

## Estimation of Genetic Parameters for Body Weight in Chinese Simmental Cattle Using Random Regression Model\*

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**ABSTRACT :** The random regression model methodology was applied into the estimation of genetic parameters for body weights in Chinese Simmental cattle to replace the traditional multiple trait models. The variance components were estimated using Gibbs sampling procedure on Bayesian theory. The data were extracted for Chinese Simmental cattle born during 1980 to 2000 from 6 national breeding farms, where records from 3 months to 36 months were only used in this study. A 3 orders Legendre polynomial was defined as the submodel to describe the general law of that body weight changing with months of age in population. The heritabilities of body weights from 3 months to 36 months varied between 0.31 and 0.48, where the heritabilities from 3 months to 12 months slightly decreased with months of age but ones from 13 months to 36 months increased with months of age. Specially, the heritabilities at eighteenth and twenty-fourth month of age were 0.33 and 0.36, respectively, which were slightly greater than 0.30 and 0.31 from multiple trait models. In addition, the genetic and phenotypic correlations between body weights at different month ages were also obtained using regression model. (*Asian-Aust. J. Anim. Sci. 2004. Vol 17, No. 7 : 914-918*)

**Key Words :** Body Weight, Random Regression Model, Genetic Parameter, Chinese Simmental

### INTRODUCTION

Simmental cattle were introduced into China at the beginning of last century for improving the Chinese local yellow cattle, which have become the so called Chinese Simmental. In the past two decades, the open nucleus breeding system was established to develop the dairy-beef type Simmental breed so that the body weights became as important as the milk production in the breeding project. However, in practice, only the body weights at eighteenth and twenty-fourth month of age were genetically evaluated using multiple traits model. The records for genetic evaluation included the real body weights at eighteenth and twenty-fourth month of age and the estimated body weights adjusted to eighteen and twenty-four months of age. Such genetic evaluation did not take those body weights into account except eighteenth and twenty-fourth month of age, and more estimation error arose from the adjustment of body weights.

The random regression methodology (Henderson 1982; Schaeffer et al., 1994) has been proposed for modeling traits that are measured over time, such as milk production, growth traits, survival data, fertility and genotype by environment interaction (Schaeffer 2002). Covariance functions (Kirpatrick et al., 1990) model the phenotypic,

genetic and residual variances and covariances between measurements on a trait taken over time. Meyer and Hill (1997) have shown the equivalence between random regression models and covariance functions. The theoretical aspects of random regression models (RRM) have been discussed by Crowder and Hand (1991). A key element in a RRM is the function submodel for the random regressions, which can result in quite different estimates of genetic parameters (Misztal et al., 2000; Guo, 2002). The orthogonal polynomials were used often, because the correlations between parameters are lower than with other functions. One choice is the normalized Legendre polynomial (Kirpatrick et al., 1990).

The objective of this study was to apply the random regression methodology to estimate the genetic parameters for body weights of Chinese Simmental and to compare the estimates from such model with the traditional approach.

### MATERIALS AND METHODS

#### Data

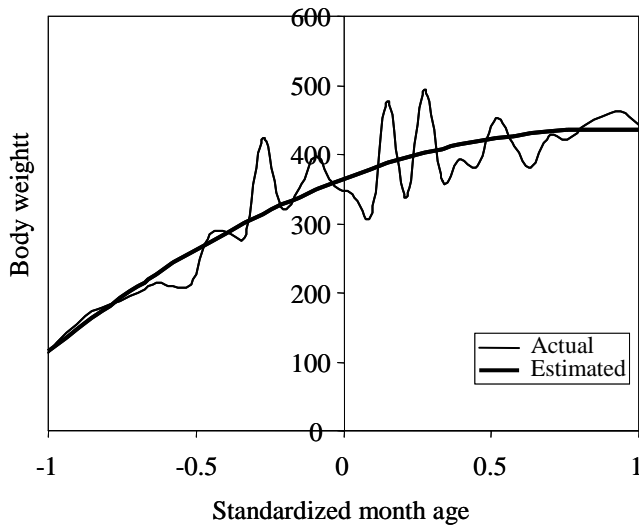
Records for body weight, calving data and pedigree information were extracted for the Chinese Simmental cattle born during 1980 to 2000 from 6 national breeding farms. The raw data had about 10,000 records for body weight. In the editing process, the records at less than 3 months of age were deleted from the raw data set to avoid effect of common environment from dam on birth and weaning weights (Meyer, 2000; Albuquerque et al., 2001). Body weight records at greater than 36 months of age were also deleted because they were not the traits of interest and there were few records at those months of age. In order to decrease disequilibrium of data as more as possible, the

