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Research Article

Estimation of genetic parameters and genetic evaluation of Hanwoo lean meat traits using BLUP

Gwang Hyeon Lee[1,2,3,4], Hong Sik Kong[1,2,3,4*]
[1]Department of Applied Biotechnology, The Graduate School of Hankyong National University, Anseong 17579, Korea
[2]Genomic Informatics Center, Hankyong National University, Anseong 17579, Korea
[3]Gyeonggi Regional Research Center, Hankyong National University, Anseong 17579, Korea
[4]Hankyong and Genetics, Anseong 17579, Korea

*Corresponding author: Kebinkhs@hknu.ac.kr

Abstract

The goal of Hanwoo breeding is to produce large quantities of high-quality beef at a low cost. Breeding research has led to an increase of more than 100 kg in the average carcass weight of Hanwoo cattle. However, carcass weight includes bone and inedible fat, which differ from the percentage of lean meat. Enhancing the percentage of lean meat is essential for improving meat efficiency. Therefore, this study aimed to enhance the productivity of Hanwoo cattle by analyzing 1,905 Hanwoo cattle. This study investigated the correlations between carcass traits (carcass weight, eye muscle area, back fat thickness, and marbling score) and lean meat traits (weight and percentage). Additionally, genetic parameters for lean meat weight and percentage were estimated using the Best Linear Unbiased Prediction (BLUP) method. Based on the estimated genetic parameters, breeding value analysis was conducted. Furthermore, accuracy and correlation analyses between the estimated breeding values and the phenotypic data were performed. The accuracies of the estimated breeding values for carcass traits such as carcass weight, eye muscle area, backfat thickness, and marbling score, were 0.380, 0.373, 0.338, and 0.366, respectively; whereas for lean meat traits, namely weight and percentage, the accuracies were 0.381 and 0.373, respectively. Although the accuracy was relatively low, establishing a larger reference population is expected to enable more precise genetic evaluation. Based on the results of this study, improving lean meat traits is expected to significantly enhance Hanwoo beef productivity.

Keywords: Hanwoo, SNP chip, Lean meat trait, Genetic parameter, Breeding value

INTRODUCTION

Producing high-quality beef in large quantities at a low cost is the most critical aspect of the Hanwoo industry. Improvements in meat quality and weight have significantly increased the average carcass weight of Hanwoo cattle. Jung et al. (1996) reported in their study on the castration effects of Hanwoo and Holstein cattle that the carcass weight of castrated Hanwoo was 324.70±38.89 kg. Lee et al. (1997) analyzed factors affecting the percentage of Hanwoo primal cuts and reported an average carcass weight of 324.18±37.49 kg. Recent studies have reported an average carcass weight of 448.38±49.26 kg in research estimating the genetic parameters of carcass traits (Sun, 2021). This study analyzed 65,299 castrated Hanwoo cattle shipped from the Gyeongnam region between 2009 and 2020. Additionally, a study investigating the percentage of primal cuts by gender in 180 Hanwoo reported an average carcass weight of 467.60±45.66 kg for steers (Seo et al., 2019). It can be observed that the carcass weight of Hanwoo has increased by more than 100 kg compared to the past. Although the carcass weight of Hanwoo cattle has

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significantly increased through breeding improvements, the critical factor for productivity is the amount of meat produced through deboning. Yun et al. (1994) conducted a correlation analysis between carcass traits and primal cuts and reported that while an increase in carcass weight leads to an increase in primal cut weight, it tends to result in a decrease in the primal cut percentage. An increase in carcass weight signifies an increase in the amount of meat as well as the quantities of bones, inedible fat, and other non-edible components. While an increase in carcass weight leads to an increase in the overall weight of primary cuts, the percentage of primary cuts, calculated relative to the carcass weight (including inedible parts), may decrease. Consequently, if breeding improvements focus solely on increasing the carcass weight, the percentage of lean meat produced during processing may decline.

Therefore, this study examined the correlations between carcass traits (carcass weight, eye muscle area, back fat thickness, and marbling score) and lean meat traits (weight and percentage) to enhance the efficiency of Hanwoo beef production. Additionally, genetic parameters for lean meat weight and yield in Hanwoo carcasses were estimated using the Best Linear Unbiased Prediction (BLUP) method, and breeding value analysis was conducted based on these genetic parameters. An accuracy analysis of the estimated breeding values was conducted along with a correlation analysis between the estimated breeding values and phenotypic data. The results of this study provide fundamental data for predicting the lean meat yield of Hanwoo carcasses.

