

# Estimation of Genetic Parameters of Body Weights in Hanwoo Steers (Korean Cattle), *Bos Taurus Coreanae* Using Random Regression Model

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## 임의회귀모형을 이용한 한우 거세우 체중의 유전모수 추정

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### 요 약

본 연구는 임의회귀모형을 이용하여 한우 거세우 체중에 대해서 유전모수 추정을 하고 이것을 단 형질 개체모형의 결과와 비교해 보고자 실시하였다. 분석에 이용한 자료는 총 1,372두의 한우 거세우의 체중 자료로, 농협중앙회 가축개량사업소에서 실시한 한우 후대검정우의 기록이다. 이차의 임의회귀 모형에 적용한 결과 유전력이 총 800일령까지의 검정기간에 대해 0.17~0.30의 범위로 나타났다. 개체모형을 통해 얻은 유전력은 0.24~0.36의 범위로 나타났다. 측정일간의 영구환경효과의 상관은 검정일령이 늘어남에 따라 함께 증가하는 경향을 보였다. 반면, 측정일간의 유전상관의 경우 검정초기에는 0.30 정도의 약한 음의 상관을 보이지만, 검정이 이뤄짐에 따라 상관이 점차 증가하여 검정이 종료될 무렵이면 거의 고정되는 것으로 나타났다. 임의회귀모형과 개체모형의 결과를 비교해보면 두가지 모형 모두 비슷한 경향을 보여 큰 차이를 보이지 않았다. 따라서, 임의회귀모형을 한우에 대한 국가유전능력평가에 사용하는 것이 가능할 것으로 사료된다.

(Key words : Genetic parameters, Hanwoo, Random regression model)

### I. INTRODUCTION

The current genetic evaluation of beef cattle for growth utilized multi trait animal model methodology wherein animals are evaluated for weights at certain ages (BIF, 2002). However, actual weighing dates are noted and recorded at certain ages thereby pre-adjusting weights to

fixed ages. All records that are outside of the specific age range interval are not used which lowers the accuracy of evaluation. Furthermore Nobre et al. (2003a) reported pre-adjustments of weights to fixed ages are for the mean only but not the variances.

In the United States random regression models have been proposed as an alternative to multi-

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trait models for genetic evaluation of growth data. Nobre et al. (2003b) reported that analysis of weights as a longitudinal trait may result in increased accuracy of evaluation by eliminating the need for pre-adjustments by its ability to incorporate all weights with appropriate covariances.

In Korea, the national genetic evaluation of Hanwoo utilized multi-trait animal model in a two stage testing programs. First stage is the performance testing in which young bull calves of current proven bulls were harvested at six months of age and would undergo performance testing up to 12 month of age. The second stage is the progeny testing wherein cows registered in the program were inseminated with semen of young bulls and its male calves were purchased from farms and castrated at about 3 months of age. Station progeny testing were undertaken by the Hanwoo Genetic Improvement conducted at the Livestock Improvement Main Center of the National Agricultural Cooperative Federation (LIMC-NACF), a three month old steer has to be weighed at least 4 times throughout the whole progeny testing program. These weights were treated as separate traits. The purpose of this study was to estimate the genetic parameters of growth in Hanwoo steers using random regression model and eventually compare it with single trait animal model.

## II. MATERIALS AND METHODS

Hanwoo progeny testing data from the 23<sup>rd</sup> up to the 31<sup>st</sup> progeny testing covering the year 1972 up to 2001 were used. Birth weights were recorded and weighing was undertaken at three, six, twelve, eighteen and twenty two months of age. Preliminary data analysis was conducted using SAS v9.1 using the following model :

$$Y = \mu + \text{BYS} + \text{BP} + e$$

Y = observations of traits;  $\mu$  = mean of observ-

ations;  $\text{BYS}$  = fixed effect of birth year (1972 ...2001), season (summer, winter);  $\text{BP}$  = fixed effect of birth place (four region) and  $e$  = random error

The random regression model could be written in matrix notation Normalized Legendre Polynomial (Kirkpatrick et al., 1990) as :

$$P_j(D_i^*) = \frac{1}{2^j} \sqrt{\frac{2j+1}{2}} \cdot \sum_{m=0}^{j/2} (-1)^m \binom{j}{m} \binom{2j-2m}{j} (D_i^*)^{j-2m}$$

where,

$j^{\text{th}}$  normalized Legendre polynomial,  $P_j$  is given by the formula

$$D_i^* = u + \frac{v-u}{D_{\max} - D_{\min}} (D_i - D_{\min})$$

where [.] indicates that fractional values are rounded down to the nearest integer (Beyer, 1976 as cited by Kirkpatrick et al., 1990). These polynomials were defined over the interval [-1, 1], and so  $u = -1$  and  $v = 1$ .  $D_{\min}$  = minimum age,  $D_{\max}$  = maximum age,  $D_i$  = weighing date.

