Estimation of Genetic Parameters on Pre-weaning Growth Traits in Hanwoo

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한우의 이유전 성장형질에 관한 유전모수 추정

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요   약

본 연구에서는 축산연구소 한우시험장에서 1970년부터 2005년까지 출생한 한우 4,627두의 이유전 성장형질(생시체중, 이유시 체중, 이유전 일당증체량)에 대한 유전모수를 추정하기 위해 실시하였다. 유전모수 추정은 두 가지 모형을 이용하여 실시되었는데, 모형 1에서 추정한 개체효과의 유전력은 0.34, 이유시 체중에서 0.26, 이유전 일당증체량에서 0.20이었다. 모형 2를 이용하여 추정한 개체 유전효과의 유전력과 모체 유전효과의 유전력은 생시체중에서 0.14와 0.06, 이유시 체중에서 0.07과 0.04 그리고 포유기 일당증체량에서 0.05와 0.04이었고, 개체효과와 모체효과간의 유전상관계수는 생시체중에서 0.58, 이유시 체중에서 0.75 그리고 포유기 일당증체량에서 0.61 이었다. 모형 1을 이용하여 추정한 생시체중과 이유시 체중 간, 생시체중과 포유기 일당증체량 간, 그리고 이유시 체중과 포유기 일당증체량 간의 유전상관은 각각 0.76, 0.62 및 0.99였다. 포유기 일당증체량과 이유시 체중 사이의 유전상관계수가 높게 추정된 결과는 포유기 일당증체량에 대한 선발을 통해 한우 집단의 이유시 체중을 효과적으로 증대시킬 수 있을 것임을 시사한다.

(**Key words** : Birth weight, Weaning weight, ADG, Heritability, Genetic correlation)

Ⅰ. INTRODUCTION

To improve pre-weaning productivity of cattle, cow-calf producers have been trying to increase weaning weight of their calves through management and genetics (Fiss and Wilton, 1993). Pre-weaning ability of an animal is determined by inherent genes from its parents and milking production and mothering ability of its dam called maternal effect. Most of the literature reported that the maternal ability of beef cows had been shown to be a critical component for pre-weaning growth of their calves (Freking and Marshall, 1992; Fiss and Wilton, 1993; Mallinckrodt et al., 1993; Brown and Brown, Jr. 2002).

The objective of this study was to estimate genetic relationships between pre-weaning growth traits in Hanwoo.

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Ⅱ. MATERIALS AND METHODS

A total of 4,627 records on pre-weaning growth traits, birth weight (BW), weaning weight (WW), pre-weaning daily gain (ADG) of Hanwoo's born from 1970 to 2005 were collected from Hanwoo Experiment Station, National Livestock Research Institute. BW of calf was measured within 24h after birth and age at measuring WW ranged from 90 to 150 days of age.

Variance components and heritabilities of BW, WW and ADG were estimated with two models.

Model 1 : $y = X\beta + Z_d u_d + e$

Model 2 : $y = X\beta + Z_d u_d + Z_m u_m + Z_{pe} u_{pe} + e$

Where, y is a N×1 vector of observations, β is a vector of fixed effects-contemporary group (birth year-season-sex), age of dam and weaning age of calf, u_d is a vector of additive genetic effect, u_m is a vector of maternal genetic effect, u_{pe} is a vector of permanent environmental effect. And X, Z_d, Z_m, Z_{pe} are incidence matrices linking fixed effects and random effects with observations.

The (co)variance structures of random effects for Model 1 was

$$Var\begin{bmatrix} u_d \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_d^2 & 0 \\ 0 & I\sigma_e^2 \end{bmatrix}$$

and that for Model 2 was

$$Var\begin{bmatrix} u_d \\ u_m \\ u_{pe} \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_d^e & A\sigma_{dm} & 0 & 0 \\ A\sigma_{dm} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Where σ_d^2 is direct genetic variance, σ_m^2 is maternal genetic variance, σ_{dm} is covariance between direct and maternal genetic effect, σ_{pe}^2 is permanent environmental variance, and σ_e^2 is random residual variance. A is a numerator relationship matrix among animals in pedigree file, and the I matrices are identity matrices.