MATERIALS AND METHODS

1. Materials and Data collection

In this study, data from 1,905 Hanwoo steers slaughtered between 2018 and 2021 in the Jeollabuk-do region and processed at the Jeonju Gimje Wanju Livestock Cooperative Meat Processing Plant were analyzed. To estimate breeding values using the BLUP method, phenotypic information on carcass traits (carcass weight, eye muscle area, back fat thickness, and marbling score) were collected from the Korea Institute for Animal Products Quality Evaluation website. Pedigree and individual information were collected from the Korea Animal Improvement Association, Hanwoo Genetic Improvement Center, and Animal Products Traceability website. Information on lean meat weight was obtained by summing the weights of each primary cut (tender loin, loin, strip loin, neck, clod, top round, bottom round, brisket, shank, and rib) from individual animals provided by the Jeonju Gimje Wanju Livestock Cooperative Meat Processing Plant. The lean meat percentage was calculated as the proportion of lean meat weight to carcass weight.

2. Statistical analysis

1) Construction of a numerator relationship matrix

The Numerator Relationship Matrix (NRM) was constructed based on pedigree information and represented the probability that two randomly selected individuals within a population inherited genes that were identical by descent (IBD) from a common ancestor (Falconer and Mackay, 1996). The additive genetic relationship between the two individuals was probabilistically expressed as twice the proportion of their shared ancestry. The NRM was constructed using the PreGSF90 program, which is a part of the BLUPF90 software family.

2) Estimation of genetic parameters and breeding values

The genetic parameters were estimated using the REMLF90 program of the BLUPF90 software family. The breeding values were estimated using the estimated genetic parameters and the BLUPF90 program. Genetic parameters for the carcass traits of Hanwoo cattle (carcass weight, eye muscle area, backfat thickness, and marbling score), as well as lean meat weight and percentage, were estimated simultaneously using multivariate analysis. The additive genetic and residual variances for each trait were estimated using the following linear model matrix:

$$Y_P = X\beta + Zu + e \qquad Var\begin{pmatrix} u \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_\alpha^2 & 0 \\ 0 & I\sigma_e^2 \end{pmatrix}$$

Y_P: Observation of each trait (carcass traits, lean meat weight, and lean meat percentage).

X: Coefficient matrix for fixed effects (birth year, birth month, slaughter year, slaughter month, and slaughter age).

Z: Coefficient matrix for additive genetic effects

β: Estimates of fixed effects

u: Genetic effect

e: Residual effect

A: Individual relationship matrix

I: Identity matrix with diagonal elements equal to 1.

where Y_P represents the observed values for carcass and lean meat traits, X is the coefficient matrix for fixed effects, Z is the coefficient matrix for additive genetic effects, β is the estimates of fixed effects, u represents genetic effects, and e represents the residual effects. Additionally, A is the relationship matrix of individuals, I is the identity matrix with diagonal elements equal to 1, and σ_α^2 and σ_e^2 are the genetic variance and residual variance, respectively.

3) Estimation of heritability

The heritability of each trait, estimated using the BLUP method, was calculated using genetic variance and residual variance. Heritability was expressed as the ratio of genetic to phenotypic variance. To calculate heritability, the genetic and residual variance values provided by the REMLF90 parameter estimation results were used using the following formula:

$$Heritability(h^2) = \frac{\sigma_\alpha^2}{\sigma_P^2} \qquad \sigma_P^2 = \sigma_\alpha^2 + \sigma_e^2$$

h^2: Heritability

σ_α^2: Additive genetic variance

σ_e^2: Residual variance

where, σ_α^2 and σ_e^2 represent additive genetic variance and residual variance (variance due to environmental effects and non-additive genetic effects), respectively. *heritability* (h^2) was calculated as the ratio of genetic variance to phenotypic variance ($\sigma_P^2 = \sigma_\alpha^2 + \sigma_e^2$), which is obtained by summing the genetic variance and residual variance. Heritability can explain the proportion of the total phenotypic variance attributable to genetic effects.