$$y_{ijkl} = \sum_{d=0}^3 z_{dm} o_{di} + \sum_{d=0}^3 z_{dm} l_{dj} + \sum_{d=0}^3 z_{dm} p_{dk} + \sum_{d=0}^3 z_{dm} a_{dk} + e_{ijkl}$$

where :

$y_{ijkl}$  =  $i^{\text{th}}$  observation of the  $j^{\text{th}}$  animal of the  $k^{\text{th}}$  dam and  $l^{\text{th}}$  record;  $o_{di}$  = progeny testing batch;

$l_{dj}$  = birth place;  $p_{dk}$  = permanent environmental;  $a_{dk}$  = animal effect;  $e_{ijkl}$  = residual effect. All random regression models fitted Legendre polynomials of test in days (tid) as independent variables. It involved fitting a set of regression coefficients on age or functions thereof for each animal as random effects. Orders of polynomial fit up to  $k=3$  were considered. The analyses fitted three sets of random regression coefficients due to animal's direct genetic effects, animal's permanent environmental effects and due to phenotypic effects. Regression coefficients for

phenotypic animal effects were the only one considered. The computations were undertaken using DMU package (Madsen and Jensen, 1994).

A single trait animal model using Derivative Free Restricted Maximum Likelihood (DFREML) by Meyer, 1998 was fitted using the following model :

$$Y = \mu + \text{BYS} + \text{BP} + e$$

Y=observations of traits; BYS = fixed effect of birth year (1972 ... 2001), season (summer, winter); BP= fixed effect of birth place (four region) and e=random error. Six covariables were fitted that corresponds to the age of the animal at weighing time. The weighing dates were thus noted hence the age were known.

### III. RESULTS AND DISCUSSION

A total of 1,372 steers with data from a pedigree of 21,282 animals were used. All the fixed effects fitted were significant ( $P < 0.05$ ) therefore all (birth year season and birth place) were fitted for both random regression model and single trait animal model. Results of the random regression model revealed during the early stages of test the direct genetic variances slightly decreased up to about 180 days then continuously increased with increasing test in days (Fig. 1).

Similar, trend for both phenotypic variance and permanent environmental variance were followed (Figures 2 and 3). The results corroborated with the reports of Jaffrezic et al. (2004) in their study on the analysis of growth curves of Charolais herd at INRA. They found that variances strongly increased with age.

Estimates of direct genetic, permanent environmental and phenotypic correlations between test in days are shown in Figures 4, 5 and 6. The estimates of additive genetic correlation (Fig. 4) between adjacent test in days exhibited an increasing pattern although at early stage of test at 256 days showed weak  $-0.09$  but as the

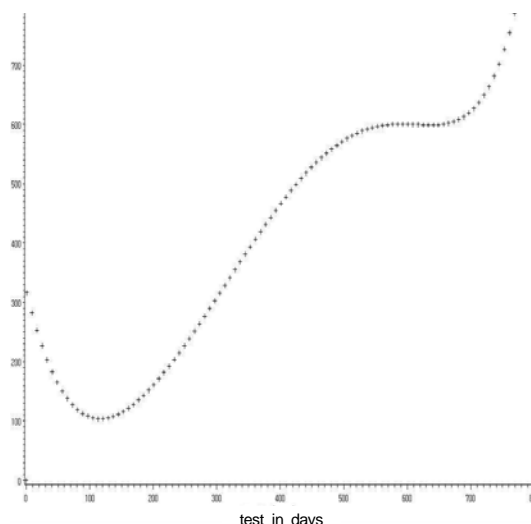


Fig. 1. Estimates of additive genetic variance of weights in Hanwoo steers using RRM.

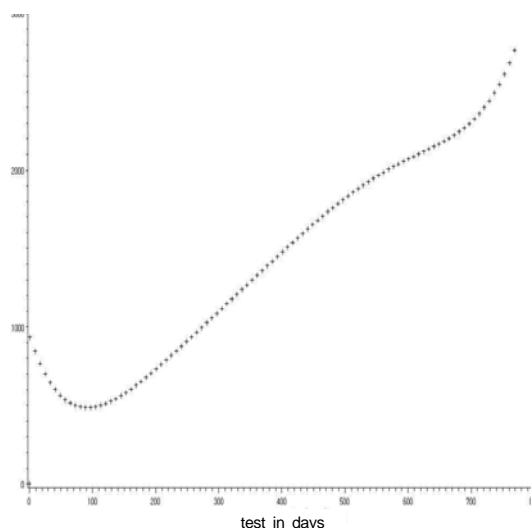


Fig. 2. Estimates of phenotypic variance of weights in Hanwoo steers using RRM.