Table 1. Distribution of records by birth year, birth season and sex

Year	N	Year	N	Season	N	Sex	N
1970~1980	669	1994	174	Winter	241	Female	2,405
1981	96	1995	194	Spring	2,326	Male	2,222
1982	139	1996	212	Summer	1,316		
1983	103	1997	188	Fall	580		
1984	115	1998	228	Unknown	164		
1985	73	1999	183				
1986	151	2000	206				
1987	137	2001	214				
1988	128	2002	167				
1989	174	2003	137				
1990	117	2004	147				
1991	124	2005	86				
1992	146	Unknown	164				
1993	155						
Total			4,627		4,627		4,627

Winter : Dec.~Feb., Spring : Mar.~May, Summer: Jun~Aug., Fall : Sep.~Nov.

MTDFREML program (Boldman et al, 1995) was used for genetic parameter estimation. Global maximum likelihood estimates were iteratively estimated using estimates from previous run as priors with each run to go until the variation was less then 10^{-11}. Two trait analyses using model 1 were performed to obtain covariance among traits.

Ⅲ. RESULT AND DISCUSSION

Table 2 reports summary statistics for BW, WW and ADG in this sample.

The averages of BW, WW and ADG were 24.39 kg, 91.77 kg and 0.547 kg, respectively.

Additive direct genetic variances of pre-weaning traits estimated from model 1 are shown in Table 3. Heritability estimates for BW, WW and ADG from model 1 were 0.34, 0.26 and 0.20, respectively. Heritability estimates for BW, WW and ADG in this study were within the range of literature values. Ferreira et al. (1999) estimated direct heritabilities of direct BW and

direct WW as 0.28 and 0.16 in Hereford. Aziz et al. (2005) reported that heritabilities of BW and 120d weight in Japanese Black cattle were 0.38 and 0.65. Koots et al. (1994) summarized published genetic parameter estimates and reported that weighted average estimates of heritability for BW, WW and ADG were 0.31, 0.24 and 0.29, respectively.

Additive genetic, maternal genetic and permanent environmental variances of pre-weaning traits estimated from model 2 are shown in Table 4. Maternal heritability estimates ranged from 0.04 to 0.06. Direct heritability estimates ranged from 0.05 to 0.14 for BW, WW and ADG. Genetic correlations between direct and maternal genetic effects were estimated positive; 0.58, 0.75 and 0.61 for BW, WW and ADG, respectively. It is suggested that maternal effect for WW and ADG may positively interact with direct genetic effect during selection process.

Meyer (1992) reported that genetic correlations between direct and maternal genetic effect for BW were 0.038 in Hereford and 0.285 in Angus

Table 2. Simple statistics of pre-weaning traits, age of dam and age at weaning

Trait	n	mean	std	Max	min
BW	4,191	24.39	3.76	40	10
WW	3,136	91.77	20.31	26	179
ADG	3,133	0.547	0.153	1.287	0.045
AOD	4,346	1,960.5	1,015.2	6,881	461
Wage	3,136	122.9	11.2	150	90

BW : Birth weight (kg), WW : Weaning weight (kg), ADG : Preweaning daily gain (kg), AOD : Age of dam (day), Wage : Weaning age of calf (day).

Table 3. Additive direct genetic variance of pre-weaning traits

Trait	σ_d^2	σ_e^2	σ_t^2	h^2
BW	3.73	7.33	11.06	0.34
WW	68.65	191.01	259.66	0.26
ADG	0.003	0.012	0.016	0.20

σ_d^2 : Direct genetic variance, σ_e^2 : Environmental variance, $\sigma_t^2 = \sigma_d^2 + \sigma_e^2$, h^2 : Direct heritability.

Table 4. Additive direct genetic, maternal genetic and permanent environmental variance of pre-weaning traits

Trait	σ_d^2	σ_m^2	σ_{dm}	σ_{pe}^2	σ_e^2	σ_p^2	h_d^2	h_m^2	r_{dm}
BW	1.55	0.62	0.57	0.10	7.99	10.82	0.14	0.06	0.58
WW	17.82	10.30	10.15	14.71	190.03	243.01	0.07	0.04	0.75
ADG	0.001	0.001	0.000	0.001	0.012	0.015	0.05	0.04	0.61

σ_d^2 : Direct genetic variance, σ_m^2 : Maternal genetic variance, σ_{dm}: Direct maternal genetic covariance, σ_{pe}^2: Permanent environmental variance, σ_e^2 : Environmental variance, σ_p^2 : Phenotypic variance, h_d^2 : Direct heritability, h_m^2: Maternal heritability, r_{dm} : Correlation between direct and maternal effect.

and those for WW were -0.587 in Hereford, 0.223 in Angus and -0.783 in Zebu Cross. Ferreira et al. (1996) reported that genetic correlation between direct and maternal was -0.33 for WW. Koots et al. (1994) reported that weighted genetic correlation between direct and genetic effects for WW was -0.20.