4) Estimation of accuracy

The accuracy of the estimated breeding values was verified using the two methods described below. Accuracy was estimated using the prediction error variance of the estimated breeding values for each individual, along with the genetic variance for each trait, as estimated using BLUPF90 and REMLF90. The calculation formula is as follows:

$$Accuracy = \sqrt{1 - PEV/\sigma_\alpha^2}$$

where, *Accuracy* represents the accuracy of the estimated breeding value, *PEV* is the prediction error variance of the estimated breeding value for each individual, and, σ_a^2 is the additive genetic variance for each trait. The accuracy of the estimated breeding values was evaluated by conducting a correlation analysis between the estimated breeding values obtained using the BLUP method and phenotypic data. Correlation analysis was conducted using the Pearson correlation coefficient, and the calculated correlation coefficient was interpreted using the Realized Accuracy theory, where a value closer to 1 indicates a higher accuracy of the estimated breeding values. The correlation coefficient is calculated as follows:

$$p_{X,Y} = \frac{cov(X,Y)}{\sigma_X \sigma_Y}$$

where, $p_{X,Y}$ represents the correlation coefficient between the two datasets, *cov* is the covariance between them, and σ_X and σ_Y represent the variances of the estimated breeding values and the phenotypic data, respectively.

3. Formation of reference and test populations

The analysis included 1,905 animals. Owing to the small size of the reference population, 200 animals were randomly selected from each of the nine groups, with the remaining 105 animals forming one additional group, resulting in a total of 10 evaluation groups. The remaining animals were used as the reference populations. Analysis was conducted for each group, resulting in 10 analyses. Analyses were conducted on carcass traits (carcass weight, eye muscle area, back fat thickness, and marbling score) and lean meat traits (weight and percentage).

RESULTS AND DISCUSSION

1. Basic statistical analysis

Before conducting the analysis, a quantile–quantile plot (Q-Q plot) of the phenotypic data of the reference population was drawn using the R program to check for normality. The results are shown in Figure 1. Although some data points deviated from normality for each trait, they were included in the reference population to represent the diversity of individuals and were used in the analysis. The basic statistics for carcass traits (carcass weight, eye muscle area, backfat thickness, and marbling score) and lean meat traits (weight and percentage) were calculated and are presented in Table 1. A total number of animals were used for analysis was 1,905. The averages for carcass weight, eye muscle area, backfat thickness, marbling score, lean meat weight, and lean meat percentage were 446.43 ± 44.33 kg, 93.39 ± 10.20 cm², 12.95 ± 5.11 mm, 6.10 ± 1.94score, 248.66 ± 25.08 kg, and 55.78 ± 3.15%, respectively. According to basic statistics from previous studies, Kim et al. (2018) reported the average and standard deviation for carcass weight, lean meat weight, and percentage as 471.77 ± 40.64 kg, 294.46 ± 27.64 kg, and 62.43 ± 2.78%, respectively, for steers raised and slaughtered in the Gyeongbuk region. Seo et al. (2019) reported the descriptive statistics for carcass weight, lean meat weight, and percentage as 467.60 ± 45.66 kg, 294.47 ± 30.76 kg, and 63.01 ± 3.13%, respectively, for steers aged 26 to 35 months. Lee (2023) reported the average and standard deviation for carcass weight, lean meat weight, and yield as 448.64 ± 54.60 kg, 286.30 ± 30.90 kg, and 63.96 ± 2.80%, respectively, for Hanwoo steers. Compared with previous studies, the average carcass weight, lean meat weight, and lean meat percentage in this study were lower. Higher carcass weight was associated with greater lean meat weight, whereas the lean meat percentage could still be lower, even with increased carcass weight.

