JABG. 2023 September, 7(3)55-64
https://doi.org/10.12972/jabng.20230007

Print ISSN 1226-5543
Online ISSN 2586-4297

Research Article

Estimation the genetic parameters and evaluating the correlation between the maternal linear type traits and the birth weight of the progeny in Hanwoo cows

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ABSTRACT

This study aimed to investigate the correlation between the linear type traits of mother cows (dams) and the birth weight(BW) of the progeny. The study used data collected between 2002 and 2018 by the Korea Animal Improvement Association (KAIA). This study evaluated the data specifically with respect to 19 traits. A statistical model was established to estimate the correlation between the maternal linear classification traits and the progeny BW. The significance of each statistical variable was analyzed using the generalized linear model (GLM) method in the SAS package 9.1.3 software, while the genetic parameters were estimated using the BLUPF90 Family program. The BW of Hanwoo cows increased by approximately 0.4 kg each year; however, the BW heritability was moderate (0.23). The linear classification traits showed values of 0.34, 0.37, 0.11, 0.45, 0.31, and 0.40, for ST (Vertical distance from the apex of the rump to the ground), BL (Horizontal distance between anterior shoulder point to the posterior extremity of the pin bone), RA (The slope from the rump to the pin bone), RL (Horizontal distance from the anterior rump to the tip of the pin bone), PBW (Lateral width of pin bone), and FS (Final score), respectively, with moderate heritability for all traits, except RA. The BW of the progeny showed phenotypic correlations of 0.06, -0.01, 0.03, and 0.04, and genetic correlations of 0.09, 0.03, 0.02, and -0.04 with ST, BL, RL, and PBW, respectively. The average parity in Hanwoo cows increased from 2.5 in 2016 to 2.8 in June 2020. There is a low genetic correlation between the maternal linear classification traits and the BW of the progeny. An increase in the parity of dams and a greater accumulation of progeny BW data and test records could lead to the accurate evaluation of the BW as a breeding objective trait.

Key words: linear type traits, birth weight, genetic parameters, Hanwoo cows, parity, economic trait

INTRODUCTION

Various selective breeding operations such as performance and progeny testing for seed stock and female replacement have been improved the linear type and carcass traits in Hanwoo cattle. In Hanwoo breeding program, BW is an essential objective trait for predicting the growth potential (Roh et al., 2004; Choi et al., 2006; Koo et al., 2008).The linear type for cow such as hip height (HH) and body length (BL) growth standard for Hanwoo cow has been increased 106% and 113%, respectively, over the past 30 years (Lee, 1985; Lee, 2017). In paticular, it is interpreted that there has been more research on systematic evaluation of Hanwoo cows linear traits and improvement than carcass traits in recent years (Misztal,

Received May 26, 2023 **Revised** June 29, 2023 **Accepted** July 27, 2023

1992; Gutierrez and Goyache, 2002; Veerkamp, 2002; Lee, 2011; Cho et al, 2014; Lee et al, 2017). The KAIA uses the linear classification system in Korea. It was adopted in 2008, for improving the linear type traits of Hanwoo cows, by enhancing 19 linear type traits and 6 body parts, for better overall quality of cows. The classification used a grade scale of 1–9. For all organisms, BW is the first trait measured upon birth, and a key trait for predicting the growth potential of an individual animal. Hanwoo farms interested in genetic improvement for cow would benefit from measuring BW systematically; however, obtaining this data at small farms would be difficult because of the lack of weighing system. Therefore, very limited researches have published because the data collection is relatively difficult (Reynolds et al., 1991; Johnston et al., 1992; Veseth et al., 1993; Gregory et al., 1995; Franke et al., 2001; Eriksson et al., 2004; Celso et al., 2019). Cow breeding operation aimed at improving the carcass qualities and linear type traits, which are key economic traits for Hanwoo cows. Therefore, investigating a genetic correlation between linear type of cow and birth weight for progeny may help set up a selection index for dam replacement in breeding program.