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**Figure 1.** Estimated and actual values of phenotypic means (kg) across months of age on 2 orders Legendre polynomial.

calving time period was divided into 2 levels (1980 to 1990 and 1991 to 2000), the season of calving was divided into 3 levels (Nov., Dec. Jan. and Feb. as level one; Mar., Apr., May and Oct. as level two and the others as level three), and 23 classes of THSS were defined after the THSSs less than 50 records were deleted from the combinations (THSSs) of time period (T), herd (H), season of calving (S) and sex of calf (S). Then a total of 6,379 records on 2,208 Chinese Simmental cattle and 10,568 animals in pedigree were used to estimate the genetic parameters for body weight.

### Submodel

The Legendre polynomial was chosen to describe the growth curves of Chinese Simmental. The function is

$$P(t) = \sum_{m=0}^{q-1} b_m P_m(t)$$

In general, for  $m$  integral

$$P_m(t) = \frac{1}{2^m} \sum_{r=0}^{m/2} \frac{(-1)^r (2m-2r)!}{r!(m-r)!(m-2r)!} t^{m-2r}$$

Where  $m/2=m/2$  if  $m$  is even, and  $m/2=(m-1)/2$  if  $m$  is odd.

The first five Legendre polynomials are therefore:

$$P_0(t) = 1, P_1(t) = t, P_2(t) = \frac{1}{2}(3t^2 - 1), P_3(t) = \frac{1}{2}(5t^3 - 3t), P_4(t) = \frac{1}{8}(35t^4 - 30t^2 + 3)$$

### Random regression model

The single-trait RRM for body weights was

$$y_{ijt} = \sum_{m=0}^{q-1} \beta_{im} P_m(t) + \sum_{m=0}^{q-1} a_{jm} P_m(t) + \sum_{m=0}^{q-1} p_{jm} P_m(t) + e_{ijt}$$

Where  $y_{ijt}$  is the body weight at  $t$  months of age on  $j$  individual belonging to subclass  $i$  of (THSS);  $\beta_{km}$  are fixed regression coefficients;  $a_{jm}$  are the additive genetic random regression coefficients which are specific to each individual in the pedigree;  $p_{jm}$  is the permanent environmental random regression coefficients which are specific to each individual with record;  $e_{ijt}$  are the residual effects for each observation.

In matrix notation the model can be written as

$$y = Xb + Za + Qp + e$$

Where  $b$  denotes the vector of  $\beta_{im}$ ,  $a$  is the  $q$  by 1 vector of random regression coefficients for each individual in the pedigree,  $p$  is the  $q$  by 1 vector of permanent environment effects for individuals with records.  $e$  is the vector of residual effects and  $X$ ,  $Z$  are  $Q$  the incidence and covariables matrices. Assume that