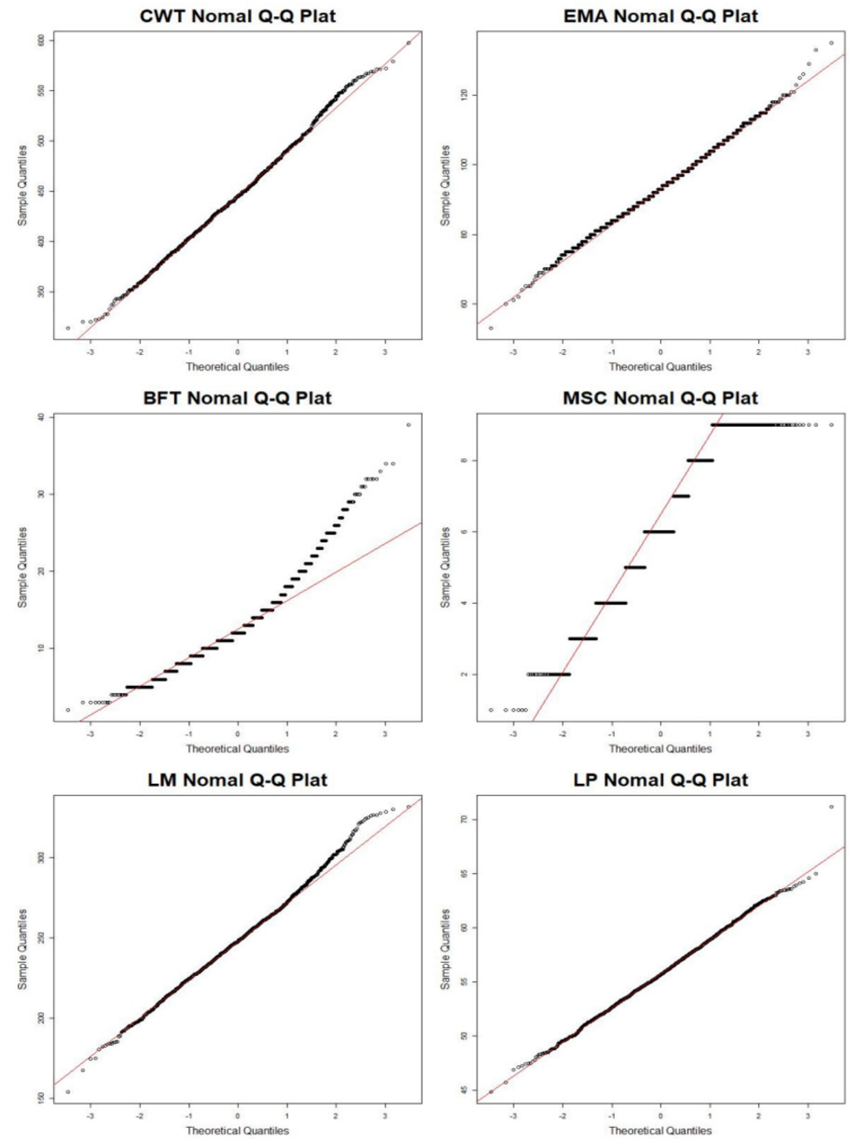

Figure 1. Normal Quantile-Quantile (Q-Q) plot of carcass and lean meat traits for the reference population

Table 1. Basic statistics for the carcass traits: lean meat weight and percentage

Trait	No.	Min	Max	Mean	S.D
CWT (kg)	1,905	314.0	597.0	446.43	44.38
EMA (cm^2)		53.0	135.0	93.39	10.20
BFT (mm)		2.0	39.0	12.95	5.11
MSC (score)		1.0	9.0	6.10	1.94
LM (kg)	1,905	154.1	331.6	248.66	25.08
LP (%)		44.9	71.2	55.78	3.15

CWT: Carcass weight; EMA: Eye muscle area; BFT: Backfat thickness; MSC: Marbling score; LM: Lean meat; LP: Lean meat percentage; S.D, standard deviation.

2. Genetic parameter

The genetic parameters (genetic variance, residual variance, and heritability) estimated in this study for carcass traits (carcass weight, eye muscle area, backfat thickness, and marbling score), lean meat weight, and percentage are summarized in Table 2. The estimated genetic variances for carcass weight, eye muscle area, back fat thickness, and marbling score were 946.00, 42.99, 7.55, and 1.56, respectively, and the residual variances were 923.90, 56.75, 17.98, and 2.23, respectively. Heritability was estimated using genetic and residual variances, and carcass weight, eye muscle area, back fat thickness, and marbling score were 0.51, 0.43, 0.30, and 0.41, respectively. The estimated genetic variances for lean meat weight and percentage were 296.00 and 3.02, respectively, while the residual variances were 284.80 and 10.41, respectively. The heritability calculated using these variances were 0.51 for lean meat weight and 0.22 for lean meat percentage, indicating that lean meat weight showed higher heritability than lean meat percentage. Koh (2013) reported a heritability of 0.225 for lean meat in Hanwoo cattle in Gangwon-do, Korea. Koh et al. (2014) reported heritabilities of 0.48 and 0.33 for lean meat weight and percentage, respectively, in Hanwoo steers raised in Gangwon-do and slaughtered between 2009 and 2012. The heritability of lean meat yield reported by Koh (2013) closely matches that found in this study. Additionally, the pattern of heritability for lean meat weight and yield reported by Koh et al. (2014) is consistent with the pattern observed in this study. The heritability of lean meat weight was similar to that of the carcass weight.