steers aged it approaches unity. Furthermore, the plot exhibited a smooth surface dominated by large values which formed nearly unity. The weak negative genetic correlation at early stage seems to have no biological meaning although strong negative genetic correlation at early stage in beef cattle was reported by Jaffrezic et al. (2004). Estimates of permanent environmental

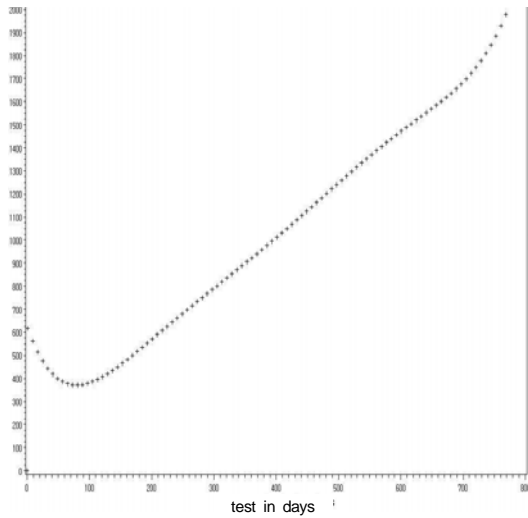


Fig. 3. Estimates of permanent environmental variance of weights in Hanwoo steers using RRM.

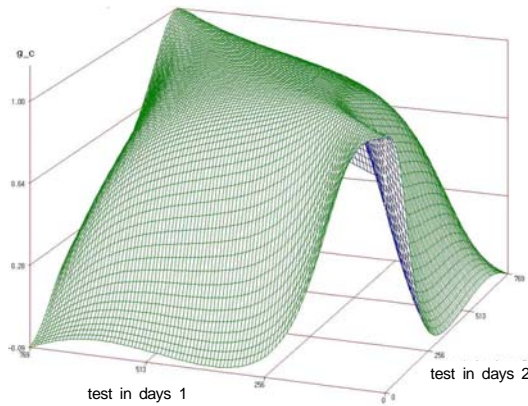


Fig. 4. Estimates of additive genetic correlation between two adjacent test in days in Hanwoo steers using RRM.

correlations tended to increase with increasing test in days. Unlike in the direct genetic correlation that at early stage the estimate was slightly negative it was 0.30 then increased to approach unity at later stage of test. Smooth surface of the plot could be attributed to the large values of covariances between adjacent test in days. The estimates of phenotypic correlation exhibited narrow differences as the test in days increased from 256 to 769. However, the values at

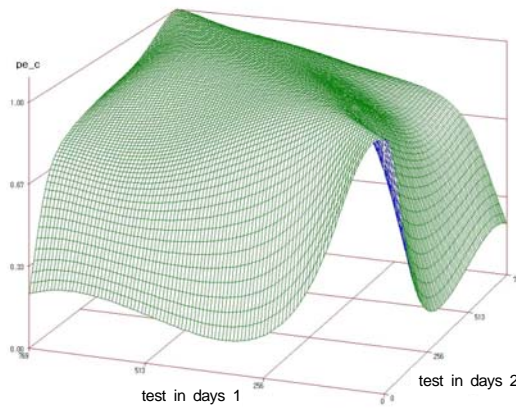


Fig. 5. Estimates of permanent environmental correlation between two adjacent test in days in Hanwoo steers using RRM.

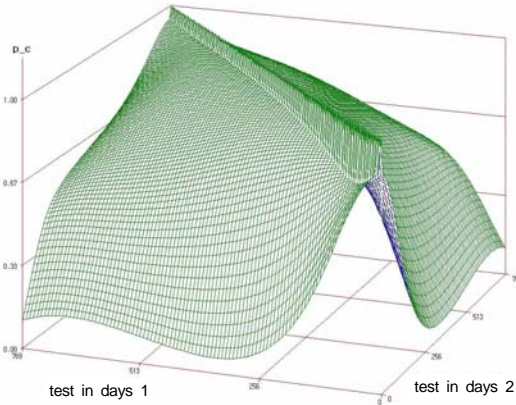


Fig. 6. Estimates of additive phenotypic correlation between two adjacent test in days in Hanwoo steers using RRM.

the early stage of test was lower than the permanent environmental correlation although at the later stage it did not approach unity. The smooth surface of the plot was due to the large covariance values between two adjacent test days.