MATERIALS AND METHODS

Data

To investigate the correlations between the maternal linear type traits and the BW of progeny in Hanwoo cows, the study used KAIA linear classification data and the BW data collected between 2002 and 2018, through a cow test farm project. The BW data from 342,659 animals from the cow test farm project and the pedigree registration data of 302,474 animals among them were used. For evaluating the linear classification scores, we selected 840,155 animals with maternal scores that were registered between 2013 to the present. The study used data from 4,681 animals, after removing the outliers. The criteria for removing outliers were: cows that were unregistered or with basic registration, animals with missing records, data with the duration between the date of calving and the classification date exceeding 365 days (1 year), data from herd-year-season (HYS) contemporary group (CG) with ≤ 5 animals, and data deviating from the standard deviation range of 3 (3SD). Although it cannot be concluded that the data exceed the 3 SD ragne of the standard deviation does not follow a normal distribution, it also excludes data that are considered outliers. The number of records by birth year, linear classification year, classifier, and birth region are presented in Table 1. The BW data included the data between2013 and2020, while the maternal classification records included data between2013 and2019. Seven classifiers and records from six birth regions (provinces) were used. The SAS 9.1.3 package program and Microsoft Office Excel 2010 were used for data handling and basic statistical analysis, while the estimates of genetic parameters were evaluated using the restricted maximum likelihood (REML) method using the BLUPF90 program (Misztal, 2007).

Table 1. Number of records by birth year, classification year, classifier, and birth region

B_year*	Obs.	C_year	Obs.	Classifier	Obs.	Region	Obs.
2013	175	2013	415	A	324	GW	5
2014	485	2014	647	B	389	GG	195
2015	813	2015	778	C	25	GB	42
2016	852	2016	971	D	V	JB	408
2017	727	2017	1105	E	1376	CN	2453
2018	962	2018	638	F	1845	CB	1578
2019	651	2019	127	G	596		
2020	16						
Total	4681		4681		4681		4681

*B_year, birth year; Obs, observation number; C_year, classification year; Region, birth region; GW, Gangwon; GG, Gyeonggi; GB, Gyeongbuk; JB, Jeonbuk; CN, Chungnam; CB, Chungbuk

Linear classification traits

This study evaluated the data collected between 2013 and 2019, with respect to 19 traits. The variables include ST and BL, which were measured using the quantitative values among the 19 linear type traits. RA, RL, and PBW were measured to evaluate the calving ease. The udder volume was excluded, because it changes according to the suckling period. The FS represents the comprehensive indicator of the linear classification traits, which were graded on a 9-point scale (1–9 points). The detailed information of the variables is as follows:

ST	Vertical distance from the apex of the rump to the ground
BL	Horizontal distance between anterior shoulder point to the posterior extremity of the pin bone
RA	The slope from the rump to the pin bone
RL	Horizontal distance from the anterior rump to the tip of the pin bone
PBW	Lateral width of pin bone

Statistical model

To estimate the correlation between the maternal linear classification traits and the progeny BW, the following statistical model was fitted to correct environmental factors affecting the traits.

$$Y_{ijklmno} = \mu_i + HYS_{ij} + SEX_{ik} + SY_{il} + SS_{im} + CM_{in} + D_{ijklmno} + m_{ijklmno} + mpe_{ijklmno} + a_{ijklmno} + e_{ijklmno}$$

Here,

$Y_{ijklmno}$	Observed value
μ_i	Group average
HYS_{ij}	Effect of birth region, year, and season on BW
SEX_{ik}	Effect of sex on BW
SY_{il}	Effect of classification year on the tested traits
SS_{im}	Effect of classification season on the tested traits
CM_{in}	Effect of classifier on the tested traits
$D_{ijklmno}$	Covariate effect from classification date to calving date (in days)
$m_{ijklmno}$	Maternal effect on BW
$mpe_{ijklmno}$	Effect of permanent maternal environment on BW
$a_{ijklmno}$	Individual effect
$e_{ijklmno}$	Random error of each measured value

The significance of each statistical variable was analyzed using the generalized linear model (GLM) method in the SAS package 9.1.3 software, while the genetic parameters were estimated using the BLUPF90 Family program (Misztal, 2007), which was developed based on the EM-REML algorithm. The heritability estimates for the additive genetic effects based on the models were calculated as follows:

$$\hat{h}^2 = \frac{\hat{\sigma_a^2}}{\hat{\sigma}_a^2 + \hat{\sigma}_e^2}$$

Here, $\hat{h}^2$ is heritability, $\hat{\sigma}_a^2$ is additive genetic variance, and $\hat{\sigma}_e^2$ is the error variance. The genetic correlation between the traits was estimated based on the variance/covariance estimates using the following functional equation:

$$r_{G(i,j)} = \frac{Cov_{a(i,j)}}{\sqrt{\sigma^2_{a(i)} \times \sigma^2_{a(j)}}}(i \neq j)$$

The phenotypic correlation between the traits was estimated using the following functional equation.

$$r_{p(i,j)} = \frac{\left[Cov_{a(i,j)} + Cov_{e(i,j)}\right]}{\sqrt{\left[\sigma^2_{a(i)} \times \sigma^2_{e(i)}\right]\left[\sigma^2_{a(j)} \times \sigma^2_{e(j)}\right]}}(i \neq j)$$

Here, $\hat{\sigma}^2_a$ is additive genetic variance, r_G is genetic correlation, and r_p is phenotypic correlation.