Table 2. Estimated genetic parameters for the carcass and lean meat traits

	Trait	Genetic variance(s)	Residual variance(s)	Heritability
Carcass traits	CWT	946.00	923.90	0.51
	EMA	42.99	56.76	0.43
	BFT	7.55	17.98	0.30
	MSC	1.56	2.23	0.41
Lean meat traits	LM	296.00	284.80	0.51
	LP	3.02	10.41	0.22

CWT: Carcass weight; EMA: Eye muscle area; BFT: Backfat thickness; MSC: Marbling score; LM: Lean meat; LP: Lean meat percentage.

The genetic and phenotypic correlations for carcass traits (carcass weight, eye muscle area, back fat thickness, and marbling score), lean meat weight, and lean meat percentage are presented in Table 3. The phenotypic correlations of lean meat weight with carcass weight, eye muscle area, back fat thickness, and marbling score were 0.84, 0.53, 0.88, and 0.18, respectively, whereas the genetic correlations were 0.90, 0.78, 0.05, and 0.38, respectively. The phenotypic correlations between lean meat percentage and carcass weight, eye muscle area, backfat thickness, and marbling score were -0.26, 0.10, -0.37, and 0.02, respectively, while the genetic correlations were -0.24, 0.48, -0.58, and 0.31, respectively. The phenotypic and genetic correlations between lean meat weight and percentage were 0.30 and 0.20, respectively. Choy et al. (2010) reported phenotypic correlations of 0.95, 0.70, and 0.28 between lean meat weight and carcass weight, eye muscle area, and back fat thickness, respectively, in Hanwoo steers slaughtered at the National Institute of Animal Science abattoir between 1996 and 2008. They also reported phenotypic correlations between lean meat percentage and carcass weight, eye muscle area, and backfat thickness as -0.24, 0.01, and -0.55, respectively. Lee et al. (2013) reported phenotypic correlations of 0.92, 0.61, 0.15, and 0.06 between lean meat weight and carcass weight, eye muscle area, backfat thickness, and marbling scores, respectively. Lee et al. (2016) reported phenotypic correlations of carcass weight with lean meat weight and percentage as 0.91 and -0.21, respectively. They also reported phenotypic correlations of eye muscle area with lean meat weight and percentage as 0.53 and 0.25, and phenotypic correlations of backfat thickness with lean meat weight and percentage as 0.23 and -0.42, respectively. Comparing the results of this study with those of previous studies, we observed that phenotypic and genetic correlations were generally similar.

Table 3. Phenotypic (above the diagonal) and genetic (below the diagonal) correlations between the carcass and lean meat traits

Trait	CWT	EMA	BFT	MSC	LM	LP
CWT		0.48	0.30	0.17	0.84	-0.26
EMA	0.56		-0.02	0.35	0.53	0.10
BFT	0.31	-0.12		0.03	0.08	-0.37
MSC	0.25	0.56	-0.01		0.18	0.02
LM	0.90	0.78	0.05	0.39		0.30
LP	-0.24	0.48	-0.58	0.31	0.20	

CWT: Carcass weight; EMA: Eye muscle area; BFT: Backfat thickness; MSC: Marbling score; LM: Lean meat; LP: Lean meat percentage.

Lean meat weight was highly correlated with carcass weight and eye muscle area, likely because both traits are related to meat weight. Backfat thickness, on the other hand, showed a very low correlation with lean meat weight, which may be because backfat thickness is associated with fat content rather than lean meat, and thus has a weaker relationship with lean meat percentage. The lean meat percentage was negatively correlated with carcass weight and backfat thickness. The negative correlation with carcass weight is likely due to the lean meat percentage being calculated as the ratio of lean meat weight to carcass weight; therefore, if only the carcass weight increases, the percentage may decrease. Backfat thickness is related to fat content, and an increase in backfat thickness implies a decrease in the proportion of lean meat in the carcass, which explains this negative correlation. Lean meat weight and percentage showed a low correlation with each other, possibly because, even if lean meat weight increased, a large amount of bone, inedible fat, and other parts removed during processing could have led to a lower percentage.