$$y | b, a, p, R \sim N(Xb + Za + Qp, R)$$

and

$$(a \ p \ e)^T \sim N(0, V)$$

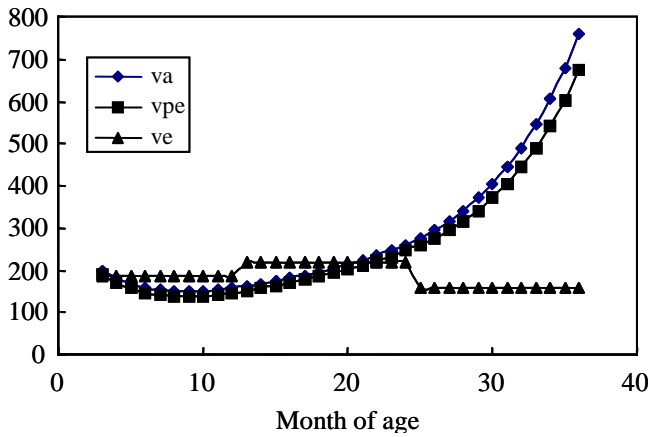
with

$$V = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & R \end{bmatrix}$$

where  $G$  is the  $q$  orders covariance matrix of random genetic regression coefficients, assumed to be same for all individuals;  $A$  is the additive genetic relationship matrix among the individuals in the pedigree;  $I$  is a identity matrix;  $P$  is the  $q$  orders covariance matrix of the random permanent environment coefficients; and  $R$  is the diagonal matrix with different residual variances were allowed for different time intervals within measuring period, defined as 3 to 12 months of age, 13 to 24 months of age, 25 to 36 months of age, and  $R = \text{diag}(\sigma_{e3-12}^2, \sigma_{e13-24}^2, \sigma_{e25-36}^2)$ . Residual effects on different months of age were uncorrelated both within and between individuals.

### Estimation of parameters

The Gibbs sampling algorithm described by Jomrozik and Schaeffer (1997) for a single trait RRM was implemented for this study. Covariance matrixes of additive genetic, permanent environment random regression coefficients and residual variances of RRM for body weight were estimated using GIBBS via DMU package (Madsen



**Figure 2.** Estimates of genetic, permanent environment, residual variances for body weights over months of age.

and Jensen, 2000). 50,000 and 30,000 rounds, respectively, for total iteration and burn-in period were given in editing DRIVE FILE of DMU, i.e., a single chain length 50,000 was generated where the first 30,000 iterates of the chain were discarded as the burn-in period and remaining 20,000 iterates were used for the estimation of means of the marginal distribution of the variances and covariances components as described by Sorenson et al. (1995).

Covariance functions for genetic and permanent environment effects can be established, respectively, as

$$g(t_i, t_j) = T_i' \hat{G} T_j \quad pe(t_i, t_j) = T_i' \hat{P} T_j$$

Where  $T_i = [1 \quad P_1(i) \quad \Lambda \quad P_{q-1}(i)]$

Then, let  $i=j$ , the estimates of genetic and permanent environment variances for body weight at the given month age  $i$  were obtained, respectively, and likewise, if  $i \neq j$ , the estimates of genetic and permanent environment variances for body weight between the given month age  $i$  and  $j$  were also obtained then.

Heritability at the given month age  $i$  was calculated as

**Table 1.** Estimates of means and standard deviations of posterior distributions of variances and covariances for random regression coefficients

Parameters	Genetic		Permanent environment		Residual	
	Means	SD	Means	SD	Means	SD
$\sigma_{00}$	211.4	57.42	193.6	37.02		
$\sigma_{01}$	95.4	24.46	88.0	25.45		
$\sigma_{02}$	22.68	12.11	14.2	11.02		
$\sigma_{03}$	37.6	32.57	39.8	11.47		
$\sigma_{11}$	147.1	45.48	138.5	37.90		
$\sigma_{12}$	44.4	32.27	33.1	13.27		
$\sigma_{13}$	18.8	11.48	21.8	7.03		
$\sigma_{22}$	75.7	13.89	70.5	8.85		
$\sigma_{23}$	22.5	32.11	12.3	12.02		
$\sigma_{33}$	53.9	60.69	57.9	12.67		
$\sigma_{e3-12}$					184.8	37.43
$\sigma_{e13-24}$					219.5	39.10
$\sigma_{e25-36}$					159.3	26.48

$$h_i^2 = \frac{g(t_i, t_i)}{g(t_i, t_i) + pe(t_i, t_i) + \sigma_i^2}$$

The phenotypic covariance functions is

$$P(t_i, t_j) = g(t_i, t_j) + pe(t_i, t_j) = T_i' \hat{G} T_j + T_i' \hat{P} T_j$$