RESULTS AND DISCUSSION

Data structure analysis

The pedigree of the individuals was analyzed based on the number of sires and dams, average inbreeding coefficient, and distribution of the inbreeding coefficient range. The results are presented in Table 2. and with an average inbreeding coefficient of 0.37 (Table 2). Among the 4,835 animals used in the analysis, the number of dams was 4,306. This indicates the availability of a very high number of maternal pedigree records, which enabled high-quality genetic analysis, compared to earlier studies. However, the number of animals with both the classification and BW records was low, accounting for only around 8%.

Table 2. Data on the number of animals studied and the inbreeding percentage

Item	Herd
No. of animals	4681
No. of sires	314
No. of dams	4306
Average inbreeding %	0.37

A normal distribution was assumed for the statistical analysis of quantitative traits. Accordingly, a normality test was performed on progeny the BW and FS; the linear classification traits in the five body parts of dams were used in the analysis. For the normality tests, estimations were based on Kolmogorov-Smirnov statistics (D) of the SAS univariate procedure, shown in Table 3. D≥0.05 indicated a normal distribution and D < 0.05 indicated a non-normal distribution. Normality tests showed that the D value of BW was 0.1080, while the D values for the linear classification traits ST, BL, RA, RL, and PBW were 0.154, 0.144, 0.203, 0.173, and 0.183, respectively. All the values exceeded 0.05; and therefore, normality was established for all the traits.

Table 3. Kolmogorov-Smirnov test for BW and linear type traits

Value	Obs.	K-S D* (*Pr*>D)					
		BW	ST	BL	RA	RL	PBW
D	4681	0.180	0.154	0.144	0.203	0.173	0.183
P		0.01	0.01	0.01	0.01	0.01	0.01

* K-S D: Kolmogorov-Smirnov statistic, No., number of observations. D >0.05,normal distribution; D < 0.05,not normal distribution; BW, birth weight; ST, stature; BL, body length; RA, rump angle; RL, rump length; PBW, pin bone width.

General analysis

The basic statistics for BW, linear classification traits, and FS are presented in Table 4. With respect to the basic statistics for each trait, the results indicated 27.32±2.20 kg for BW and 5.84±1.28 points, 5.80±1.33 points, 6.17±1.13 points, and 5.84±1.15 points for the linear classification traits ST, BL, RA, RL, and PBW, respectively. FS is a comprehensive indicator of linear classification and it had 80.03±1.68 points. The duration between the date of linear classification and the date of calving was 172.06±111.10 days. With respect to ST and BL, which are general external traits, the average ST score (5.84 points) was in the range of 128–130 cm, while the average BL score (5.80 points) was in the range of 150–153 cm. In an earlier report on the general appearance of Hanwoo cows, Choi et al. (1996) reported an ST of 118.93cm and BL of 134.9 cm; the results from the present study indicated that the overall size of Hanwoo cows has increased. Lee et al. (2011) reported 5.50±1.43 points, 6.01±1.39 points, 5.71±1.87 points, 5.81±1.34 points, and 5.37±1.34 points for ST, BL, RA, RL, and PBW, respectively. Cho et al. (2014) reported 5.45±1.30 points, 5.91±1.25 points, 5.78±1.33 points, 5.81±1.25 points, and 5.18±1.20 points for the same linear classification traits. Jeoung (2017) reported 5.73±1.35 points, 5.86±1.33 points, 5.81±1.35 points, 5.42±1.31 points, and 78.87±1.94 points for ST, BL, RL, PBW, and FS, respectively. These results from the present study were similar to that from these earlier studies. This similarity could be attributed to the use of classification data from the same period. The BW statistics and trends by birth year and season are presented in Table 5. There was an increase in the mean BW of newborn calves from 23.73 kg in 2013 to 29.50 kg in 2020, which represents a total increase of 5.8 kg and an average annual increase of 0.37 kg.