3. Breeding value and accuracy

The estimated breeding values for lean meat weight and percentage, accuracy of the estimated breeding values, and correlation coefficients between the breeding values and phenotypes are summarized in Table 4. The average estimated breeding values for carcass traits (carcass weight, eye muscle area, back fat thickness, and marbling score), lean meat weight, and lean meat percentage were 4.894, 0.882, 0.113, 0.116, 2.787, and 0.004, respectively. The accuracies of the estimated breeding values were 0.380, 0.373, 0.338, 0.366, 0.381, and 0.373. The accuracy of the estimated breeding values was highest for lean meat weight. The correlation coefficients between the estimated breeding values and phenotypic performance for carcass weight, eye muscle area, back fat thickness, marbling score, lean meat weight, and percentage were 0.236, 0.222, 0.189, 0.188, 0.262, and 0.143, respectively, with lean meat weight showing the strongest correlation. As no previous studies have evaluated the genetic potential for lean meat weight and percentage, comparisons were made with the accuracy of breeding values for carcass traits (carcass weight, eye muscle area, backfat thickness, and marbling score). Lee et al. (2022) conducted a genetic evaluation of cows using a reference population of 9,849 Hanwoo steers slaughtered nationwide between 2013 and 2018 constructed using the BLUP method. The accuracies of the estimated breeding values for carcass weight, eye muscle area, back fat thickness, and marbling score were 0.424, 0.430, 0.426, and 0.426, respectively. Kim et al. (2022) reported the accuracy of breeding values for carcass weight, eye muscle area, backfat thickness, and marbling score as 0.48, 0.51, 0.51, and 0.59, respectively, in a study estimating the reliability of genetic evaluations for carcass traits using ssGBLUP. In comparison, the accuracy of the estimated breeding values for lean meat weight and percentage in this study was lower than those reported in previous studies. Lee et al. (2022) used a reference population of 9,849 heads for their analysis, whereas Kim et al. (2022) used data from approximately 500,000 heads, which likely resulted in the higher accuracy observed in the present study. To accurately estimate breeding values for lean meat traits, it is essential to establish a sufficiently large reference population.

Table 4. Estimated breeding values and accuracy for the carcass and lean meat traits

Trait	No.	EBV2)	S.E.3)	Accuracy	Correlation
CWT (kg)	1,905	4.894	28.325	0.380	0.236
EMA (cm^2)		0.882	6.057	0.373	0.222
BFT (mm)		0.113	2.576	0.338	0.189
MSC (score)		0.116	1.156	0.366	0.188
LM (kg)		2.787	15.843	0.381	0.262
LP (%)		0.004	1.605	0.373	0.143

CWT: Carcass weight; EMA: Eye muscle area; BFT: Backfat thickness; MSC: Marbling score; LM: Lean meat; LP: Lean meat percentage.

CONCLUSION

Currently, genetic improvement of Hanwoo cattle focuses primarily on carcass traits such as carcass weight, eye muscle area, backfat thickness, and marbling score. This significantly enhances meat quality and weight; however, research on lean meat consumption remains limited. In the present study, the accuracy of the estimated breeding values for carcass and lean meat traits was lower than that reported in previous studies, mainly because of the smaller size of the reference population. However, the breeding value accuracies for both carcass and lean meat traits showed a similar trend. With a sufficiently large reference population, the breeding values for lean meat traits can be estimated with high accuracy. To achieve this, data collection on lean meat traits is necessary; however, practical challenges remain. Currently, it is legally necessary to measure and record data for the four major carcass traits, making it relatively easy to obtain data for analysis. However, no such legislation exists for other traits, and measurements must be taken individually at processing plants, requiring additional labor and time, which makes it practically challenging to record these traits. Further discussion is required to address these issues. By addressing these challenges and securing a sufficient dataset and reference population, it is possible to achieve more accurate predictions of lean meat traits, which, in turn, are expected to lead to more efficient increases in meat production.

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