Genetic (co)variance components and genetic (phenotypic) correlation coefficients between pre-weaning traits from bi-variable analyses are shown in Table 5. Genetic (phenotypic) correlation coefficients between BW and WW, between BW

and ADG, and between WW and ADG were $0.76\,(0.34)$, $0.62\,(0.17)$ and $0.99\,(0.97)$, respectively.

Heritability estimates from single trait analyses and from two trait analyses came out to be the same. ADG and WW can be thought of as the same traits because genetic correlation between these was close to unity. Genetic correlation coefficients were higher than phenotypic correlation coefficients between BW and WW and between BW and ADG in the study. Our results accord with the results of Aziz et al. (2005) where direct genetic correlation coefficients among birth

Table 5. Estimates of (co)variance components among pre-weaning traits

Traits	σ_{d1}^2	σ_{d2}^2	σ_{d12}	σ_{e1}^2	σ_{e2}^2	σ_{e12}	σ_{p1}^2	σ_{p2}^2	σ_{p12}
BW×WW	3.76	61.72	11.52	7.33	187.40	7.69	11.08	249.12	19.21
BW×ADG	3.745	0.003	0.064	7.331	0.012	0.004	11.076	0.015	0.068
WW×ADG	65.656	0.003	0.439	184.363	0.012	1.452	250.019	0.015	1.892

	h_{d1}^2		h_{d2}^2		r_{d12}		r_{p12}	
BW×WW	0.34		0.25		0.76		0.37	
BW×ADG	0.34		0.19		0.62		0.17	
WW×ADG	0.26		0.20		0.99		0.97	

BW : Birth weight (kg), WW : weaning weight (kg), ADG : Pre-weaning daily gain (kg)
$\sigma_{d1\,(or\,2)}^2$: Direct genetic variance of traits 1 (or 2), σ_{d12}: Genetic covariance between trait 1 and trait 2, $\sigma_{e1\,(or\,2)}^2$: Environmental variance of trait 1 (or 2), σ_{e12} : Environmental covariance between trait 1 and trait 2, $\sigma_{p1\,(or\,2)}^2$: Phenotypic variance of trait 1 (or 2), σ_{p12} : Phenotypic covariance between trait 1 and trait 2, $h_{d1\,(or\,2)}^2$: Direct heritability of trait 1 (or 2), r_{d12} : Genetic correlation between two traits, r_{p12} : Phenotypic correlation between two traits.

weight, weight at 90 days of age, weight at 120 days of age were higher than phenotypic correlation coefficients. Gregory et al. (1995, b) reported genetic and phenotypic correlation coefficient between birth weight and weight at 200 days of age similar to our results in female mixed breed population. However, they (Gregory et al. 1995, a) showed lower genetic correlation coefficients than phenotypic correlation coefficients between birth weight and pre-weaning average daily gain, and between birth weight and weight at 200 days of age in intact male population of beef cattle. This was due to negative genetic correlation between birth weight and 200 days weight. In the paper by Koots et al. (1994), genetic (phenotypic) correlation coefficients were 0.50 (0.46) between BW and WW, 0.26 (0.18) between BW and ADG and 0.98 (0.98) between WW and ADG. This supports close correlation between ADG and WW found in our study. This means that WW is more of a function of ADG than of sole genetic potential embedded in BW. Therefore, to increase WW, we need to select breeding stock with superior genetic potential of pre-weaning ADG.

Ⅳ. ABSTRACT

A total of 4,627 records on pre-weaning growth traits, birth weight (BW), weaning weight (WW) and pre-weaning daily gain (ADG) of Hanwoo's born form 1970 to 2005 were collected from Hanwoo Experiment Station, National Livestock Research Institute. Variance components and heritabilities of BW, WW and ADG were estimated with two models; Model 1 included only direct genetic effect while Mode1 2 included direct genetic, maternal genetic and permanent environmental effects. Direct heritability estimates of BW, WW and ADG estimated by model 1 were 0.34, 0.26 and 0.20, respectively. In model 2, direct heritability and maternal genetic heritability estimates were 0.14 and 0.06 for BW, 0.07 and 0.04 for WW and 0.05 and 0.04 for ADG. Estimates of genetic correlation between direct and maternal effect for BW, WW and ADG were 0.58, 0.75 and 0.61, respectively. Genetic correlation coefficients between BW and WW, between BW and ADG, and between WW and ADG were 0.76, 0.62 and 0.99, respectively.

(**Key words** : Birth weight, Weaning weight, ADG, Heritability, Genetic correlation)

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