Table 4. Basic statistics of each trait

Traits*	Obs.	Mean	SD	MIN	MAX
BW	4681	27.32	2.20	18	39
ST		5.88	1.27	1	9
BL		5.81	1.32	1	9
RA		6.17	1.13	1	9
RL		5.84	1.15	1	9
PBW		5.47	1.21	1	9
FS		80.05	1.67	68.64	86.13
Int		165.25	106.58	0	365

*BW, birth weight; ST, stature; BL, body length; RA, rump angle; RL, rump length; PBW, pin bone width; FS, final score; Int, duration between the linear-type test date and the date of calving.

Table 5. Mean and standard deviation of the birth weight classified according to the birth year and season

B_year	Obs.	Mean±SD	B_season	Obs.	Mean±SD
2013	175	26.73±1.80	Spring	864	27.49±2.15
2014	485	26.92±2.09	Summer	2015	27.24±2.19
2015	813	26.69±2.07	Autumn	1092	27.36±2.30
2016	852	26.98±2.26	Winter	710	27.33±2.14
2017	727	27.79±2.10			
2018	962	28.20±2.11			
2019	651	28.18±2.21			
2020	16	29.50±0.52			

There were more offspring produced during summer and autumn, compared to that during spring and winter. However, the mean BW was superior among the offspring produced during spring and autumn, compared to that for offspring produced during summer and winter. Lee (2012) reported a mean BW of 26.43 and 26.40 kg for the offspring produced during autumn and spring, respectively, which were slightly higher than that for the offspring produced during summer and winter. The results from the present study are consistent with that in the earlier reports. The differences in BW could be attributed to the differences in the breeding environment, sex, and breed of animals in the basic data used in the analysis. FS is the value derived from the scores of individual linear classification traits; it was used to investigate the correlation between the linear classification traits and BW. Four score groups were defined and the mean and SD for BW and linear classification traits for each group were evaluated (Table 6). The groups were classified as FS < 76 points, ≥ 76 but < 78, ≥ 78 but < 80, and ≥ 80 points. Classification of the basic statistics for the linear classification traits, based on FS indicated considerable differences among the groups. Previously mentioned; each trait should be high for the overall FS score to be high. The total linear classification score indicates the maternal linear type scores. Among the groups, the < 76 points group had a mean progeny BW of 27.17±2.07 kg, while ≥ 76 but < 78, ≥ 78 but < 80, and ≥ 80 groups had 27.14±2.06 kg, 27.24±2.17 kg, and 27.35±2.23 kg, respectively. This indicates an indirect correlation between the maternal linear type traits and the BW and the phenotypic data of the progeny.

Table 6. Basic statistics of the linear traits classified based on the final score group

Group	Obs.	BW	ST	BL	RA	RL	PBW
>76	117	27.17 ± 2.07	3.39 ± 0.96	3.26 ±0.96	4.97 ± 1.36	3.36 ± 0.84	2.62 ± 0.96
76~78	410	27.14 ± 2.06	4.3 ± 0.90	4.23 ± 1.00	5.53 ± 1.22	4.32 ± 0.75	3.79 ± 0.84
78~80	1,151	27.24 ± 2.18	5.16 ± 0.87	5.26 ± 0.93	5.98 ± 1.22	5.31 ± 0.75	5.00 ± 0.76
80<	3,003	27.35 ± 2.23	6.44 ± 1.01	6.31 ± 1.14	6.37 ± 0.99	6.34 ± 0.93	5.98 ± 0.96

Estimation of environmental effects

To assess the effects of birth region/year/season CGs, sex, and the period (in days) between the maternal classification and calving, analytical models were established using the classification traits that correlated with the progeny BW. Classification year, classification season, and the classifier were grouped by the traits that correlated with the linear classification traits to perform analysis of variance (ANOVA). ANOVA was performed using the GLM in the SAS 9.1.3 package program, the results of which are shown in Tables 7 and 8.

Table 7. Analysis of variances between each trait and the birth weight

Source*	DF	MS	FV
HYS	88	122.244	51.74**
Sex	1	985.871	417.28**
Int	1	22.097	10.62*

*HYS, Herd-Year-Season group; Int, linear-type test date to the date of calving; DF, degree of freedom; MS, mean square; FV, F-value; **: p<.0001, *: p<0.05.

