

Genetic Relationship Between Weaning Weight and Carcass Traits in Hanwoo

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한우의 이유시 체중과 도체형질과의 유전적 관계

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요 약

본 연구는 한우에서 이유시 체중과 도체형질들 간의 상관관계를 구명하고자 실시하였다. 조사된 도체 형질은 배최장근 단면적, 등지방두께, 21단계로 구분하여 평가한 근내지방도(근내지방도 I)와 7단계로 구분하여 평가한 근내지방도(근내지방도 II), 그리고 7단계로 구분하여 평가한 육색 등이었다. 유전모수의 추정에는 DFREML 방법을 적용하여 실시하였는데 이유시 체중에 대한 통계모형은 동기우 그룹효과(년도-계절-성) 외에 이유시 송아지 일령 및 어미소 일령의 1차식 효과와 2차식 효과를 고정효과로 포함하였고 개체 효과를 임의효과로 포함하였다. 도체형질에 대한 통계 모형은 동기우 그룹효과(년도-계절-성) 외에 도축시 일령의 1차식 효과를 고정효과에 포함하였고 개체효과를 임의효과로 포함하였다. 조사된 형질별 유전력 추정치는 이유시 체중이 0.25, 배최장근 단면적이 0.20, 등지방두께가 0.20, 근내지방도 I 이 0.32, 근내지방도 II 가 0.32 그리고 육색이 0.22였다. 이유시 체중과 배최장근 단면적, 등지방두께, 근내지방도 I, 근내지방도 II 및 육색 간의 유전(표현형) 상관계수는 각각 0.75 (0.16), 0.18 (0.05), -0.41 (-0.09), -0.40 (0.11) 및 -0.07 (0.05)였다. 본 연구 결과는 이유시 체중이 무거운 방향으로 단형질 선발을 진행할 경우 등심단면적이 넓어지고, 등지방두께가 두꺼워지며 근내지방도가 감소하는 도체를 생산하는 후손집단이 형성될 가능성이 있음을 시사하고 있다.

(Key words : Weaning weight, Carcass trait, Heritability, Genetic correlation)

I. INTRODUCTION

To satisfy customers' tastes, production of quality beef is a very important in beef cattle breeding along with calf growth, which is also an economically important issue for cow-calf producers. However there is controversy in

relationship between body growth and carcass parameters at different slaughter end points (Choy et al., 2005). Splan et al. (2002) reported that selection to increase maternal or direct weaning weight would have been expected to increase carcass weight, rib eye area, and fat thickness and that selection for direct weaning weight only

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would be expected to slightly decrease marbling. Before we proceed selection of animals with higher carcass quality, which is an important focus in Hanwoo, studies on how growth traits may develop in response to the selection with emphases on meat quality, or vice versa, should be researched.

The objective of this study was to estimate the genetic relationships between weaning weight and carcass traits in Hanwoo.

II. MATERIALS AND METHODS

1. DATA

The data of carcass traits and weaning weight (WW) were collected from a total 581 Hanwoo's; 472 bulls and 109 steers which were born between 1989 and 2003 at Hanwoo Experiment

Station of National Livestock Research Institute, Korea. Age at weaning weight measurement ranged from 90 to 150 days of age. Carcass records used were eye muscle area (EMA, cm²), back fat thickness (BFT, mm), marbling score I (MS I, 1 (poor) to 21 (best) grade), marbling score II (MS II, 1 (poor) to 7 (best) grade) and meat color score (Mcolor, 1 (bright) to 7 (dark)). All slaughtering processes and carcass evaluations were performed in accordance with the guidelines of beef grading system of Ministry of Agriculture, Korea.

Distribution of animals slaughtered by season of birth and sex for each birth year is shown in Table 1.

2. STATISTICAL ANALYSES

Multiple trait animal models were used to

Table 1. Distribution of animals slaughtered by season of birth and sex for each birth year

Year	Season				Sex		Total
	Winter	Spring	Summer	Autumn	Bull	Steer	
1989	0	0	15	8	23	0	23
1990	1	9	11	7	28	0	28
1991	0	16	9	6	31	0	31
1992	0	14	24	14	52	0	52
1993	2	5	11	4	22	0	22
1994	0	21	4	2	27	0	27
1995	0	17	5	1	25	0	23
1996	0	18	13	6	27	10	37
1997	0	16	0	0	16	0	16
1998	0	25	12	5	17	25	42
1999	14	5	2	8	19	0	19
2000	0	17	27	7	35	26	61
2001	0	12	35	16	63	0	63
2002	4	49	28	1	59	19	78
2003	0	18	37	0	30	29	59
Total	21	242	233	85	472	109	581

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

estimate heritabilities and genetic correlations. The linear models used for this analysis in uni-variable expression for each trait plugged in bi-variable analyses were;

(1) Weaning weight

$$Y_{ij} = \mu + SBY_i + \beta_1 AOD + \beta_2 AOD^2 + \beta_3 WCA + \beta_4 WCA^2 + u_{ij} + e_{ij}$$

where, Y_{ij} is record of j^{th} individual of i^{th} birth year-season-sex (SBY_{*i*}), μ is an overall mean, β_1 and β_2 are regression coefficients of linear and quadratic effects for age of dam (AOD), β_3 and β_4 are linear and quadratic regression coefficients for weaning age of calf (WCA), u_{ij} is an additive genetic effect, and e_{ij} is a random residual.

