmental factors affecting ultrasound measures of longissimus muscle area and backfat thickness in Nelore cattle. Livestock Science 117, 147–154. https://doi.org/10.1016/j.livsci.2007.12.006.