Table 8. Analysis of variances among each trait and the linear type traits

Source*	DF	ST		BL		RA		RL		PBW		FS	
		MS	FV	MS	FV	MS	FV	MS	FV	MS	FV	MS	FV
LY	6	33.0	24.4**	96.3	64.5**	5.5	4.7**	52.8	50.3**	34.3	26.3**	38.6	15.8**
LS	3	18.2	13.4**	13.7	9.19**	19.1	16.5**	10.9	10.4**	4.7	3.6**	53.5	21.8**
Classifier	6	52.9	39.1**	40.4	27.1**	57.1	49.2**	40.1	38.2**	9.1	6.9**	92.8	37.8**
Int	1	32.6	24.1**	26.5	17.8**	45.6	39.3**	42.6	40.5**	83.4	63.9**	191.1	77.9**

* LY: linear test year; LS: linear test season.

BW significantly correlated with the differences in birth region/year/season CGs and sex (P<.0001) and with the environmental effects of the duration (in days) between the maternal classification and calving (P<.005). The classification traits significantly correlated with the environmental effects (P<.0001); therefore, they were included in the statistical analysis model for the genetic parameter estimation.

The phenotypic correlation between the BW of the progeny and the maternal linear type traits is shown in Table 9. There was a low negative correlation (-0.13) between BW and RA and a low positive correlation (0.1) between BW and FS. However, there was no correlation with the other linear classification traits; and there was no significant difference between BW and BL. In the linear classification of Holstein cows, used for milk production through progeny production, the ideal RA requires the pin bone to be slightly lower than the rump, because cows with the pin bone slightly lower than the rump tend to have easier calving. The low correlation between BW and the linear classification traits could be attributed to the differences in the linear type traits between the time of classification and calving, as there were differences in the date of maternal linear classification and calving.

Table 9. Phenotypic correlations between the birth weight and linear traits

Traits	BW	ST	BL	RA	RL	PBW
ST	0.06^{**}					
BL	-0.01^{NS}	0.81^{**}				
RA	-0.13^{**}	0.15^{**}	0.22^{**}			
RL	0.03^{*}	0.78^{**}	0.79^{**}	0.16^{**}		
PBW	0.04^{*}	0.66^{**}	0.64^{**}	0.23^{**}	0.70^{**}	
FS	0.10^{**}	0.77^{**}	0.70^{**}	0.32^{**}	0.76^{**}	0.78^{**}

**: p<.0001, *: p<0.05, NS: Not significant.

We evaluated the phenotypic correlations among the linear classification traits. There is a high positive correlation of ≥ 0.60, among ST, BL, RL, and FS, and a moderate positive correlation of 0.15~0.32 with RA. Therefore, the correlations among the linear classification traits were significant. Lee et al. (2011) reported phenotypic correlations of 0.18~0.80 among ST, BL, RA, RL, PBW, and FS, while Jeoung (2017) reported phenotypic correlations of 0.49~0.76 among ST, BL, RL, and PBW. The results from the present study corroborated the results from the earlier reports. However, Shin (2018) reported phenotypic correlations of 0.78~0.94 among ST, BL, RL, PBW, and FS, which is higher than that observed in the present study.

Genetic parameter estimation

The genetic deviation, heritability of the linear classification traits, and BW are presented in Table 10. The heritability of BW, ST, BL, RA, RL, PBW, and FS were 0.23, 0.34, 0.37, 0.11, 0.45, 0.31, and 0.40, respectively, indicating a moderate heritability for all traits except RA, which showed a low heritability.

Table 10. Variance components and heritability estimates of each trait

Components*	BW	ST	BL	RA	RL	PBW	FS
	0.57	0.47	0.58	0.12	0.50	0.42	1.01
	0.63						
	0.33						
	0.92	0.92	0.98	1.02	0.61	0.92	1.52
	2.45	1.39	1.56	1.14	1.11	1.34	2.53
	0.23	0.34	0.37	0.11	0.45	0.31	0.40

* : Additive genetic variance, : Maternal variance, : Maternal permanent environment variance, : Residual variance, : Phenotype variance, : Heritability

Lee et al. (2018) evaluated Hanwoo calves born in Gangwon Province Livestock Research Institute between 2006 and 2016 and estimated a BW heritability of 0.26. Kim (2012) reported that the BW heritability among female and male calves was 0.14, and 0.17, respectively, in the Hanwoo calves born between 1970 and 2011. Lee (2012) reported a BW heritability of 0.63 in female calves, which was higher than that observed in the present study.