## RESULTS AND DISCUSSION

### Choosing a submodel

In order to choose a submodel, three steps were adopted: firstly, a visual inspection of the phenotypic means of body weights plotted against months of age was used to determine the possible order of Legendre polynomial that fit this plot; secondly, the selected possible orders of Legendre polynomials were fitted to the means and statistical selection criteria were obtained; and finally, comparing statistical selection criteria, an appropriate order of Legendre polynomial was defined as the submodel in the random regression model. In this study, the 2, 3, 4 orders

**Table 2.** Estimates of genetic ( $g$ ), permanent environment ( $pe$ ), residual ( $\sigma_e^2$ ), phenotypic ( $P$ ) variances, heritabilities ( $h^2$ ) and ratio of permanent environment (PE) for body weights at selected months of age

Age	$g$	$pe$	$\sigma_e^2$	$P$	$h^2$	PE
3	199.7	188.9	184.8	573.4	0.35	0.48
6	159.1	147.3	184.8	491.2	0.32	0.48
9	149.1	137.1	184.8	471.0	0.32	0.48
12	156.8	145.1	184.8	486.7	0.32	0.48
15	173.5	162.6	219.5	555.5	0.31	0.43
18	195.1	184.6	219.5	599.1	0.33	0.44
21	221.9	210.8	219.5	652.1	0.34	0.44
24	258.8	244.5	219.5	722.7	0.36	0.45
27	314.9	293.6	159.3	767.9	0.41	0.29
30	404.2	370.0	159.3	933.6	0.43	0.31
33	544.8	489.8	159.3	1,193.9	0.46	0.34
36	759.3	673.0	159.3	1,591.6	0.48	0.36

**Table 3.** Estimates of genetic (upper triangle) and phenotypic (lower triangle) correlations between body weights at selected months of age with covariance functions

Age	3	6	9	12	15	18	21	24	27	30	33	36
3	1	0.963	0.863	0.744	0.643	0.572	0.530	0.509	0.499	0.492	0.485	0.476
6	0.959	1	0.967	0.894	0.818	0.755	0.706	0.663	0.621	0.575	0.527	0.480
9	0.853	0.961	1	0.978	0.934	0.887	0.838	0.783	0.718	0.642	0.561	0.482
12	0.726	0.883	0.973	1	0.987	0.959	0.919	0.863	0.788	0.696	0.596	0.498
15	0.584	0.757	0.874	0.928	1	0.991	0.964	0.917	0.845	0.751	0.645	0.539
18	0.516	0.698	0.832	0.906	0.886	1	0.990	0.958	0.898	0.812	0.711	0.607
21	0.476	0.653	0.789	0.872	0.867	0.897	1	0.988	0.948	0.879	0.791	0.697
24	0.457	0.616	0.742	0.825	0.830	0.874	0.906	1	0.986	0.941	0.874	0.795
27	0.360	0.463	0.547	0.606	0.616	0.659	0.699	0.731	1	0.985	0.943	0.885
30	0.374	0.4450	0.512	0.561	0.574	0.625	0.679	0.731	0.614	1	0.986	0.952
33	0.388	0.432	0.469	0.503	0.516	0.573	0.640	0.710	0.615	0.674	1	0.989
36	0.400	0.411	0.420	0.438	0.449	0.508	0.585	0.671	0.601	0.677	0.737	1

Legendre polynomial, respectively, were fitted to the body weight means. Their function and multiple correlation coefficients were obtained as follows:

$$\hat{y} = 335.0 + 160.1P_1(t) - 59.0P_2(t) \quad R^2 = 0.854$$

(12.50)      (15.42)

$$\hat{y} = 335.1 + 159.1P_1(t) - 59.0P_2(t) + 10.5P_3(t) \quad R^2 = 0.856$$

(12.76)      (15.59)      (2.86)

$$\hat{y} = 334.1 + 159.8P_1(t) - 63.0P_2(t) + 10.5P_3(t) + 24.8P_4(t) \quad R^2 = 0.864$$