(2) Carcass traits

$$Y_{ij} = \mu + SBY_i + \beta \text{ Age at slaughter} + u_{ij} + e_{ij}$$

where, Y_{ij} is record of j^{th} individual of i^{th} birth year-season-sex (SBY_{*i*}), μ is an overall mean, β is a regression coefficient for Age at slaughter in days, u_{ij} is an additive genetic effect, e_{ij} is a random residual.

The linear models for weaning weight and carcass traits including EMA, BFT, MS I, MS II and Mcolor, defined in matrix notation, were as follows;

$$y = X\beta + Z_d u_d + e$$

Where y is a $N \times 1$ vector of observations; β is a vector of fixed effects (birth year-season-sex, age of dam, weaning age of calf and age at slaughter); u_d is a vector of additive genetic effect. Incidence matrices X and Z_d relate observations to fixed effects and random effects.

The (co)variance structure of the random effects was

$$Var \begin{bmatrix} u_{d1} \\ u_{d2} \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{d1}^2 & A\sigma_{d12} & 0 & 0 \\ A\sigma_{d12} & A\sigma_{d2}^2 & 0 & 0 \\ 0 & 0 & I\sigma_{e1}^2 & I\sigma_{e12} \\ 0 & 0 & I\sigma_{e12} & I\sigma_{e2}^2 \end{bmatrix}$$

Where, $\sigma_{d1(2)}^2$ is a direct genetic variance of trait 1(2). $\sigma_{e1(2)}^2$ is a random residual variance of

trait 1(2). And σ_{d12}^2 is a direct genetic covariance between traits 1 and 2. A is a numerator relationship matrix among animals in pedigree file, and the I matrix is a $(N \times N)$ identity matrix.

MTDFREML program (Boldman et al., 1995) was used for genetic parameter estimation. Global maximum likelihood estimates were iteratively gotten using estimates from previous run as priors with each run to reach convergence criteria of 10^{-11} . Single trait and two trait analyses were performed.

III. RESULTS AND DISCUSSION

Simple statistics of weaning age of calf, weaning weight, carcass traits and age at slaughter are shown in Table 2.

The averages of carcass traits were 90.81 cm² for EMA, 8.66mm for BFT, 6.42 for MS I, 2.54 for MS II, and 4.66 for Mcolor. And average of WW was 103.64 kg.

Additive direct genetic variances and heritabilities estimated from single trait analyses are shown in Table 3 for WW and carcass traits.

Heritability estimates of carcass traits were 0.20 for EMA, 0.20 for BFT, 0.32 for MS I, 0.32 for MS II, and 0.22 for Mcolor. Heritability of WW was estimated to be 0.25. Heritabilities for EMA, BFT and MS as reported by Koots et al.(1994) were higher as compared to these results. Hirooka et al.(1996) reported that heritabilities of BFT, EMA and MS were 0.20, 0.24 and 0.4 respectively in Japanese Brown cattle. Heritability estimates of MS reported by Crews et al.(2004), Macneil et al(2001), Ríos-Utrera et al.(2005) and Kemp et al.(2002) were 0.54, 0.29, 0.40 and 0.42, respectively. On the other hand, heritability estimates reported by Roh et al.(2004) for Hanwoo steers fattened at progeny test station were 0.35 for EMA, 0.39 for BFT and 0.51 for MS. Park and Park(2003) reported that heritability estimates from Hanwoo

Table 2. Simple statistics of weaning age of calf, weaning weight, carcass traits and age at slaughter

Trait	n	mean	std	Max	Min
WCA	254	125.29	10.88	150	90
WW	254	103.64	18.02	150	43
Age at slaughter	567	743.90	62.07	935	373
EMA	569	90.81	13.38	144	61
BFT	578	8.66	5.34	38	1
MS I	558	6.42	4.41	20	1
MS II	546	2.54	1.40	7	1
Mcolor	530	4.66	0.74	7	2

WCA : weaning age of calf (day), WW : weaning weight (kg), EMA : Eye muscle area (cm²), BFT : Subcutaneous fat thickness (mm), MS I : Marbling score I , MS II : Marbling score II, Mcolor : Meat color (score)

Table 3. Additive direct genetic variance of weaning weight and carcass traits

Trait	σ_d^2	σ_e^2	h^2
WW	62.61	187.01	0.25
EMA	24.71	98.29	0.20
BFT	3.77	14.83	0.20
MS I	3.68	7.86	0.32
MS II	0.38	0.80	0.32
Mcolor	0.06	0.21	0.22