Estimates of heritability over test in days using random regression model is presented in Fig. 7. Estimated heritability slightly decreased during the early stage of test at approximately 180 days then it continuously increased up to about 460

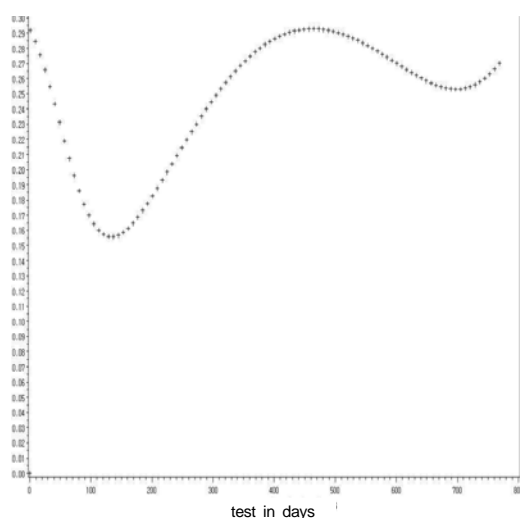


Fig. 7. Estimates of heritability of weights in Hanwoo steers using RRM.

days and slightly decreased and tapered off. Results from using single trait animal model showed estimated heritability at 6, 12, 18 and 22 months were 0.36, 0.24, 0.27 and 0.35, respectively (Table 1). Comparing the results between random regression model and the animal model showed not much differences and both followed similar pattern. The pattern is characteristic of heritability estimates in various literatures however there were some peculiarities related to the management practice in the conduct of progeny testing. At about 180 days the animals were castrated therefore it slowed down the growth accompanied by high fat deposition. In a review of univariate estimates of heritability coefficients, Koots et al. (1994) computed average values of 0.35, 0.27, 0.35 and 0.50 for birth weight, weaning weight, yearling weight and adult cow weight, respectively.

A similar pattern was obtained by Bullock et

al. (1993) with field data records of Polled Hereford cows: 0.49, 0.24, 0.30 and 0.52, respectively. In two studies of growth curves up to 2 years of age, Meyer (2000, 2001) also obtained a similar pattern for heritability coefficient estimates with random regression models. In the present study, the heritability of birth weight is 0.29 then at about 180 days decrease to 0.17 then at yearling stage increase to 0.27 then slowly tapers off to 0.26 at about 1.9 years old. However, Han (2002) using mixed model least squares and maximum likelihood reported different trends in heritability estimates of body weight in Hanwoo at birth, weaning, 12 months and 27 months were 0.21, 0.46, 0.48 and 0.22.

Studies conducted by Choi et al. (2000) estimated the genetic parameters for Hanwoo by using multi-trait animal model showed a direct heritability for birth weight, weaning weight and 6 month weight as 0.09, 0.03 and 0.02. A study conducted by Han (2002) for Hanwoo estimated genetic parameters for body weights at birth, weaning, 12 and 27 months using mixed model least squares maximum likelihood as 0.208, 0.457, 0.476 and 0.227, respectively. Almost similar results were reported by Choi et al., 1996 in their estimation of heritability at birth weight also at 4 months old the heritability value of 0.487 was revealed when they used Becker's method (1985) utilizing variance components of sire.

Use of random regression models over univariate model for genetic parameter estimation has many advantages in that it captures the

Table 1. Variance component by single trait animal model

Parameters	Body weight, months			
	6	12	18	22
Additive genetic variance	185.0	415.8	676.6	1108.4
Error variance	316.7	1334.1	1835.8	2048.5
Heritability	0.36	0.24	0.27	0.35

continuous nature of the process therefore allows prediction of the genetic values at any time even in the absence of actual measurements and its use for the national genetic evaluation of Hanwoo would offer more advantages. Furthermore weight measurements taken at early stages can be used in selection of mature weight and could therefore reduce generation interval in selection programs.

#### IV. ACKNOWLEDGEMENT

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#### V. ABSTRACT

The study aimed to estimate genetic parameters of body weights in Hanwoo steers using random regression model and compare it with single trait animal model. A total of 1,372 Hanwoo steers that belonged to progeny testing program of the Hanwoo Genetic Improvement conducted at the Livestock Improvement Main Center of the National Agricultural Cooperative Federation (LIMC-NACF) in Rep. of Korea were used. Results of the random regression model fitting quadratic function revealed heritability values from 0.17 to 0.30 for the whole testing days up to 800 days. The results of the animal model showed estimated heritability values ranged from 0.24 to 0.36. Estimates of permanent environmental correlations tended to increase with increasing test in days. Unlike in the direct genetic correlation that at early stage the estimate was slightly negative it was 0.30 then increased to approach unity at later stage of test. Comparing the results between random regression model and the animal model showed not much differences and both followed similar pattern and therefore the use of random regression model for the national genetic evaluation of Hanwoo could be implemented.

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