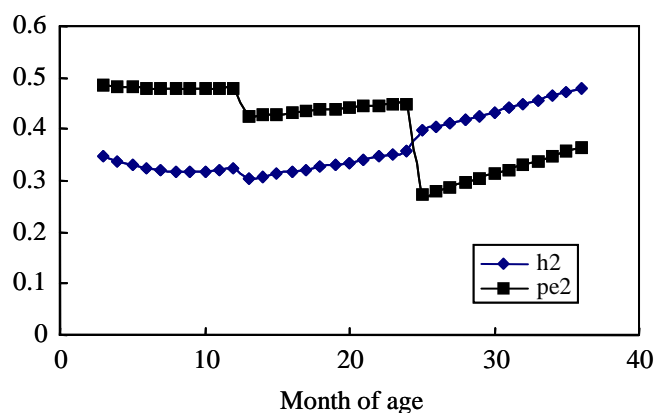
(12.66)      (15.79)      (2.69)      (20.00)

Note that below each regression coefficient is its standard error.

This shows that all of the three Legendre polynomials gives a high R (greater than 85%) and the R slightly increased as the order increased. However, because the 4 order regression coefficient was not significantly different from zero ( $p > 0.20$ ), the 3 order Legendre polynomial was determined thus as the submodel in the random regression model for body weights of Chinese Simmental, which fitting result was shown in Figure 1.

### Estimating parameters

The estimates of the means and the standard deviations of the posterior distributions of variances and correlations for the random regression coefficients were given in Table 1. The variances of random regression coefficients of the genetic and permanent environment effects on the first and second order Legendre polynomial were high significantly different from zero, as well as the third order Legendre polynomial of the permanent environment effect. But the third order Legendre polynomial of genetic effect was not significant. The estimates of genetic, permanent environment, residual variances for body weights over months of age were shown in Figure 2. The plot of genetic variances against months of age was similar to of the

**Figure 3.** Estimates of heritabilities and ratio of permanent environment for body weights over months of age.

permanent environment but their magnitudes are different, as the results in studies on Nelore cattle (Albuquerque et al., 2001). The residual variance was greater at middle months of age. More time intervals within measuring period could be defined to accurately estimate residual variance under the condition of large sample in future study.

The heritabilities of the body weights from 3 to 36 months of age varied between 0.31 and 0.48, where the heritabilities from 3 to 12 months of age slightly decreased with months of age but ones from 13 to 36 months of age increased with months of age; the ratios of the permanent environment before 24 months of age were greater than corresponding heritabilities (see Table 2 and Figure 3).

The estimates of and the phenotypic correlations between particular months of age for body weights were given in Table 3. The correlations between body weights at months of age that were close together were higher than those that were farther apart. All phenotypic correlations were greater than corresponding genetic correlations, and both phenotypic and genetic correlations were positive, as has been reported in other studies on cattle and pig (Meyer, 2000; Albuquerque et al., 2001; W. Z. Liu et al., 2002).

### Comparing with traditional method

Traditionally, the genetic parameters of body weights at eighteenth and twenty-fourth month of age were only estimated using multiple traits model for genetic evaluation. Two estimates of the heritabilities of body weights at eighteenth and twenty fourth month of age were calculated by utilizing the records between twelve and twenty-four months of age (Ren, 2001), which were 0.32 and 0.36, respectively, which were a little difference with 0.31 and 0.48 from random regression model.

### CONCLUSIONS

A preliminary application of random regression model to estimate the genetic parameters of body weights in Chinese Simmental cattle were carried out for replacing the traditional multiple trait models. A 3 orders Legendre polynomial was defined as the submodel. Theoretically, the random regression model was performed to be better than the multiple trait models. However, large records should be required to obtain stable estimates.

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