WW : weaning weight (kg), EMA : Eye muscle area (cm²), BFT : Subcutaneous fat thickness (mm), MS I : Marbling score I , MS II : Marbling score II, Mcolor : Meat color (score), σ_d^2 : Direct genetic variance, σ_e^2 : Environmental variance, h^2 : Direct heritability.

bulls' performance data set, of which carcass trait measures were collected at 22 months of age, were 0.33 for EMA, 0.51 for BFT and 0.31 for MS. The heritability estimates in this study tended to be lower than those of Roh et al. (2004). However, heritabilities for MS estimated in our study were similar to 0.31, the heritability estimate for MS reported by Park and Park (2003). Heritability estimate of MS I (0.31) was same with that of MS II (0.31), while genetic and environmental variance were smaller in MS

II in this study. This suggests that heritability estimates of MS with 7 grades or with 21 grades may lead to almost same results. Variation must be increased by triplication of measuring scale but the ratio of variance component would be kept the same with smaller changes by redistribution of MS scales within each grade in 1-7 scale.

Genetic (co)variance components and genetic (phenotypic) correlation coefficients of WW with carcass traits estimated from two trait model analyses are shown in Table 4.

Positive genetic correlations were estimated between WW and EMA or between WW and BFT. But the genetic correlation coefficient between WW and MS was negative. Woodward et al. (1992) reported that genetic (phenotypic) correlation between WW and MS was 0.16 (0.02) in Simmental. Shanks et al. (2001) reported that genetic correlation coefficients between WW direct effect and EMA were 0.19-0.42 between WW and BFT were -0.44-0.53 and between WW and MS were -0.05-0.09 in Simmental. Estimates for genetic correlation coefficients in the study by Arnold et al. (1991) were -0.28 between WW and BFT, 0.33 between WW and EMA and -0.01 between WW and MS for

Table 4. Estimates of (co)variance components between weaning weight and carcass 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}
WW×EMA	61.20	18.18	25.10	187.96	164.79	8.36	249.16	182.98	33.45
WW×BFT	62.79	3.78	2.73	186.88	15.11	0.92	249.67	18.90	3.65
WW×MS I	62.59	3.80	-6.39	187.01	7.92	1.30	249.60	11.71	-5.08
WW×MS II	62.97	0.40	-1.99	186.76	0.79	0.08	249.72	1.19	-1.91
WW×Mcolor	62.85	0.06	-0.14	186.84	0.21	0.53	249.69	0.27	0.39
	h_{d1}^2		h_{d2}^2		r_{d12}		r_{p12}		
WW×EMA	0.25		0.10		0.75		0.16		
WW×BFT	0.25		0.20		0.18		0.05		
WW×MS I	0.25		0.32		-0.41		-0.09		
WW×MS II	0.25		0.33		-0.40		-0.11		
WW×Mcolor	0.25		0.23		-0.07		0.05		

WW : weaning weight (kg), EMA : Eye muscle area (cm²), BFT : Subcutaneous fat thickness (mm), MS I : Marbling score I, MS II : Marbling score II, Mcolor : Meat color (score), σ_{d1} (or σ_{d2})² : Direct genetic variance of trait 1 (or 2), σ_{d12} : Genetic covariance between trait 1 and trait 2, σ_{e1} (or σ_{e2})² : Environmental variance of trait 1 (or 2), σ_{e12} : Environmental covariance between trait 1 and trait 2, σ_{p1} (or σ_{p2})² : Phenotypic variance of trait 1 (or 2), σ_{p12} : Phenotypic covariance between trait 1 and trait 2, h_{d1} (or h_{d2})² : Direct heritability of trait 1 (or 2), r_{d12} : Genetic correlation between two traits, r_{p12} : Phenotypic correlation between two traits.

Hereford steers.

Results from this study suggest that selection for weaning weight would lead to progeny population having carcass with large EMA, thick BFT and decreased MS.

IV. ABSTRACT

The objective of this study was to evaluate the genetic relationship between weaning weight (WW) and carcass traits. Carcass traits were eye muscle area (EMA), back fat thickness (BFT), marbling score 1 (MS1) in 21 grade scales, marbling score 2 (MS2) in 7 grade scales and meat color scores (Mcolor). Parameters were estimated by REML procedure with MTDFREML package. Models included contemporary group as defined by the same year-season-sex at birth, linear covariates of age (days) at weaning, age of dam (days) and age at slaughter (days) as fixed

effects and animal random effects for all the traits. Heritability estimates of WW, EMA, BFT, MS1, MS2 and Mcolor were 0.25, 0.20, 0.20, 0.32, 0.32 and 0.22, respectively. Genetic (phenotypic) correlation coefficients of WW with EMA, BFT, MS1, MS2 and Mcolor were 0.75 (0.16), 0.18 (0.05), -0.41 (-0.09), -0.40 (0.11) and -0.07 (0.05), respectively. Results from this study suggest that single trait selection for weaning weight would lead to progeny population having carcass with large EMA, thick BFT and decreased MS.

(Key words : Weaning weight, Carcass trait, Heritability, Genetic correlation)

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