Lee et al. (2011) reported ST, BL, RA, RL, PBW, and FS heritability of 0.40, 0.42, 0.31, 0.19, 0.17, and 0.30, respectively. The ST, BL, and RA heritability were higher than that in the present study (0.34, 0.37, and 0.11, respectively),while of the RL, PBW, and FS heritability were lower than that in the present study (0.45, 0.31, and 0.40, respectively). Cho et al. (2014) reported ST, BL, RL, and PBW heritability of 0.16, 0.13, 0.07, and 0.06, respectively, which were lower than that in the present study. Jeoung (2017) reported ST, BL, and PBW heritabilities of 0.33, 0.35, and 0.31, respectively, which were similar to that in the present study; however, the RL heritability was 0.25, which was lower than that in the present study. Shin (2008) reported an ST heritability of 0.33, which was similar to that in the present study, while the BL, RL, PBW, and FS heritabilities were 0.29, 0.25, 0.24, and 0.24, respectively, which were lower than that in the present study.

The genetic correlations between the BW of the progeny and the maternal linear classification traits are presented in Table 11. BW showed a low genetic correlation with ST, BL, RL, PBW, and FS (0.09, 0.03, 0.02, -0.04, and -0.02, respectively), but there was a negative genetic correlation with RA (–0.19). There were strong positive genetic correlations among all the traits (0.83–0.90), except RA, which had a relatively moderate correlation (0.25~0.36). Lee et al. (2011) reported that ST has a genetic correlation of 0.92, 0.32, 0.89, 0.84, and 0.82 with BL, RA, RL, PBW, and FS, respectively, and 0.46–0.91, with the remaining traits. Jeoung (2017) reported that ST has a genetic correlation of 0.73, 0.48, and 0.52, with BL, RL, and PBW, respectively, and a genetic correlation of 0.53–0.65, with the remaining traits. Shin (2018) reported that ST has a genetic correlation of 0.77, 0.60, 035, and 0.65, with BL, RL, PBW, and FS, respectively, and a genetic correlation of 0.49–0.66 with BL, RL, PBW, and FS. These differences in the correlation could be attributed to the differences in the analytical method and the animals used in the analyses; therefore, additional studies are required to establish concrete correlations. Jeoung (2018) reported that there is almost no genetic correlation between maternal linear classification traits and the progeny carcass traits (castrated).The results from the present study, corroborates the early report, as the results indicated no correlation between the maternal linear classification traits and progeny BW.

Table 11. Genetic correlation between the birth weight and the linear traits

Traits	BW	ST	BL	RA	RL	PBW
ST	0.09					
BL	0.03	0.89				
RA	-0.19	0.27	0.27			
RL	0.02	0.86	0.92	0.25		
PBW	-0.04	0.79	0.82	0.36	0.90	
FS	-0.02	0.83	0.86	0.39	0.85	0.83

CONCLUSION

The BW of Hanwoo cows increased by approximately 0.4 kg each year, indicating that the body weight and linear type traits of Hanwoo cows are increasing. The mean BW increased with an increase in the mean FS, which is a comprehensive indicator for maternal linear type traits. Animals with excellent linear type traits would produce better progeny traits and therefore, the linear type traits could be used for screening and selection. However, the BW heritability was moderate (0.23). The linear classification traits, which represent maternal linear type traits, showed values of 0.34, 0.37, 0.11, 0.45, 0.31, and 0.40,for ST, BL, RA, RL, PBW, and FS, respectively, with moderate heritability for all traits, except RA. Traits with heritability ≥ 0.30 could be improved within a relatively shorter time, compared to the other traits.BW had a heritability of ≥ 0.20and it could be improved to enhance the progeny production. The BW of the progeny showed phenotypic correlations of0.06, -0.01, 0.03, and 0.04, and genetic correlations of 0.09, 0.03, 0.02, and -0.04 with ST, BL, RL, and PBW, respectively, with the linear classification traits representing maternal linear type traits, in Hanwoo cows. The average parity in Hanwoo cows has gradually increased from 2.5 in 2016 to 2.8 in June 2020; but there is a lack of progeny information for testing dams. From a policy perspective, multiple births by excellent dams are desirable. The parity of dams is expected to increase in the future, which would allow further testing of dams and a greater accumulation of progeny BW data and test records. This could lead to meaningful results that enable accurate evaluation of BW, as an economic trait.

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